

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 19:17:03 ; Search time 1681.18 Seconds
(without alignments)
15701.003 Million cell updates/sec

Title: US-09-591-500-4

Perfect score: 907

Sequence: 1 gggttcgggtttattgatt.....ctctaatactgccccctgaa 907

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.man.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
c 1	836.2	92.2	164945	9	AC089987	AC089987 Homo sapi
2	825.4	91.0	1052	6	AR009985	AR009985 Sequence
3	825.4	91.0	1052	6	I91514	I91514 Sequence 1
4	825.4	91.0	1052	6	I96074	I96074 Sequence 1
5	825.4	91.0	1052	9	HSU73477	U73477 Human acid1
6	822.2	90.7	1136	9	BC007200	BC007200 Homo sapi
7	811.6	89.5	904	9	HSU71084	U71084 Homo sapien
8	796.4	87.8	916	9	HSPHAPI	X75090 H.sapiens m
9	767.4	84.6	925	9	AF025684	AF025684 Homo sapi
10	716	78.9	5785	9	AF008216	AF008216 Homo sapi
11	716	78.9	70449	9	AC105250	AC105250 Homo sapi
12	702.4	77.4	162482	9	AC022740	AC022740 Homo sapi
13	700.8	77.3	149015	9	AC107992	AC107992 Homo sapi
14	700.8	77.3	186886	2	AC016297	AC016297 Homo sapi
c 15	681.2	75.1	750	9	HSU60823	U60823 Human poten
16	623	68.7	1017	10	RATLANP	D32209 Rat mRNA fo
17	607.8	67.0	863	10	AF022957	AF022957 Mus muscu
18	585	64.5	980	6	AR009986	AR009986 Sequence
19	585	64.5	980	6	AX305936	AX305936 Sequence
20	585	64.5	980	6	I91515	I91515 Sequence 3
21	585	64.5	980	6	I96075	I96075 Sequence 3
22	585	64.5	980	10	MMU73478	U73478 Mus musculu
23	571.2	63.0	771	9	BC000608	BC000608 Homo sapi
24	481.8	53.1	1656	9	AY007110	AY007110 Homo sapi
25	484.8	51.2	101819	2	AC129809	AC129809 Rattus no
26	464.8	51.2	170170	2	AC106610	AC106610 Rattus no
27	405	44.7	759	6	AR009987	AR009987 Sequence
28	405	44.7	759	6	I91516	I91516 Sequence 4
29	405	44.7	759	6	I96076	I96076 Sequence 4
30	395.8	43.6	79457	2	AC098396	AC098396 Rattus no
31	330.2	36.4	1011	9	HSPHAPI2A	Y07569 H.sapiens m
32	330.2	36.4	1035	9	BC013003	BC013003 Homo sapi
33	330.2	36.4	1371	9	BC019658	BC019658 Homo sapi
34	330.2	36.4	1371	9	HSAPRIL	Y07969 H.sapiens m
35	330.2	36.4	1475	9	HSU70439	U70439 Human silve
36	330.2	36.4	3980	9	BC000476	BC000476 Homo sapi
37	313.6	34.6	168182	2	AC068338	AC068338 Homo sapi
c 38	313.6	34.6	200445	2	AC105137	AC105137 Homo sapi
c 39	310	34.2	198926	10	AL683843	AL683843 Mouse DNA
40	291.6	32.1	238142	2	AL611930	AL611930 Mus muscu
41	288	31.8	1225	10	AB025581	AB025581 Rattus no
42	282.4	31.1	1397	10	BC003489	BC003489 Mus muscu
43	282.4	31.1	1408	10	BC005628	BC005628 Mus muscu
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ALIGNMENTS

RESULT 1
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LOCUS AC089987 164945 bp DNA linear PRI 07-MAY-2002
DEFINITION Homo sapiens 12q BAC Rpl1-722Pl1 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
ACCESSION AC089987
VERSION AC089987.26 GI:14277204
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 164945)
AUTHORS Muzny D.M., Adams C., Adio-Oduola B., Ali-Osman F.R., Allen C.,
Alsbrooks S.L., Amaratunge H.C., Are J.R., Banks T., Barbaria J.,

Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flag, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, J., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louised, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marondel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhney, E., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G., Miner, S., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogburn, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Perez, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shm, C., Shoshkari, N., Sisson, I., Sodergren, E., Sonalike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczka, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Kuchelapati, R., Weinstein, G., and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 164945)
Worley, K.C.

Direct Submission
Submitted (07-FEB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 164945)
Worley, K.C.

Direct Submission
Submitted (01-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 164945)
Worley, K.C.

Direct Submission
Submitted (05-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 164945)
Worley, K.C.

Direct Submission
Submitted (29-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 164945)
Worley, K.C.

Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
7 (bases 1 to 164945)
Worley, K.C.

TITLE
JOURNAL

COMMENT

Direct Submission
Submitted (07-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 1, 2001 this sequence version replaced gi:14150337.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

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	/db_xref="taxon:9606"
	/chromosome="12q"
	/clone="RP11-722P11"
repeat_region	1..1733
	/rpt_family="L1P11"
repeat_region	1734..1758
	/rpt_family="(CAA)n"
repeat_region	1759..2636
	/rpt_family="L1P11"
repeat_region	2662..3133
	/rpt_family="L1M4"
repeat_region	3133..3390
	/rpt_family="L1M4"
repeat_region	3391..3687
	/rpt_family="L1P16"
repeat_region	3688..3957
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repeat_region	3958..4351
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	/rpt_family="AluSq/x"
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repeat_region 6913. .7132
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complement(7133. .7601)
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7602. .7798
/rpt_family="L1PA12"
7827. .8021
/rpt_family="L1ME1"
complement(8905. 9362)
/rpt_family="L1R10B"
complement(11383. .14064)
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/rpt_family="L1ME2"
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/rpt_family="L1R45"
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/rpt_family="MER21B"
complement(17882. .18603)
/rpt_family="MER4D"
complement(18602. .18905)
/rpt_family="MER21B"
complement(18968. .19344)
/rpt_family="L1"
complement(19345. .19647)
Query Match 92.2%; Score 836.2; DB 9; Length 164945;
Best Local Similarity 96.7%; Pred. No. 3.8e-164;
Matches 877; Conservative 0; Mismatches 23; Indels 7; Gaps 2;

Qy 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTCGCGCGGGAGCCTCTGCAGAGAGAGAGCGC 60
Db 138983 GGGTTCGGGGTTTATTGATTGAATTCGGCTCGCTCGCTCAGGAGCCTCTGC -AGAGAAAGCGT 138926

Qy 61 GAGAGATGGAGTGGCAGAGCGATTCAATTAGAGCTCGGGAACGGGACGCCCTCTGATG 120
Db 138925 GAGAGATGGAGTGGCAGAGCGAAATGGATTCAATTAGAGCTCGGGAACAGGCGCCCTCCGATG 138866

Qy 121 TGAAGAACTTGTCTGCACACACAGTCGGTCAATGAAGGCAAACTCGAAGSCCTCACAG 180
Db 138865 TGAAGAACTTGTCTGCACACACAGTCAGTCAATGAAGGCAAACTCGAAGSCCTCACAG 138806

Qy 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACAATCAAGCTAGCGCTCACCTCAATTCGCAA 240
Db 138805 ATGAATTTGAAGAACTGGAATTTCTTAAGTACAATCAAGCTAGCGCTCACCTCAATTCGCAA 138746

Qy 241 ACTTACCAAGTTAAACAACTTAAAGAGCTTGAAGCTTAAGCAGTAAACAGAGCCTCAGTGG 300
Db 138745 ACTTGCACAAAGTTAAACAACTTAAAGAGCTTGAAGCTTAAGCAGTAAACAGAGCCTCAGTGG 138686

Qy 301 CCCTAGAGATTATGGCAGAAAGTCTCCAAACCTCATACATCTAAATTTAAGTGCACACA 360
Db 138685 CCCTAGAGATTATGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGCACACA 138626

Qy 361 AAATTAAGAGCTCAGCACAATAGAGCCCTGAAAGAGTTAGAAAACCTCGAGAGCTTAG 420
Db 138625 AAATTAAGAGCTCAGCACAATAGAGCCCTGAAAGAGTTAGAAAACCTCGAGAGCTTAG 138566

Qy 421 ACCTTTTTCACCTTGGAGGTAAACCACTGAACAACCTACTTGAGAGAGAGATGTTCAAGCTCC 480
Db 138565 ACCTTTTTCACCTTGGAGGTAAACCACTGAACAACCTACTTGAGAGAGAGATGTTCAAGCTCC 138506

Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTCAACTCGG 540
Db 138505 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTCAACTCGG 138446

Qy 541 ATGGTGAGGGCTTTGTGGATGCGCTGGATGACAAGAGAGAGGATGAGGATGAGGAGGAGT 600
Db 138445 ATGGTGAGGGCTTTGTGGATGCGCTGGATGACAAGAGAGAGGATGAGGATGAGGAGGAGT 138386

Qy 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGGACGTTG 660
Db 138385 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGGACGTTG 138326

Qy 661 AAGAGGAGGAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 138325 AAGAGGAGGAGTGAAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 138266

Qy 721 TAGATGATGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 138265 TAGATGATGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAGGAGGAGGAGGAGGAGGAGGAG 138206

Qy 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 138205 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 138146

Qy 841 CCTTTTGTGATTTTACTGTTTGTAGCGGTACCCCTCTCCCCCGCCACTCTAATCTCTGCC 900
Db 138145 CCTTTTGTGATTTTACTGTTTGTAGCGGTATCCCTTCTCTCTCTCTCTCTCTCTCTCTCT 138091

Qy 901 CCCTGAA 907
Db 138090 CCCTGAA 138084

RESULT 2
AR009985
LOCUS AR009985 Sequence 1 from patent US 5756676.
DEFINITION AR009985
ACCESSION AR009985
VERSION AR009985.1 GI:3968790
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack,G.R.
TITLE Mammalian protein associated with uncontrolled cell division
JOURNAL Patent: US 5756676-A 1 26-MAY-1998;
FEATURES
Location/Qualifiers
1. 1052
BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN

Query Match 91.0%; Score 825.4; DB 6; Length 1052;
Best Local Similarity 94.4%; Pred. No. 4.2e-162;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 1 GGGTTTCGGGGTTTATTGATTGAATTCGGCTGCGCGGGAGCCTCTGTCAGAGAGAGAGCGC 60
Db 32 GGGTTTCGGGGTTTATTGATTGAATTCGGCGCGCGGGAGCCTCTGTCAGAGAGAGAGCGC 91

Qy 61 GAGAGATGGAGATGGCAGACGCGATTTCATTAGAGCTGCGGAGCGGAGCGCCCTCTGATG 120
Db 92 GAGAGATGGAGATGGCAGACGCGATTTCATTAGAGCTGCGGAGCGGAGCGCCCTCTGATG 151

Qy 121 TGAAGAAGACTTCTCTCGTGAACAACAGTCGGTCAATGAAGGCAAACTCGAAGSCCTCACAG 180
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QY	241	ACTTACCAAGTTAAACAACCTTAAGAAGCTTGAACCTAAGCAGTAAACAGAGCCTCAGTGG	300
Db	272	ACTTACCAAGTTAAACAACCTTAAGAAGCTTGAACCTAAGCAGTAAACAGAGCCTCAGTGG	331
QY	301	GCCTAGAAGTATTGGCAGAAAAGTGTCCAAAACCTCATACATCTAAATTTAAGTGGCAACA	360
Db	332	GCCTAGAAGTATTGGCAGAAAAGTGTCCAAAACCTCATACATCTAAATTTAAGTGGCAACA	391
QY	361	AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG	420
Db	392	AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG	451
QY	421	ACCTTTTACATTGCGAGGTAAACCAACCTGAACAACTACTGAGAGAAGATGTTCAAGCTCC	480
Db	452	ACCTTTTCAATTGCGAGGTAAACCAACCTGAACAACTACTGAGAGAAGATGTTCAAGCTCC	511
QY	481	TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTAACTCGG	540
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QY	601	ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT	660
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Db	932	CCCTGAA 938	
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DEFINITION	Sequence 1 from patent US 5726018.		
ACCESSION	I91514		
VERSION	I91514.1 GI:3935984		
KEYWORDS	unknown.		
SOURCE	unknown.		
ORGANISM	unknown.		
REFERENCE	1 (bases 1 to 1052)		
AUTHORS	Pasternack,G.R.		
TITLE	Nucleic acid based assays to detect a novel mammalian protein		
JOURNAL	associated with uncontrolled cell division		
FEATURES	Patent: US 5726018-A 1 10-MAR-1998;		
source	Location/Qualifiers		
	1..1052		
BASE COUNT	326 a	196 c	316 g 214 t

ORIGIN			
Query Match 91.0%; Score 825.4; DB 6; Length 1052;			
Best Local Similarity 94.4%; Pred. No. 4.2e-162;			
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;			
QY	1	GGGTTCGGGGTTTATTTGATTGAATTCGGCTGGCGGGGAGCCTCTGCGAGAGAGAGCGC	60
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QY	121	TGAAGAACTTGTCTCTGACAAACAGCTCGGTGCAATGAAGGCAAACTCGAAGGCTCACAG	180
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QY	181	ATGAATTTGAAGAACTGGAATTCCTTTAAGTACAATCAACGTAGGCCCTCAGCTCAATCGCAA	240
Db	212	ATGAATTTGAAGAACTGGAATTCCTTTAAGTACAATCAACGTAGGCCCTCAGCTCAATCGCAA	271
QY	241	ACTTACCAGAACTTAAACAACCTTAAAGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA	300
Db	272	ACTTACCAGAACTTAAACAACCTTAAAGAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA	331
QY	301	GCCTAGAAATTTGGCAGAAAAGTGTCCAAAACCTCATACATCTAAATTTAAGTGGCAACA	360
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QY	541	ATGGTGAGGGCTTTGTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT	600
Db	572	ATGCTGAGGGCTACGTGGAGGGCTTGATGTGAGGAGGAGGATGAGGATGAGGAGGAGT	631
QY	601	ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT	660
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QY	661	AAGAGGAGGAGCTGAGTGGAGACGAGGAGGAGGAGGATGAGGATGAGGAGGAGGAGT	720
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QY	721	TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGATGAGGATGAGGAGGAGGAGT	780
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QY	841	CCTTTTGTGATTTACTGTTTTTAGCCGCTACCCCTCTCCCTCCCTCCCTCCCTCCCTCCCT	900
Db	872	CCTATTGTGATTTACTGTTTTTAGCCGCTACCCCTCTCCCTCCCTCCCTCCCTCCCTCCCT	931
QY	901	CCCTGAA 907	
Db	932	CCCTGAA 938	
RESULT 4			
I96074			

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Q	y	781	AAGAAACTGAAGATGAGGGGAGAGACGATCGCTAAGTGGTAATAATCTATTTTGAAAAATT	840	
D	b	812	GAGAACCTGAAGATGAGGGGAGAGATGATGACTAAGTGGTAACCTATTTTGAAAAATT	871	
Q	y	841	CCTTTTCGTATTTTACATGTTTTTTAGCCGTACCCTCTCCCCCCCCTCTAATCCTGCC	900	
D	b	872	CCTATTGTGATTTGACTGTTTTTTACCATATCCCTCTCCCCCCCCTCTAATCCTGCC	931	
Q	y	901	CCCTGAA	907	
D	b	932	CCCTGAA	938	
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H	S	U	HSU73477		PRI 02-JAN-1997
L	O	C	LOCUS	1052 bp	mRNA linear complete cds.
D	E	F	DEFINITION	Human acidic nuclear phosphoprotein pp32	
A	C	C	ACCESSION	U73477	
V	E	R	VERSION	U73477.1	GI:1763272
K	E	Y	KEYWORDS		
S	O	U	SOURCE	Homo sapiens.	
O	R	G	ORGANISM	Homo sapiens	
R	E	F	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
A	U	T	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
T	I	T	TITLE	Chen, T.-H., Brody J.R., Romantsev, F.E., Yu, J.-G., Kayler, A.E., Voneiff, E., Kuhnajda, F.P. and Pasternack, G.R. Structure of pp32, an Acidic Nuclear Protein Which Inhibits Oncogene-Induced Formation of Transformed Foci Mol. Biol. Cell (1996) In press	
J	O	U	JOURNAL	2 (bases 1 to 1052)	
R	E	F	REFERENCE	Chen, T.-H., Brody J.R., Romantsev, F.E., Yu, J.-G., Kayler, A.E., Voneiff, E., Kuhnajda, F.P. and Pasternack, G.R. Direct Submission Submitted (04-OCT-1996) Pathology, The Johns Hopkins University School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA	
T	I	T	TITLE	Location/Qualifiers	
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D	b	32	GGGTTCCGGGGTTTATTGATTCAATTCGCCGGCGGGAGCCTCTGCAGAGAGAGAGCGC	91	
Q	y	61	GAGAGATGGAGATGGGCAGACGGATTCAATTTAGAGCTCGGGAACGGGACGCCCTCTGATG	120	
D	b	92	GAGAGATGGAGATGGGCAGACGGATTCAATTTAGAGCTCGGGAACAGGACGCCCTCTGATG	151	
Q	y	121	TGAAGAACTTGTCTCTGGACAACAGTCGGTTCGAATGAAGCAAACCTCGAAGCCTCACAG	180	
D	b	152	TGAAGAACTTGTCTCTGGACAACAGTCGGTTCGAATGAAGCAAACCTCGAAGCCTCACAG	211	

Qy	361	AAATTAAGAGCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAAACTCGAGAGCTTAG	420
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Qy	481	TCCTGCACTACATATCTCAACGGCTGTGACCCGGATGACNAGGAGGCCCTTAAGCTGG	540
Db	549	TCCCCCAACTCACATATCTGACGGCTATGACCGGGACGACAAGGAGGCCCTGACTCGG	608
Qy	541	ATGGTGAGGGCTTCTGTGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGT	600
Db	609	ATGCTGAGGGCTACGTGAGGGCTGTGGATGATGAGGAGGAGGATGAGGATGAGGAGGT	668
Qy	601	ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGCTG	660
Db	669	ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGTG	728
Qy	661	AAGAGGAGGCTGAGTGGAGGAGGAGGAGGAGGAGGATGAGGTTATACAAATGAGAGG	720
Db	729	AAGAGGAGGCTGAGTGGAGGAGGAGGAGGAGGATGAGGTTATACAAATGAGAGG	788
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Qy	841	CCTTTTGTGATTTACTGTTTTAGCCGTACCCCTCCTCCGCCCTCAATCTAATCCTGCC	900
Db	909	CCTATTGTGATTTACTGTTTTTACCCATATCCCTCTCCTCCGCCCTCAATCCTGCC	968
Qy	901	CCCTGAA	907
Db	969	CCCTGAA	975
RESULT 7			
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LOCUS	HSU71084	904 bp	DNA linear PRI 09-FEB-1999
DEFINITION	Homo sapiens pp32r2 protein (pp32r2) gene, complete cds.		
ACCESSION	U71084		
VERSION	U71084.1	GI:4249365	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Kadkol,S.S., Brody,J.R., Pevsner,J., Bai,J. and Pasternack,G.R.		
JOURNAL	Modulation of oncogenic potential by alternative gene use in human		
REFERENCE	prostate cancer		
AUTHORS	Nat. Med. (1999) In press		
TITLE	Rebel,J.M.J., Kayler,A.E., Kadkol,S.S., Kuhajda,F.P. and		
JOURNAL	Direct Submission		
REFERENCE	Submitted (17-SEP-1996) Pathology, The Johns Hopkins University		
AUTHORS	School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA		
TITLE	Rebel,J.M.J., Kayler,A.E., Kadkol,S.S., Kuhajda,F.P. and		
JOURNAL	Direct Submission		
REFERENCE	Submitted (09-FEB-1999) Pathology, The Johns Hopkins University		
AUTHORS	School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA		
TITLE	Sequence update by submitter		
REMARK	On Feb 9, 1999 this sequence version replaced gi:1916631.		
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Qy	139	ACAACAGTCGGTCGAATGAAGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGG	198
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Qy	199	AATTCCTTAAGTACAATCAACGTAGGCTCACCTCAATTCGCAAACTTACCAAGTTAAACA	258
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Qy	259	AACCTTAAGAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGGCCCTAGAGTATTGCGAG	318
Db	240	AACCTTAAGAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGGCCCTAGAGTATTGCGAG	299
Qy	319	AAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAATTAAGAGCTCAGCA	378
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Qy	379	CAATAGAGCCCTGAAAAAGTTAGAAAACTCGAGAGCTTAGACCTTTTCACTTGGCAGG	438
Db	360	CAATAGAGCCCTGAAAAAGTTAGAAAACTCGAGAGCTTAGACCTTTTCACTTGGCAGG	419
Qy	439	TAACCAACCTGACAACTACTGAGAGAGATGTTCAAGCTCCTCCTCGCAACTCACATATC	498
Db	420	TAACCAACCTGACAACTACTGAGAGAGATGTTCAAGCTCCTCCTCGCAACTCACATATC	479
Qy	499	TCAAGGGCTGTGACCCGGATGACAAGGAGGCCCTCAACTCGGATGCTGAGGGCTTTGTGG	558
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Qy	559	AGTGCTGTGATGACAAAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGG	618
Db	540	AGTGCTGTGATGACAAAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGATCAGG	599
Qy	619	TAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT	678
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Qy	679	GAGAGGAGGAGGAGGAGGATGAGGTTATAACCAATGAGAGGAGTATGATGAGGAGGAGT	738
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RESULT 8
LOCUS HSPHAPI 916 bp mRNA linear PRI 19-JUL-1994
DEFINITION H.sapiens mRNA for HLA-DR associated protein I (PHAPI).
ACCESSION X75090.1 GI:403006
VERSION HLA-DR associated protein I; PHAPI.
KEYWORDS Homo sapiens.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS Kratzin,H.D.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-1993) H.D. Kratzin, Max Planck Inst. for
Experimental Med., Dept. for Immunochimistry, Hermann-Rein-str. 3,
37075 Goettingen, FRG
2 (bases 1 to 916)
Vaesen,M., Barnikol-Watanabe,S., Gotz,H., Awini,L.A., Cole,T.,
Zimmermann,B., Kratzin,H.D. and Hilschmann,N.
Purification and characterization of two putative HLA class II
associated proteins: PHAPI and PHAPII
Biochem. Hoppe-Seyler 375 (2), 113-126 (1994)
94250340
PUBMED 8192856
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Matches 827; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

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QY 61 GAGAGATGGAGATGGGAGAGGATTCATTATAGCTGCGGAACGGAGCGCCCTCTGATG 120
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RESULT 9
LOCUS AF025684
DEFINITION Homo sapiens cerebellar leucine rich acidic nuclear protein (LANP)
ACCESSION AF025684
VERSION AF025684.1 GI:2589220
KEYWORDS mRNA, complete cds.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS Matilla,A., Koshy,B.T., Cummings,C.J., Isobe,T., Orr,H.T. and
Zoghbi,H.Y.
TITLE The cerebellar leucine-rich acidic nuclear protein interacts with
ataxin-1
JOURNAL Nature 389 (6654), 974-978 (1997)
MEDLINE 98013170
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DEFINITION	Homo sapiens candidate tumor suppressor pp32r1 (PP32R1) gene, complete cds.		
ACCESSION	AF008216		
VERSION	AF008216.1 GI:2738512		
KEYWORDS	Homo sapiens.		
SOURCE	Homo sapiens		
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REFERENCE	1 (bases 1 to 5785)		
AUTHORS	Kadkol,S., Brody,J.R., Pevsner,J., Bai,J. and Pasternack,G.R.		
TITLE	Modulation of oncogenic potential by alternative gene use in human prostate cancer		
JOURNAL	Nature Medicine (1999) In press		
REFERENCE	2 (bases 1 to 5785)		
AUTHORS	Kochevar,G.J., Brody,J.R. and Pasternack,G.R.		
TITLE	The Structure of a Gene Encoding pp32r1, a New Member of the pp32 Family		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 5785)		
AUTHORS	Kochevar,G.J., Brody,J.R. and Pasternack,G.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-JUN-1997) Pathology, Johns Hopkins University School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA		
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QY 301 GCCTAGAAGTATTGGCAGAAAAGTGCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
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QY 361 AAATTTAAGACCTCAGACACANTAGACCCCTGAAAAGTTAGAAAAACCTCGAGAGCCTTAG 420
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QY 421 ACCTTTTCACTTCGAGAGTAAACCAACTGAACAACTACTGAGAGAGAGATGTTCAAGCTCC 480
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QY 481 TCCTGCAACTCACATATCTCAAGCGGTGTGACCCGGATGACAGAGAGGCGCCCTAACTCGG 540
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Db 4916 ATATTGAGGACCACTGGAGGGCGCTGGATGACAGAGGAGGAGGCTGASCATGAGGAGGAGT 4975
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QY 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGGAGACGNG 660
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QY 661 AAGAGGAGACGTGAGTGAGAGCGAGGAGGAGAGGATGAAGGTTATAACAATGGAGAGG 720
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RESULT 11
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LOCUS Homo sapiens BAC clone RP11-39C10 from 4, complete sequence.
DEFINITION AC105250 AC011026
ACCESSION AC105250.3 GI:19310326
VERSION
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 70449)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 70449)
AUTHORS Desai,A., Creason,K. and Kozlowicz,A.
TITLE The sequence of Homo sapiens BAC clone RP11-39C10
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 70449)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (26-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 70449)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 9, 2002 this sequence version replaced gi:18376931.
COMMENT -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
-----
Center project name: H_NH0039C10
Drafting Center: WIBR
-----
NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
MAPPING INFORMATION:
Source: The RP11-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.chori.org
```

VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

NEIGHBORING SEQUENCE INFORMATION. The clone sequenced to the left is RP11-360H22, 2000 bp overlap; the clone sequenced to the right is RP11-808H17, 2000 bp overlap. Actual start of this clone is at base position 97207 of RP11-360H22; actual end is at base position 22714 of RP11-808H17.

The sequence of AC011026 has been incorporated into AC105250.

FEATURES

Location/Qualifiers

source

source	1, 70449 /organism="Homo sapiens" /db_xref="taxon:9606" /map="A" /clone="RP11-39C10" 617, 834 /rpt_family="L1" 1499, 1638 /rpt_family="MIR" 3032, 3085 /rpt_family="CT-rich" 3232, 3677 /rpt_family="L1" 3678, 3708 /rpt_family="(TATG)n" 3709, 3963 /rpt_family="L1" 6214, 6589 /rpt_family="MaLR" 6661, 6768 /rpt_family="MER1_type" 7008, 7616 /rpt_family="L1" 10369, 10416 /rpt_family="GA-rich" 11049, 11115 /rpt_family="ERV1" 11135, 11619 /rpt_family="ERV1" 11620, 11661 /rpt_family="(CATA)n" 11725, 11860 /rpt_family="MER1_type" 19019, 19050 /rpt_family="(CA)n" 19500, 19534 /rpt_family="AT-rich" 19785, 20181 /rpt_family="MaLR" 21643, 22100 /rpt_family="MaLR" 22602, 22633 /rpt_family="AT-rich" 22866, 23018 /rpt_family="L2" 23227, 23997 /rpt_family="ERV1" 24379, 24408 /rpt_family="AT-rich" 24622, 24659 /rpt_family="AT-rich" 25165, 25296 /rpt_family="MIR" 25373, 26162 /rpt_family="ERV1" 26458, 26682 /rpt_family="L1" 26934, 27094 /rpt_family="MER1_type" 27297, 27601 /rpt_family="Alu"
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Db 68532 TGAAGAACTTGCCTGGGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 68473
QY 181 ATGAATTTGAAGAACTGGAAATCTTAAAGTACATCAACGTAGAGCCCTCACCTCAATCGCAA 240
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QY 241 ACTTACCAAGTTAAACAACAACTTAAGAAGCTTGAACTAAGCAGTAACAGAGCCCTCAGTCG 300
Db 68412 ACTTACCAAGTTA---AAGTTGAGAAGCTTGAACTA-----AGAGTCTCAGGGG 68365
QY 301 GCTAGAACTANTGCGAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
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QY 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 420
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QY 481 TCCTGCAACTCACATATCTCAACGCTGTGACCCGAGTACAGAGAGCCCTTAACCTCG 540
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QY 721 TAGATGATGAGGAGATGAAGAAGCTTGTGTAAGAGAAAGGGGTGAGAAGCGAAAT 780
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QY 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGATGCTAAGTGAATATCTATTTTGAAGATTT 840
Db 67884 GAGAACTGAAGATGAGGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGAT 67825
QY 841 CCTTTGTGATTTTACTGTTTTAGCCGTACCCCTCTCCCTCCCTCCCTCCCTCCCTCCCT 896
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RESULT 12
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LOCUS AC022740 162482 bp DNA linear PRI 25-APR-2001
DEFINITION Homo sapiens chromosome 15, clone RP11-617D22, complete sequence.
ACCESSION AC022740
VERSION AC022740.4 GI:13786480
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162482)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-617D22
Unpublished
2 (bases 1 to 162482)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
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Perreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivari,T.M., Peterson,K.,
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Testfaye,S., Theodore,J.,
Tirrell,A., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J.,
Zimmer,A. and Zody,M.
Direct Submission
Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 162482)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A.,
Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K.,
Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
Iliev,I., Johnson,R., Jones,C., Karatas,A., Lander,E., Lander,W.,
Lamarez,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Sougniez,C., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Testfaye,S.,
Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zeloun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (25-APR-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 25, 2001 this sequence version replaced gi:13184169.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L5619
Center clone name: 617_D_22
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RESULT 13
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ACCESSION AC107992
VERSION AC107992.3 GI:19683511
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 149015)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Ferreira,P., FitzHugh,W., Gage,D., Diaz,J.S., Dodge,S., Faro,S.,
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Kamat,A., Karatas,A., Kells,C., Lakocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
Macdonald,P., McEwan,P., McKernan,K., Melidrim,J., Meneus,L.,
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Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
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Viel,R., Vo,A., Willson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
(27-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 22, 2002 this sequence version replaced gi:18677521.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-----Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-----Project Information
Center project name: L24554
Center clone name: 150_L8
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RESULT 14
AC016297/c
LOCUS AC016297.4 GI:15022083
DEFINITION Homo sapiens clone RP11-82L14, WORKING DRAFT SEQUENCE, 15 unordered
pieces.
ACCESSION AC016297
VERSION AC016297.4
KEYWORDS HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186886)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavskiy,L., Boukhalter,B.,
Brown,A., Castle,A., Collangelo,M., Collins,S., Collymore,A.,
Cooper,P., DeArelano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 26, 2001 this sequence version replaced gi:7139678.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4280
Center clone name: 82.L-14
----- Summary Statistics
Sequencing vector: M13; M7815; 96% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 179979 bases at least Q40
Consensus quality: 183319 bases at least Q30
Consensus quality: 184541 bases at least Q20
Insert size: 185000; agarose-fp
Quality coverage: 185486; sum-of-contigs
Quality coverage: 5.3 in Q20 bases; agarose-fp
Quality coverage: 5.3 in Q20 bas.
NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 28840: contig of 28840 bp in length
* 28841 28940: gap of 100 bp
* 28941 30179: contig of 1239 bp in length

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* 30180 30279: gap of 100 bp
* 30280 33993: contig of 3714 bp in length
* 33994 34093: gap of 100 bp
* 34094 37562: contig of 3469 bp in length
* 37563 37662: gap of 100 bp
* 37663 41176: contig of 3514 bp in length
* 41177 41276: gap of 100 bp
* 41277 76172: contig of 34896 bp in length
* 76173 76272: gap of 100 bp
* 76273 83570: contig of 7298 bp in length
* 83571 83670: gap of 100 bp
* 83671 92374: contig of 8704 bp in length
* 92375 92474: gap of 100 bp
* 92475 100960: contig of 8486 bp in length
* 100961 101060: gap of 100 bp
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* 124450 124549: gap of 100 bp
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* 142963 143062: gap of 100 bp
* 143063 164019: contig of 20957 bp in length
* 164020 164119: gap of 100 bp
* 164120 182765: contig of 18646 bp in length
* 182766 182865: gap of 100 bp
* 182866 186886: contig of 4021 bp in length.
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Best Local Similarity 89.1%; Pred. No. 7e-136;
Matches 798; Conservative 0; Mismatches 77; Indels 21; Gaps 3;

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REFERENCE	1 (bases 1 to 750)
AUTHORS	Li,M., Makkinje,A. and Damuni,Z.
TITLE	Molecular identification of IlpP2A, a novel potent heat-stable inhibitor protein of protein phosphatase 2A
JOURNAL	Biochemistry 35 (22), 6998-7002 (1996)
MEDLINE	96240314
PUBMED	8679524
REFERENCE	2 (bases 1 to 750)
AUTHORS	Li,M., Makkinje,A. and Damuni,Z..
TITLE	Direct Submission
JOURNAL	Submitted (13-JUN-1996) Cellular & Molecular Physiology, Pennsylvania State University College of Medicine, 500 Univeristy Drive, Hershey, PA 17033, USA
FEATURES	Location/Qualifiers
source	1..750 /organism="Homo sapiens" /db_xref="taxon:9606" /tissue_type="kidney"
CDS	1..750 /codon_start=1 /product="potent heat-stable protein phosphatase 2A inhibitor IlpP2A" /protein_id="AAC50570.1" /db_xref="GI:1408224"
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Matches 707; Conservative	0; Mismatches 43; Indels 0; Gaps 0;
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QY	366 AAAGACCTCAGCAATAGAGCCCTGNAARAAGTTAGAAAACCTCGAGAGCTTAGACCTT 425
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QY	486 CAAC TCACATATCTCAACGGGTGTGACCCGGATGACAAGGAGGCCCTTAAC TCGGATGGT 545
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QY	546 GAGGCGTTTGGAGTGCCTGGATCACAGGAGGAGGATGAGGATGAGGAGGAGTATGAT 605
Db	481 GAGGCGTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGATGATGAT 540

PT	Treatment of cancer comprising restoration of pp32 function in malignant cells -
PT	

Qy 1 GGGTTCGGGTTTATTGATTGATTGCGCTGCGCGGGAGCCCTCTCCAGAGAGAGAGCCG 60
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Qy 32 GGGTTCGGGTTTATTGATTGATTGCGCTGCGCGGGAGCCCTCTCCAGAGAGAGAGCCG 91
Db |||||
Qy 61 GAGAGATGGAGATGGGACAGCGATTCAATTAGCTGCGGAAACGGGAGCCCTCTGATG 120
Db |||||
Qy 92 GAGAGATGGAGATGGGACAGCGATTCAATTAGCTGCGGAAACGGGAGCCCTCTGATG 151
Db |||||
Qy 121 TGAAGAACTTTCCTGGACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCCTCACAG 180
Db |||||
Qy 152 TGAAGAACTTTCCTGGACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCCTCACAG 211
Db |||||
Qy 181 ATGAATTTGAAGAACTTTCCTGGACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCCTCACAG 240
Db |||||
Qy 212 ATGAATTTGAAGAACTTTCCTGGACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCCTCACAG 271
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Qy 241 ACTTACCAAAAGTTAAACAACTTTAAGAACTTGAAGCTTAAGCAATACAGAGCTCAGTGG 300
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Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGGATGACAGAGAGGCCCTTAACCTCGG 540
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Qy 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
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Qy 812 GAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 871
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Qy 841 CCTTTTGTGATTTACTGTTTATAGCGGTACCCCTCTCCCGCCCTCTTAATTCCTGCC 900
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RESULT 3
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AC AAX81536;
XX AAX81536;
DT 26-AUG-1999 (first entry)
XX

DE Nucleotide sequence of normal human phosphoprotein 32 (pp32).
XX
KW Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;
KW prostatic adenocarcinoma; antineoplastic activity;
KW transformation suppression; malignant potential; neuroendocrine;
KW neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.
XX
OS Homo sapiens.
XX
PN WO9929906-A2.
XX
PD 17-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US26433.
XX
PR 12-DEC-1997; 97US-0069677.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Brody JR, Kadkol SS, Kocheavar GJ, Pasternack GR;
XX
DR WPI; 1999-385626/32.
XX
PT Phosphoprotein 32 (pp32) related genomic sequences
XX
PS Example 2; Fig 3; 65pp; English.
XX
CC The present sequence represents a human phosphoprotein 32 (pp32)
CC nucleotide sequence. The specification describes pp32 variants,
CC nucleated pp32r1 and pp32r2. The pp32r1 and pp32r2 sequences are
CC associated with cancer in prostate, especially prostatic adenocarcinomas.
CC Normal pp32 exerts antineoplastic activity through suppression of
CC transformation. Cancer-associated pp32 variants augment, rather than
CC inhibit, transformation. Determining the presence of a gene encoding
CC residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a
CC diagnostic method for predicting malignant potential of neuroendocrine,
CC neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.
XX
SQ Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;

Query Match 91.0%; Score 825.4; DB 20; Length 1052;
Best Local Similarity 94.4%; Pred. No. 2.5e-175;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
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Db |||||
Qy 32 GGGTTCGGGTTTATTGATTGATTGCGCTGCGCGGGAGCCCTCTCCAGAGAGAGAGCCG 91
Db |||||
Qy 61 GAGAGATGGAGATGGGACAGCGATTCAATTAGAGCTGCGGAAACGGGAGCCCTCTGATG 120
Db |||||
Qy 92 GAGAGATGGAGATGGGACAGCGATTCAATTAGAGCTGCGGAAACGGGAGCCCTCTGATG 151
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Qy 332 GCCTAGAACTTTCCTGGACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCCTCACAG 391
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Db |||||
Qy 392 AAATTAAGAACTTTCCTGGACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCCTCACAG 451
Db |||||
Qy 421 ACCTTTTCACCTTGGAGGTACCAACCTGAACAACTACTGAGAGAGATGTTCAAGCTCC 480
Db |||||

Db 812 GAGAACCTGAGATGAGGGAGAGATGACTAAGTGGATACCTATTTTGAAAAATT 871

Qy 841 CCTTTTGTGATTTACGTGTTTTAGCGGTACCCCTCTCCCCGCCACTCTAATCTGCC 900

Db 872 CCTATTGTGATTTGACTGTTTTTACCATATCCCTCTCCCCGCCCTCTAATCTGCC 931

Qy 901 CCCTGAA 907

Db 932 CCCTGAA 938

RESULT 5

ABK84424

ID ABK84424 standard; cDNA; 1052 BP.

XX AC ABK84424;

XX 14-AUG-2002 (first entry)

XX Human cDNA differentially expressed in granulocytic cells #995.

DE Human; ss; granulocytic cell; DNA chip; bacterial infection;

XX viral infection; parasitic infection; protozoal infection;

KW fungal infection; sterile inflammatory disease; psoriasis;

KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;

KW cardiac reperfusion injury; renal reperfusion injury; ARDS;

KW adult respiratory distress syndrome; inflammatory bowel disease;

KW Crohn's disease; ulcerative colitis; periodontal disease;

KW granulocyte activation; chronic inflammation; allergy.

XX Homo sapiens.

XX OS

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US30821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

PI WPI; 2002-435328/46.

XX DR

XX Detecting granulocyte activation by detecting differential expression

PT of genes associated with granulocyte activation, which serves as

PT diagnostic markers that is useful for monitoring disease states and

PT drug toxicity -

XX Claim 1; SEQ ID No 995; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation

CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by

CC DNA chip analysis as given in the specification, and comparing

CC the expression level to an expression level in an unactivated

CC GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent

CC that alters the expression of at least one gene in Gs; (2) screening (M3)

CC for an agent capable of modulating GCA or an inflammation (especially

CC chronic) in a tissue, an allergic response in a subject, exposure of a

CC subject to a pathogen or sterile inflammatory disease using the

CC gene expression profile; (3) detecting (M4) an inflammation (especially

CC chronic) in a tissue, an allergic response in a subject, exposure of a

CC subject to a pathogen or sterile inflammatory disease, by detecting the

CC level of expression in a sample of the tissue of gene(s) from Gs, where

CC the level of expression of the gene is indicative of inflammation;

CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,

CC an allergic response in a subject, exposure of a subject to a pathogen

CC or sterile inflammatory disease, by contacting a tissue having

CC inflammation with an agent that modulates the expression of gene(s)

CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for

CC modulating GA; M3 is useful for screening an agent capable of modulating

CC GCA preferably in an inflammation in a tissue; M4 is useful for

CC detecting an inflammation (especially chronic) in a tissue, an allergic

CC response in a subject, exposure of a subject to a pathogen or sterile

CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,

CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal

CC reperfusion injury, ARDS, adult respiratory distress syndrome,

CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,

CC periodontal disease; also bacterial infection, viral infection,

CC parasitic infection, protozoal infection, fungal infection and M5 is

CC useful for treating one of the above conditions. The present

CC sequence represents a gene differentially expressed in granulocytes.

CC Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic

CC format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;

Query Match 91.0%; Score 825.4; DB 24; Length 1052;

Best Local Similarity 94.4%; Pred. No. 2.5e-175;

Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTGCAGAGAGAGCGC 60

Db 32 GGGTTCGGGGTTTATTGATTGAATTCGGCGGGAGCCCTCTGCAGAGAGAGCGC 91

Qy 61 GAGAGATGAGATGGCGACGCGATTCATTAGAGTCGCGAACGGGAGCCCTCTGTATG 120

Db 92 GAGAGATGAGATGGCGACGCGATTCATTAGAGTCGCGAACGGGAGCCCTCTGTATG 151

Qy 121 TGAAGAAGCTGTCTCTGGACACAGTCGTCGAATGAAGCAAACTCGAAGCGCTCACAG 180

Db 152 TGAAGAAGCTGTCTCTGGACACAGTCGTCGAATGAAGCAAACTCGAAGCGCTCACAG 211

Qy 181 ATGAATTTGAAGAAGCTGGAAATCTTTAAGTACAATCAACCTAGGCGCTCACCTCAATCGCAA 240

Db 212 ATGAATTTGAAGAAGCTGGAAATCTTTAAGTACAATCAACCTAGGCGCTCACCTCAATCGCAA 271

Qy 241 ACTTACAAAGTTAAACAAACTTAAAGAGCTTGAACCTAAGCAGTACAGAGCCTCAGTCG 300

Db 272 ACTTACAAAGTTAAACAAACTTAAAGAGCTTGAACCTAAGCAGTACAGAGCCTCAGTCG 331

Qy 301 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAAATTTAAAGTGGCAACA 360

Db 332 GCCTAGAAGTATTGGCAGAAAAGTGTCCGAACTCTACGATCTAAATTTAAGTGGCAACA 391

Qy 361 AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 420

Db 392 AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCAAGAGCTTAG 451

Qy 421 ACCTTTTCACTTCGGAGGTTAACCAACTGTAACAACTACTTGAGAGAAAGATGTTCAAGCTCC 480

Db 452 ACCTTTTCACTTCGGAGGTTAACCAACTGTAACAACTACTTGAGAGAAAGATGTTTCAAGCTCC 511

Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGAGAGGCCCTTAAGTTCGG 540

Db 512 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGAGAGGCCCTTAAGTTCGG 571

Qy 541 ATGGTGAGGCTTTGTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600

Db 572 ATGGTGAGGCTACGTGGAGGCTGTGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631

Qy 601 ATGATGAAGATCTCAGGTAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660

Db 632 ATGATGAAGATCTCAGGTAATGAAGATGAGGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 691

Qy 661 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATGAAGGTTATAACAATGGAGAGG 720

Db 692 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATGAAGGTTATAACAATGGAGAGG 751

Qy 721 TAGATGATGAGGAGGATGAAGAGAGGCTTGGTGAAGAAGAAAGGGGTTCAGAACCGCAAAAT 780

Db 752 TAGATGACGAGGAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCAAGAGCGGAAAC 811
QY 781 AAGAACTGAAGATGAGGAGAGACGATCCCTAAGTGAATAATCTATTTGAAAAATT 840
Db 812 GAGAACCTGAAGATGAGGAGAGAGATGACTAAGTGAATAACCTATTTGAAAAATT 871
QY 841 CCATTGTGATTTACTGTTTTAGCCGTACCCCTCTCCCCCCCCACACTCTAATCCTGCC 900
Db 872 CCTATTGTGATTTGACTGTTTTTACCACATATCCCTCTCCCCCCCCCTCTAATCCTGCC 931
QY 901 CCTGTAA 907
Db 932 CCTGTAA 938

RESULT 6
AA576389
ID AA576389 standard; cDNA; 1155 BP.
XX
AC AA576389;
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #12193.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR P-PSDB; ABG12202.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 12193; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC imaging of sites expressing (II) and its binding partners are useful in medical
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA564197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1155 BP; 340 A; 219 C; 347 G; 249 T; 0 other;

Query Match 88.4%; Score 801.6; DB 23; Length 1155;
Best Local Similarity 93.4%; Pred. No. 5.4e-170;
Matches 848; Conservative 0; Mismatches 59; Indels 1; Gaps 1;

QY 1 GGGTTCGGGGTTTATGATTCGAATTCGGCTGGCGCGGAGGCTCTGCAGAGAGAGAGCGC 60
Db 57 GGGTTCGGGGTTTATGATTCGAATTCGGCTGGCGCGGAGGCTCTGCAGAGAGAGAGCGC 116
QY 61 GAGAGATGGAGATGGCAGACGGATTTCATTTAGAGCTGCGGAACGGACGCCCTCTCATG 120
Db 117 GAGAGATGGAGATGGCAGACGGATTTCATTTAGAGCTGCGGAACGGACGCCCTCTCATG 176
QY 121 TGAAGAAGACTTGTCTCTGGACCAACAGTCGGTGAATGAAGCAAACTCGAAGGCTCTACAG 180
Db 177 TGAAGAAGACTTGTCTCTGGACCAACAGTCGGTGAATGAAGCAAACTCGAAGGCTCTACAG 236
QY 181 ATGAATTTGAAGAAGACTTGAATTTAGTACAATCAACGTAGGCTCACCTCAATCGCAA 240
Db 237 ATGAATTTGAAGAAGACTTGAATTTAGTACAATCAACGTAGGCTCACCTCAATCGCAA 296
QY 241 ACTTACCAAGCTTAAACAACTTAAAGAGCTTGAACCTAAGCAGTAACAGAGCCTCTAGTGG 300
Db 297 ACTTACCAAGCTTAAACAACTTAAAGAGCTTGAACCTAAGCAGTAACAGAGCTCTAGGCG 356
QY 301 GCCTAGAGATTTGGCAGAAAAGTGTCCAAACC-TCATCATCTATAATTTAAATGGCAAC 359
Db 357 GCCTAGAGATTTGGCAGAAAAGTGTCCAAACCCTTCCGCCATCTAATTTAAAGSTGGCAAC 416
QY 360 AAAATTTAAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACTTCGAGAGCTTA 419
Db 417 AAAATTTAAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACTTCGAGAGCTTA 476
QY 420 GACCTTTTTCACCTTCGAGAGTAACCAACCTGAACAACTACTGAGAGAGAGATGTTCAAGCTC 479
Db 477 GACCTTTTTCACCTTCGAGAGTAACCAACCTGAACAACTACTGAGAGAGAGATGTTCAAGCTC 536
QY 480 CTCCTGCAACTCACAATATCTCAACGGCTGTGCCGGATGACAAGGAGGCCCTCACTACTCG 539
Db 537 CTCCTGCAACTCACAATATCTCAACGGCTGTGCCGGATGACAAGGAGGCCCTCACTACTCG 596
QY 540 GATGCTGAGGGCTTTGTGGAGTGCCTGATGACAAGGAGGAGGATGAGGATGAGGAGGAG 599
Db 597 GATGCTGAGGGCTTACGTGGAGGGCTTGATGAGGAGGAGGATGAGGATGAGGAGGAG 656
QY 600 TATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGCGT 659
Db 657 TATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGG 716
QY 660 GAAGAGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAAGGTTATACATGAGAG 719
Db 717 GAAGAGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAAGGTTATACATGAGAG 776
QY 720 GTAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAA 779
Db 777 GTAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAA 836
QY 780 TAGAAGACTGAAGATGAGGAGGAGGAGGATGCTTAAGTGAATAATCTATTTTGAATAAT 839
Db 837 CGAAGACTGAAGATGAGGAGGAGGAGGATGATGACTAAGTGAATAATCTATTTTGAATAAT 896
QY 840 TCCCTTTGTCATTTTACTGTTTTTACCGGTACCCCTCTCCCCCCCCACTCTAATCCTGC 899
Db 897 TCCCTTTGTCATTTTACTGTTTTTACCGGTACCCCTCTCCCCCCCCACTCTAATCCTGC 956
QY 900 CCCTGTAA 907
Db 957 CCCTGTAA 964

RESULT 7	
AAV1743	
ID	AAV1743 standard; cDNA; 916 BP.
XX	
AC	AAV1743;
XX	
DT	15-MAR-1999 (first entry)
XX	
DE	Human V3 loop HIV receptor P30/PHAPI cDNA.
XX	
KW	HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;
KW	P30 protein; PHAPI; infection; therapy; diagnosis; ss.
KW	
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	104..853
FT	/*tag- a
XX	
PN	W09840480-A1.
XX	
XX	17-SEP-1998.
XX	
XX	12-MAR-1998; 98WO-EP01409.
XX	
XX	12-MAR-1997; 97US-0040969.
XX	
XX	(CNRS) CENT NAT RECH SCI.
PA	(INSP) INST PASTEUR.
XX	
PI	Briand J, Callebaut C, Guichard G, Hovanessian A;
PI	Jacotot E, Krust B, Muller S;
XX	
XX	WPI; 1999-034588/03.
DR	P-PSDB; AAW84053.
XX	
PT	New isolated V3 loop HIV receptor - comprises P95/nucleolin,
PT	P40/PHAPI and P30/PHAPI proteins, used to develop products for the
PT	treatment and prevention of HIV infection
XX	
XX	Claim 17; Fig 49(12); 267pp; English.
XX	
CC	This cDNA sequence codes for the P30 (or PHAPI) protein of the
CC	newly identified V3 loop HIV receptor. This novel protein complex
CC	receptor for HIV retroviruses consists of an association of 3
CC	proteins named P95/nucleolin, P40/PHAPI and P30/PHAPI (see
CC	AAW84052-54). These proteins were isolated from human CD4+ CEM
CC	T-cell extracts using an affinity matrix containing either the
CC	pseudopeptide 5(Kps1CH2)NPR)-template assembled synthetic peptide
CC	or a synthetic V3 loop peptide (see AAW84055). P30 was identified
CC	as PHAPI by amino acid sequence analysis. The invention also
CC	concerns peptidic or non-peptidic molecules having the ability to
CC	alter and/or prevent the binding of the novel HIV receptor to the
CC	HIV retrovirus, and to pharmaceutical and diagnostic compositions
CC	containing such molecules. Methods are provided for screening for
CC	new active molecules, and to methods of screening genetic defects
CC	in the expression of the V3 loop HIV receptor in individuals that
CC	survive long-term HIV infection or who are HIV-resistant. Such
CC	genetically defective polynucleotides can be used in gene therapy.
XX	
SQ	Sequence 916 BP; 296 A; 167 C; 275 G; 178 T; 0 other;
Query Match	87.8%; Score 796.4; DB 20; Length 916;
Best Local Similarity	94.2%; Pred. No. 7.4e-169;
Matches 827; Conservative	0; Mismatches 51; Indels 0; Gaps 0;
QY	1 GGGTTCGGGGTTATTGATTGAATTCGGCTGGCGGGGAGCCTCTGCAGAGAGAGAGCGC 60
DB	39 GGGTTCGGGGTTATTGATTGAATTCGCCCGCGGGAGCCTCTGCAGAGAGAGAGCGC 98
QY	61 GAGAGATGGAGATGGCGAGACGGATTTCATTTAGAGCTCGCGAAGCGGACGCCCTCTGATG 120
DB	99 GAGAGATGGAGATGGCGAGACGGATTTCATTTAGAGCTCGCGAAGCGGACGCCCTCTGATG 158

QY	121	TGAAGAACCTTGTCTCTGGACAACAGTCGGTCGAATGAAGGCAAACTCGAAGGCCTCACAG	180
DB	159	TGAAGAACCTTGTCTCTGGACAACAGTCGGTCGAATGAAGGCAAACTCGAAGGCCTCACAG	218
QY	181	ATGAATTTGAAGAACTGGAATTTCTTAAGTACAATCAACGTAGGCCTCACCTCAATCGCAA	240
DB	219	ATGAATTTGAAGAACTGGAATTTCTTAAGTACAATCAACGTAGGCCTCACCTCAATCGCAA	278
QY	241	ACTTACCAAAAGTTAAACAAACTTAAGAAGCTTGAAGCTTAAGCAAGTAACAGACCTTCAGTGG	300
DB	279	ACTTACCAAAAGTTAAACAAACTTAAGAAGCTTGAAGCTTAAGCAAGTAACAGAGTCTCAGGGG	338
QY	301	GCCTAGAAGTATTGGCAGAAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA	360
DB	339	GCCTAGAAGTATTGGCAGAAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA	398
QY	361	AAATTTAAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAAACCTCAAGAGCTTAG	420
DB	399	AAATTTAAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAAACCTCAAGAGCTTAG	458
QY	421	ACCTTTTTCACITTCGAGAGTAACCAACCTGAACAACCTACTGAGAGAGAGTGTCAAGCTCC	480
DB	459	ACCTTTTTCACITTCGAGAGTAACCAACCTGAACAACCTACTGAGAGAGAGTGTCAAGCTCC	518
QY	481	TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGGAGGCCCTCAACTCGG	540
DB	519	TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGGAGGCCCTCAACTCGG	578
QY	541	ATGGTGAGGGCTTGTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGATGAGGAGGT	600
DB	579	ATGGTGAGGGCTTGTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGATGAGGAGGT	638
QY	601	ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT	660
DB	639	ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT	698
QY	661	AAGAGGAGGACGTGAGTGGAGACGAGGAGGAGGAGGATGAAGGTTATACAAATGGAGAGG	720
DB	699	AAGAGGAGGACGTGAGTGGAGACGAGGAGGAGGAGGATGAAGGTTATACAAATGGAGAGG	758
QY	721	TAGATGATGAGGAAGATGAAGAAGCTTTGGTGAAGAAAAGGGGTCAGAAGCCGAAAT	780
DB	759	TAGATGATGAGGAAGATGAAGAAGCTTTGGTGAAGAAAAGGGGTCAGAAGCCGAAAT	818
QY	781	AGAAACTGAAGATGAGGAGGAGGAGGATGCCTTAAGTGAATAATCTATTTTGAATAAT	840
DB	819	GAGAACTGAAGATGAGGAGGAGGAGGATGCCTTAAGTGAATAATCTATTTTGAATAAT	878
QY	841	CTTTTGTGATTTTACTGTTTTTGTAGCCGTACCCCTCT	878
DB	879	CTTTTGTGATTTGACTGTTTTTACCATATCCCTCT	916
RESULT 8			
AAW81537			
ID	AAW81537 standard; DNA; 889 BP.		
XX			
AC	AAW81537;		
XX			
DT	26-AUG-1999 (first entry)		
XX			
XX			
DE	Genomic sequence of phosphoprotein 32 variant pp32r2.		
XX			
KW	Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;		
KW	prostatic adenocarcinoma; antineoplastic activity;		
KW	transformation suppression; malignant potential; neuroendocrine;		
XX	neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.		
OS	Homo sapiens.		
XX			
PN	W0929906-A2.		
XX			

PD 17-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US26433.
XX
PR 12-DEC-1997; 97US-0069677.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Brody JR, Kadkol SS, Kocheavar GJ, Pasternack GR;
XX WPI; 1999-385626/32.
DR
XX
PT Phosphoprotein 32 (pp32) related genomic sequences
XX
PS Claim 1; Fig 5; 65pp; English.
XX
CC The present sequence represents the genomic sequence of phosphoprotein
CC 32 (pp32) variant pp32r2. The pp32r1 and pp32r2 sequences are associated
CC with cancer in prostate, especially prostatic adenocarcinomas. Normal
CC pp32 exerts antineoplastic activity through suppression of
CC transformation. Cancer-associated pp32 variants augment, rather than
CC inhibit, transformation. Determining the presence of a gene encoding
CC residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a
CC diagnostic method for predicting malignant potential of neuroendocrine,
CC neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.
XX
SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 78.9%; Score 716; DB 20; Length 889;
Best Local Similarity 89.2%; Pred. No. 7.4e-151;
Matches 799; Conservative 0; Mismatches 85; Indels 12; Gaps 2;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGCGCGGAGGCTCTGCAGAGAGAGCGC 60
DB 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGCGCGAGAGGCTCTGCAGAGAGAGCGC 60

QY 61 GAGAGATGAGATGGCAGACGATTCATTAGAGCTCGGGAACGGGAGCGCTCTGATG 120
DB 61 GAGAGATGAGATGGCAGACGATTCATTAGAGCTCGGGAACGGGAGCGCTCTGATG 120

QY 121 TGAAGAAGACTTGTCTGGACACAGTCGCTGAATGAAGGCAAACTCGAAGCGCTCAG 180
DB 121 TGAAGAAGACTTGTCTGGACACAGTCGCTGAATGAAGGCAAACTCGAAGCGCTCAG 180

QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAAGGAGGCTCACCTCAATCTCAG 240
DB 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAAGGAGGCTCACCTCAATCTCAG 240

QY 241 ACTTACCAAGTTAAACAACTTAAGAAGCTTGAACCTAAGCAGTAACAGACCTCAGTGG 300
DB 241 ACTTACCAAGTTAAACAACTTGAAGCTTGAACCTAAGCAGTAACAGACCTCAGTGG 300

QY 301 GCCTGAAGATTTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
DB 301 GCCTGAAGATTTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360

QY 361 AAATTAAGACCTCAGACATAGAGCCCTGAAAGATTAGAAAACCTCGAGAGCTTAG 420
DB 361 AAATTAAGACCTCAGACATAGAGCCCTGAAAGATTAGAAAACCTCGAGAGCTTAG 420

QY 349 AAATTAAGACCTCAGACATAGAGCCCTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
DB 349 AAATTAAGACCTCAGACATAGAGCCCTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408

QY 421 ACCTTTTCACTTGGGAGTAAACCACTGAACCTTACTGAGAGAAAGATGTTCAAGCTCC 480
DB 421 ACCTTTTCACTTGGGAGTAAACCACTGAACCTTACTGAGAGAAAGATGTTCAAGCTCC 480

QY 409 ACCTTTCAATGGGAGTAAACCACTGAACCTTACTGAGAGAAAGATGTTCAAGCTTC 468
DB 409 ACCTTTCAATGGGAGTAAACCACTGAACCTTACTGAGAGAAAGATGTTCAAGCTTC 468

QY 481 TCCTGCAACTCACAATCTCAACGGCTGTGACCGGATGACAGAGGCGCCCTAACTCGG 540
DB 481 TCCTGCAACTCACAATCTCAACGGCTGTGACCGGATGACAGAGGCGCCCTAACTCGG 540

QY 469 TCCTGCAACTCACAATCTCAACGGCTGTGACCGGATGACAGAGGCGCCCTAACTCAG 528
DB 469 TCCTGCAACTCACAATCTCAACGGCTGTGACCGGATGACAGAGGCGCCCTAACTCAG 528

QY 541 ATGTTGAGGGCTTTGTGGAGTGGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGT 600
DB 541 ATGTTGAGGGCTTTGTGGAGTGGCTGATGACAGAGGAGGATGAGGATGAGGAGGAGT 600

QY 529 ATATTGAGGACACCTGAGGAGGCTGATGACAGAGGAGGAGGAGGATGAGGAGGAGT 588
DB 529 ATATTGAGGACACCTGAGGAGGCTGATGACAGAGGAGGAGGAGGATGAGGAGGAGT 588

QY 601 ATGATGAAGATGCTCAGGTAATGAAGATGAGGAGGACGAGGATGAGGAGGAGGAGGAGT 660
DB 601 ATGATGAAGATGCTCAGGTAATGAAGATGAGGAGGACGAGGATGAGGAGGAGGAGGAGT 660

Db 589 ATGATGAAGATGCTCAGGTAATGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 648
QY 661 AAGAGGAGGACGTGAGTGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 649 AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 708
QY 721 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db 709 TAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 768
QY 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
Db 769 GAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 828
QY 841 CCTTTTGTGATTTTACCTGTTTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 896
Db 829 CCTATTGTGATTTGACTGTTTATACCATATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 884

RESULT 9
AAA88239
ID AAA88239 standard; DNA; 889 BP.
XX
AC AAA88239;
XX
DT 15-DEC-2000 (first entry)
XX
DE Human variant pp32r2 genomic DNA sequence.
XX
KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200045852-A1.
XX
PD 10-AUG-2000.
XX
PF 03-FEB-2000; 2000WO-US02656.
XX
PR 03-FEB-1999; 99US-0118667.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Pasternack GR, Bai J;
XX
DR WPI; 2000-514896/46.
XX
PT Treatment of cancer comprising restoration of pp32 function in
XX malignant cells -
XX
PS Example 5; Fig 5; 90pp; English.
XX
CC The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human variant pp32r2 genomic DNA sequence from
CC an example of the present invention.
XX
SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 78.9%; Score 716; DB 21; Length 889;
Best Local Similarity 89.2%; Pred. No. 7.4e-151;

Matches 799; Conservative 0; Mismatches 85; Indels 12; Gaps 2;	
QY 1	GGGTTCCGGGTTTATTGATTGAAATTCGGCTGGCGGGAGCCTCTGCAGAGAGAGAGCGC 60
Db 1	GGGTTCCGAGGTTTATTGATTGAAATTCGGCTGGCGAGAGCCTCTGCAGACAGAGAGCGC 60
QY 61	GAGAGATGGAGATGGGCACAGGATTCATTAGCTGCGGAACGGAGCGCCCTCTGATG 120
Db 61	GAGAGATGGAGATGGGCACAGGATTCATTAGCTGCGGAACGGAGCGCCCTCTGATG 120
QY 121	TGAAGAACCTTGCCCTGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGGCCCTCACAG 180
Db 121	TGAAGAACCTTGCCCTGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGGCCCTCACAG 180
QY 181	ATGAATTTGAAGAACTTGAATTTTAAAGTACAACTAACGTAGGCCCTCACCTCAATCGCAA 240
Db 181	ATGAATTTGAAGAACTTGAATTTTAAAGTACAACTAACGTAGGCCCTCACCTCAATCTCAG 240
QY 241	ACTTACCAAGTTAAACAACACTTAAAGACTTGAAGCTTCAACTAGCAGTACAGAGCCTCAGTGG 300
Db 241	ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACTA-----AGAGTCTCAGGGG 288
QY 301	GCCTAGAACTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTTAAAGTGGCAACA 360
Db 289	GCCTGGNAGTATTGGCAGAAAAGTGTCCAAACCTCAGCCTCATATATTAAAGTGGCAACA 348
QY 361	AAATTTAAAGACCTCAGCACAACTAGAGCCCTGAAAGTTAGAAAACCTCGAGAGCTTAG 420
Db 349	AAATTTAAAGACCTCAGCACAACTAGAGCCCTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
QY 421	ACCTTTTCACTTCGGAGGTAAACCACTGACAACTACTCTGAGAGAAGTGTCAAGCTCC 480
Db 409	ACCTTTTCAATTCGGAGGTAAACCACTGACAACTACTCTGAGAGAAGTGTCAAGCTTC 468
QY 481	TCCTGCAACTCACAATCTCAACGGCTGTGACCCGGATGACAAAGGAGGCCCTTAAGTCCG 540
Db 469	TCCTGCAACTCACAATCTCGACAGCTGTACTGGGACCAAGGAGGCCCTTAAGTCCAG 528
QY 541	ATGGTAGGGCTTTGGAGTGGCTGGATGACAAAGGAGGAGGATGAGGATGAGGAGGAGT 600
Db 529	ATATTGAGGACCACTGTGGAGGGCTGGATGACGAGGAGGAGGATGAGGATGAGGAGGAGT 588
QY 601	ATGATGAAGATGCTCAGTAAATGGAAGATGAGGAGGACAGGATGAGGAGGAGGAACTGG 660
Db 589	ATGATGAAGATGCTCAGTAAATGGAAGATGAGGAGGACAGGATGAGGAGGAGGAACTGG 648
QY 661	AAGAGGAGGACGTGAGTGGAGAGAGGAGGAGGAGGATGAAGGTTTATAAATGAGAGAGG 720
Db 649	AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGGATGAAGGTTTATAAATGAGAGAGG 708
QY 721	TAGATGATGAGGAGAGATGAAGAGAGCTTGGTGAAGNAGAAAGGGTCAAGACCGAAAT 780
Db 709	TAGATGCGGAGGAGAGATGAAGAGAGCTTGGTGAAGNAGAAAGGGTCAAGACCGAAAT 768
QY 781	AAGAACTGGAAGATGAGGAGGAGACACTGCCTAAAGTGAATTAATCTATTTTTGAAGAAAT 840
Db 769	GAGAACTGGAAGATGAGGAGGAGAGATGACTAAAGTAGAATAACCTATTTTTGAAGAAAT 828
QY 841	CTTTTGTGATTTTACTGTTTTTATAGCCGTATCCCTCTCTCCCTCCCTCACTTAATCC 896
Db 829	CCTATTGTGATTTGACTGTTTTTACCCTATATCCCTCTCCCTCCCTCAATCTCTGCC 884
RESULT 10	
AAA88237	
ID	AAA88237 standard; DNA; 1035 BP.
XX	
AC	AAA88237;
XX	
DT	15-DEC-2000 (first entry)
XX	
DE	Human variant pp32r1 nucleotide sequence.
XX	

KW	Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW	acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
XX	malignant; cytostatic; gene therapy; ds.
OS	Homo sapiens.
XX	WO200045852-A1.
PN	10-AUG-2000.
PD	03-FEB-2000; 2000WO-USO2656.
PF	03-FEB-1999; 99US-0118667.
PR	(UYJO) UNIV JOHNS HOPKINS.
XX	Pasternack GR, Bai J;
PI	WPI: 2000-514896/46.
XX	P-PSDB; AAB20655.
DR	Treatment of cancer comprising restoration of pp32 function in
XX	malignant cells -
PT	Example 3; Fig 3; 90pp; English.
PS	
XX	The present invention describes a method (M1) for treating malignant
CC	cells comprising restoration of pp32 function. Also described are:
CC	(1) a method (M2) of screening to determine whether a compound is an
CC	inducer of pp32 expression comprising measuring pp32 expression by
CC	cells cultured in the presence and absence of the compound; and
CC	(2) a method (M3) of screening to determine whether a compound is an
CC	inducer of pp32 function comprising measuring protein phosphatase
CC	activity in cells cultured in the presence and absence of the compound.
CC	The methods are useful for treating cancer and for identifying agents
CC	which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC	has been mapped to chromosome 15q22.3-q23. The present sequence
CC	represents the human variant pp32r1 nucleotide sequence from
CC	an example of the present invention.
XX	
SQ	Sequence 1035 BP; 322 A; 189 C; 308 G; 216 T; 0 other;
Query Match 78.9%; Score 716; DB 21; Length 1035;	
Best Local Similarity 89.2%; Pred. No. 7.7e-151;	
Matches 799; Conservative 0; Mismatches 85; Indels 12; Gaps 2;	
QY 1	GGGTTCCGGGTTTATTGATTGAAATTCGGCTGGCGGGAGCCTCTGCAGAGAGAGAGCGC 60
Db 32	GGGTTCCGAGGTTTATTGATTGAAATTCGGCTGGCAGGAGCCTCTGCACAGAGAGCGC 91
QY 61	GAGAGATGGAGATGGCAGACGGATTCATTAGAGCTGGGAACGGAGCCCTCTGATG 120
Db 92	GAGAGATGGAGATGGCAGACGGATTCATTAGAGCTGGGAACAGGGCCCTCTGATG 151
QY 121	TGAAGAACCTTCTCTGGACACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCCTCACAG 180
Db 152	TGAAGAACCTTCCCTGGACACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCCTCACAG 211
QY 181	ATGAATTTGAAGAACTGGAAATTCCTTAAGTACAACTCAACGTAGGCCCTCACCTCAATCGAA 240
Db 212	ATGAATTTGAAGAACTGGAAATTCCTTAAGTACAACTCAACGTAGGCCCTCACCTCAATCTCAG 271
QY 241	ACTTACCAAGTTAAACAACACTTAAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT 300
Db 272	ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACTA-----AGAGTCTCAGGGG 319
QY 301	GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTTAAAGTGGCAACA 360
Db 320	GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTTAAAGTGGCAACA 379
QY 361	AAATTTAAAGACCTCAGCACAACTAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 420
Db 380	AAATTTAAAGACCTCAGCACAACTAGAGCCCAATGAAGCAGTTAGAAAACCTCAAGAGCTTAG 439

QY 421 ACCTTTTCACTTGCAGGTAAACCAACCTGAACAACACTACTGAGAGAAGATGTTCAAGCTCC 480
|||||
Db 440 ACCTTTTCAATTCGAGGTAAACCAACCTGAACGACTACGGAGAAAACGCTGTTCAAGCTTC 499
QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGGAGGCCCTTAACCTGG 540
|||||
Db 500 TCCTGCAACTCACATATCTGACAGCTGTTACTGGGACCAACAAGGAGGCCCTTACTCAG 559
QY 541 ATGGTGAGGGCTTTCTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600
|||||
Db 560 ATATTGAGGACCACTGAGGGCCCTGGATGACGAGGAGGAGGGTGAGCATGAGGAGGAGT 619
QY 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAACGTG 660
Db 620 ATGATGAAGATGCTCAGCTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 679
QY 661 AAGAGGAGGAGTGAAGTGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 680 AAGAGGAGGAGTGAAGTGGAGGGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 739
QY 721 TAGATGATCAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAAAT 780
Db 740 TAGATGCGGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAAAT 799
QY 781 AGAAACTGAAGATGAGGAGGAGGAGGAGGATGCTTAAGTGGAAATAATCTATTGAAAAATT 840
Db 800 GAGAACTGAAGATGAGGAGGAGGAGGATGATGACTAAGTAGAATAACCTATTGAAAAATT 859
QY 841 CCTTTTGTGATTTACTCTTTTACCGCTACCCCTCTCCCTCCCTCCCTCTAATCC 896
Db 860 CCTATTGTGATTTGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 915

RESULT 11
AAx81535
ID AAx81535 standard; DNA; 5785 BP.
AC AAx81535;
XX
XX
DT 26-AUG-1999 (first entry)
XX
XX
DE Genomic sequence of phosphoprotein 32 variant pp32r1.
XX
XX
KW Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;
KW prostatic adenocarcinoma; antineoplastic activity;
KW transformation suppression; malignant potential; neuroendocrine;
KW neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.
XX
XX
OS Homo sapiens.
XX
XX
PN WO9929906-A2.
XX
XX
PD 17-JUN-1999.
XX
XX
PF 11-DEC-1998; 98WO-US26433.
XX
XX
PR 12-DEC-1997; 97US-0069677.
XX
XX
XX (UJYU) UNIV JOHNS HOPKINS.
XX
XX
PI Brody JR, Kadkol SS, Kocheavar GJ, Pasternack GR;
XX
XX
DR WPT; 1999-385626/32.
XX
XX
PT Phosphoprotein 32 (pp32) related genomic sequences
XX
XX
PS Claim 1; Fig 2; 65pp; English.
XX
XX
CC The present sequence represents the genomic sequence of phosphoprotein
CC 32 (pp32) variant pp32r1, which is isolated from human placenta. The
CC pp32r1 and pp32r2 sequences are associated with cancer in prostate,
CC especially prostatic adenocarcinomas. Normal pp32 exerts antineoplastic

CC activity through suppression of transformation. Cancer-associated pp32
CC variants augment, rather than inhibit, transformation. Determining the
CC presence of a gene encoding residues 146-163 of pp32r1 or pp32r2 in a
CC sample is useful for a diagnostic method for predicting malignant
CC potential of neuroendocrine, neural, mesenchymal, lymphoid, epithelial
CC or germ cell-derived tumours.
XX
XX Sequence 5785 BP; 1755 A; 1087 C; 1162 G; 1781 T; 0 other;

Query Match 78.9%; Score 716; DB 20; Length 5785;
Best Local Similarity 89.2%; Pred. No. 1.3e-150;
Matches 799; Conservative 0; Mismatches 85; Indels 12; Gaps 2;

QY 1 GCGTTTCGGGTTTATTGATTTCGGCTGGCGGGGAGCCCTCTGCAGAGAGAGAGCC 60
Db 4388 GGGTTCGAGTTTATTGATTTCGGCTGGCGAGAGCCCTCTGCAGAGAGAGAGCC 4447
QY 61 GAGAGATGGAGATGGGACGACGGATTCTATTAGAGCTGCGGAACGGGAGCCCTCTGTATG 120
Db 4448 GAGAGATGGAGATGGGACGACGGATTCTATTGAGCTGCGGAACGGGAGCCCTCTGTATG 4507
QY 121 TGAAGAAGCTTGCCTGGACACAGTCGTCGAATCAAGGCAAACTCGAAGGCCCTCACAG 180
Db 4508 TGAAGAAGCTTGCCTGGACACAGTCGTCGAATCAAGGCAAACTCGAAGGCCCTCACAG 4567
QY 181 ATGAATTTGAAGAAGCTTGAATTTCTTAAGTACAATCAACGTAGGCTCCTCACTCAATCGCAA 240
Db 4568 ATGAATTTGAAGAAGCTTGAATTTCTTAAGTAAATCAACGGAGCCCTCACTCAATCTCAG 4627
QY 241 ACTTACCAAGTTTAAACAACCTTGAAGAGCTTGAAGTAAAGAGCTTAACAGAGCCCTCAGTGG 300
Db 4628 ACTTACCAAGTTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGCTCAGGGG 4675
QY 301 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAATTTAAAGTGCACA 360
Db 4676 GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTAAAGTGGCA 4735
QY 361 AAATTAAGACCTTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCTGAGAGCTTAG 420
Db 4736 AAATTAAGACCTTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCTAAGAGCTTAG 4795
QY 421 ACCTTTTCACTTGCAGGTTAACCAACCTGAACACTACTGAGAGAGAGATGTTCAAGCTCC 480
Db 4796 ACCTTTTCAATTTGCGAGGTTAACCAACCTGAACACTACTGAGAGAGAGAGCTGTTCAAGCTTC 4855
QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGGAGGCCCTTAAGTGG 540
Db 4856 TCCTGCAACTCACATATCTCGACAGCTGTACTGGGACCACAAAGGAGGCCCTTACTCAG 4915
QY 541 ATGGTGAGGGCTTTGTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600
Db 4916 ATATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 4975
QY 601 ATGATGAAGATGCTCAGGTTAATGGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
Db 4976 ATGATGAAGATGCTCAGGTTAATGGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 5035
QY 661 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 5036 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5095
QY 721 TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAAAT 780
Db 5096 TAGATGCGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAAAT 5155
QY 781 AAGAACTGAAGATGGGAGAGAGGATGCCTAAGTGAATAATCTATTGAAAAATT 840
Db 5156 GAGAACTGAAGATGGGAGAGAGGATGCCTAAGTGAATAATCTATTGAAAAATT 5215
QY 841 CCTTTTGTGATTTTACTGTTTTTACCGCTTACCCCTCTCCCTCCCTCCCTCTAATCC 896
Db 5216 CCTATTGTGATTTGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 5271

RESULT 12
AA88236
ID AAA88236 standard; DNA; 5785 BP.
XX AC AAA88236;
XX DT 15-DEC-2000 (first entry)
XX DE Human placenta variant pp32r1 genomic DNA sequence.
XX KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
XX KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
XX KW malignant; cytostatic; gene therapy; ds.
XX OS Homo sapiens.
XX PN WO200045852-A1.
XX PD 10-AUG-2000.
XX PF 03-FEB-2000; 2000WO-US02656.
XX PR 03-FEB-1999; 99US-0118667.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Pasternack GR, Bai J;
XX DR WPI; 2000-514896/46.
XX PT Treatment of cancer comprising restoration of pp32 function in
XX PT malignant cells -
XX PS Example 3; Fig 2; 90pp; English.
XX CC The present invention describes a method (M1) for treating malignant
XX CC cells comprising restoration of pp32 function. Also described are:
XX CC (1) a method (M2) of screening to determine whether a compound is an
XX CC inducer of pp32 expression comprising measuring pp32 expression by
XX CC cells cultured in the presence and absence of the compound; and
XX CC (2) a method (M3) of screening to determine whether a compound is an
XX CC inducer of pp32 function comprising measuring protein phosphatase
XX CC activity in cells cultured in the presence and absence of the compound.
XX CC The methods are useful for treating cancer and for identifying agents
XX CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
XX CC has been mapped to chromosome 15q22.3-q23. The present sequence
XX CC represents the human placenta variant pp32r1 genomic DNA sequence from
XX CC an example of the present invention.
SQ Sequence 5785 BP; 1755 A; 1087 C; 1162 G; 1781 T; 0 other;

Query Match 78.9%; Score 716; DB 21; Length 5785;
Best Local Similarity 89.2%; Pred. No. 1.3e-150;
Matches 799; Conservative 0; Mismatches 85; Indels 12; Gaps 2;

Qy 1 GGGTTCGGGTTATTGATTAATTCGGCTGGCGGCGGAGCCCTCTCGAGAGAGAGCGC 60
Db 4388 GGGTTCGAGGTTATTGATTAATTCGGCTGGCGGCGGAGCCCTCTCGAGAGAGAGCGC 4447

Qy 61 GAGAGATGGAGATGGCGAGACGATTTCATTAGAGCTGGCGAACGGGCGCCCTCTGATG 120
Db 4448 GAGAGATGGAGATGGCGAGACGATTTCATTAGAGCTGGCGAACGGGCGCCCTCTGATG 4507

Qy 121 TGAAGAACTTGTCTCGGACCAACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCGCTCACAG 180
Db 4508 TGAAGAACTTGTCTCGGACCAACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCGCTCACAG 4567

Qy 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAAGTACAGTACCTCAATCGCAA 240
Db 4568 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAAGTACAGTACCTCAATCGCAA 4627

Qy 241 ACTTACCAGAGTTAAACAACTTAAGAGAGCTTGAAGCTTAAGCAGTAAACAGAGCGCTCAGTGG 300

Db 4628 ACTTACCAGAGTTAAACAACTTAAGTTCGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 4675
Qy 301 GCCTAGAGATTTGGCAGAGAAAGTGTCCAAACCTCATACATCTCTAAATTTAAGTGGCAACA 360
Db 4676 GCCTGGAAGTATTGGCAGAGAAAGTGTCCAAACCTTCAGGCATCTATATTAAAGTGGCAACA 4735
Qy 361 AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAAACTCTGAGAGCTTAG 420
Db 4736 AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAAACTCTGAGAGCTTAG 4795
Qy 421 ACCTTTTTCACCTTGGGAGGTAACCAACCTTGAACAACTACTGAGAGAAGATGTTCAAGTCC 480
Db 4796 ACCTTTTCACCTTGGGAGGTAACCAACCTTGAACAACTACTGAGAGAAGATGTTCAAGTCC 4855
Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTTAACCTCGG 540
Db 4856 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTTAACCTCGG 4915
Qy 541 ATGTTGAGGCGCTTGTGGAGTCCCTGGATGACAAGGAGGAGGATGAGATGAGGAGGAGT 600
Db 4916 ATATTGAGGACCACTGGAGGCGCTTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGT 4975
Qy 601 ATGATGAAGATCTCAGCTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Db 4976 ATGATGAAGATCTCAGCTAATGGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 5035
Qy 661 AAGAGGAGGAGTGTGAGTGGAGACGAGGAGGAGGAGGATGAAGGTTTAACTAAGTGGAGG 720
Db 5036 AAGAGGAGGAGTGTGAGTGGAGGAGGAGGAGGAGGATGAAGGTTTAACTAAGTGGAGG 5095
Qy 721 TAGATGATGAGGAGATGAAGAGGCTTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGT 780
Db 5096 TAGATGAGGAGGAGATGAAGAGGCTTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGT 5155
Qy 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGATGCTTAAGTGAATAATCTATTTTGAAGAAAT 840
Db 5156 GAGAACCTGAAGATGAGGAGGAGGAGGAGGATGATGACTAAGTAGAATAACCTATTTTGAAGAAAT 5215
Qy 841 CCTTTTGTGATTTTACTGTTTGTAGCCCTACCCCTCTCCGCCGCCCTCTAATCC 896
Db 5216 CCTATTGTGATTTGACTGTTTGTAGCCCTATCCCTCCGCCGCCCTCTAATCC 5271

RESULT 13
AAA15294
ID AAA15294 standard; cDNA; 750 BP.
XX AC AAA15294;
XX DT 04-SEP-2000 (first entry)
XX DE cDNA encoding a protein phosphatase 2A inhibitor.
XX KW Syndcan-4; angiotensin; proteoglycan; protein kinase C;
XX KW delta-isoenzyme; alpha isoenzyme; protein phosphatase; infarction;
XX KW endothelial cell proliferation; endothelial cell migration; anoxia;
XX KW myocardial infarction; chronic myocardial ischemia; heart tissue; ss.
OS Homo sapiens.
XX FH Key Location/Qualifiers
XX CDS 1..750
XX FT /*tag= a
XX PN WO200027416-A1.
XX PD 18-MAY-2000.
XX PF 10-NOV-1999; 99WO-US26647.
XX PR 12-NOV-1998; 98US-0190976.

PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.																																
XX																																	
PI	Simons M, Horowitz A;																																
XX																																	
DR	WPI: 2000-376307/32.																																
DR	P-PSDB; AAY93262.																																
XX																																	
PT	Stimulating angiogenesis, useful particularly for treating cardiac																																
PT	anoxia and infarction, by preventing phosphorylation of specific																																
PT	residue in syndecan-4, present in endothelial cells -																																
XX																																	
PS	Disclosure; Page 35; 73pp; English.																																
XX																																	
CC	The present sequence encodes a protein phosphatase 2A inhibitor. The																																
CC	protein phosphatase 1 is used in the method of the invention. The																																
CC	specification describes a method for stimulating angiogenesis within																																
CC	variable cells, tissues, or organs in situ. The method comprises																																
CC	treating target endothelial cells such that Ser183, in the																																
CC	intracellular cytoplasmic domain of syndecan-4 proteoglycan, is																																
CC	present in non-phosphorylated form in at least some syndecan-4 molecules.																																
CC	The cells are treated with an inhibitor of syndecan-4 protein kinase C																																
CC	(PKC) delta-isoenzyme, an agent that increases intracellular activity of																																
CC	the PKC alpha-isoenzyme, or an agent that activates at least one of																																
CC	protein phosphatases 1 or 2A. Keeping Ser183 in the non-phosphorylated																																
CC	form results in activation of protein kinase C alpha isoenzyme, which is																																
CC	essential for endothelial cell proliferation and migration in situ.																																
CC	Syndecan-4 participates in intracellular signalling through																																
CC	oligomerisation of its cytoplasmic tail and this process does not																																
CC	occur if Ser183 is phosphorylated. The method can be used in vivo or																																
CC	in vitro, to stimulate angiogenesis in cells or tissues which are																																
CC	defective or have suffered anoxia or infarction, particularly myocardial																																
CC	infarction, or chronic myocardial ischemia of heart tissue, and to																																
CC	study mechanisms involved in control of angiogenesis.																																
XX																																	
SQ	Sequence 750 BP; 260 A; 130 C; 229 G; 131 T; 0 other;																																
<table border="0"> <tr> <td>Query Match</td> <td>75.1%;</td> <td>Score</td> <td>681.2;</td> <td>DB</td> <td>21;</td> <td>Length</td> <td>750;</td> </tr> <tr> <td>Best Local Similarity</td> <td>94.3%;</td> <td>Pred.</td> <td>No. 4.3e-143;</td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>Matches</td> <td>707;</td> <td>Conservative</td> <td>0;</td> <td>Mismatches</td> <td>43;</td> <td>Indels</td> <td>0;</td> </tr> <tr> <td>Gaps</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> </table>		Query Match	75.1%;	Score	681.2;	DB	21;	Length	750;	Best Local Similarity	94.3%;	Pred.	No. 4.3e-143;					Matches	707;	Conservative	0;	Mismatches	43;	Indels	0;	Gaps							
Query Match	75.1%;	Score	681.2;	DB	21;	Length	750;																										
Best Local Similarity	94.3%;	Pred.	No. 4.3e-143;																														
Matches	707;	Conservative	0;	Mismatches	43;	Indels	0;																										
Gaps																																	
QY	66 ATGGAGATGGCAGCGGATTCAATTAGAGCTGGCGACGGAGCGCCTCTGATGTGAAA 125																																
DB	1 ATGGAGATGGCAGCGGATTCAATTAGAGCTGGCGACGGAGCGCCTCTGATGTGAAA 60																																
QY	126 GAACCTTGCTCGSACAACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCCCTCACAGATGAA 185																																
DB	61 GAACCTTGCTCGSACAACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCCCTCACAGATGAA 120																																
QY	186 TTTGAGAAGTGGAAATCTTAAGTACAATCAACGTAGGCGCTCACTCAATCGCAAACTTA 245																																
DB	121 TTTGAGAAGTGGAAATCTTAAGTACAATCAACGTAGGCGCTCACTCAATCGCAAACTTA 180																																
QY	246 CCAAAGTTAAACAAACTTAAGAAGCTTGAACCTCATACATCTAAATTTAAGTGCACAACAAAT 305																																
DB	181 CCAAAGTTAAACAAACTTAAGAAGCTTGAACCTTAAGCGCATACAGAGTCTCAGGGGCGCTG 240																																
QY	306 GAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGCACAACAAAT 365																																
DB	241 GAAGTATTGGCAGAAAAGTGTCCGAACTTCAAGACCTCAAGAGCTTAGACCTT 300																																
QY	366 AAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAAAACCTTCGAGAGCTTAGACCTT 425																																
DB	301 AAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAAAACCTTCGAGAGCTTAGACCTT 360																																
QY	426 TTCACCTTGGAGGTAAACCACTGAACAACCTACTCTAGAGAGAAGATGTTCAAGCTTCCTCGT 485																																
DB	361 TTCACCTTGGAGGTAAACCACTGAACAACCTACTCTAGAGAGAAGATGTTTCAGCTTCCTCGG 420																																
QY	486 CAACTCACATATCTCAACGGCTGTGACCCGATGACAAAGGAGGCCCTCACTCGGATGCT 545																																
DB	421 CAACTCACATATCTCGAGCGGTATGACCGGAGCAGCAAGGAGGCCCTGACTCGGATGCT 480																																
QY	546 GAGGGCTTTGTGGAGTGCTTGATGACAAGGAGGAGGATGAGGATGAGGAGGAGTATGAT 605																																

22-NOV-2001.

18-MAY-2001; 2001WO-JP04192.

18-MAY-2000; 2000JP-0145977.

(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
WPI; 2002-034733/04.
P-PSDB; ABB57251.

Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes -

Claim 2; Page 1714-1716; 2690pp; English.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring the expression levels of particular genes (AB199202 to AB199912), encoding the protein sequences in ABB57020 to ABB57374 or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.

Sequence 980 BP; 312 A; 169 C; 302 G; 197 T; 0 other;

Query Match 64.5%; Score 585; DB 24; Length 980;
Best Local Similarity 83.0%; Pred. No. 1,6e-121;
Matches 693; Conservative 0; Mismatches 135; Indels 7; Gaps

QY 50 AGAGAGAGCGGAGAGATGGAGATGGGACAGCGAGTTCATTAGAGCTCGGAGACGGGAC 109
DB 10 AGAGAGAGCGGAGAGATGGAGATGGGACAGCGAGTTCATTAGAGCTCGGAGACGGGAC 69
QY 110 GCCCTCTGATGTGAAGAACTTCTCTGGACACAGCTCGTGAATGAAGGCAAACTCGA 169
DB 70 GCCCTCTGATGTGAAGAGCTGGTCTGGATTAAGTCAATTAAGGCAAACTCGA 129
QY 170 AGGCTCTACAGATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAAGCTCAATTT 229
DB 130 AGGCTCTACAGATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAAGCTCAATTT 189
QY 230 CTCATTCGCAAACTTACCAAGTAAACAACTTAAGAGCTTGAAGTCAAGTCAAGTCAAG 289
DB 190 CTCCTATTTCCAACTTACCAAGTAAACAACTTAAGAGCTTGAAGTCAAGTCAAGTCAAG 249
QY 290 AGGCTCAGTGGGCTAGAAGTATTGGCAGAAAAGTGTCCAAAGCTCATCATCTAAATTT 349
DB 250 AATCTCAGGGAGCTGGAAGTATTGGCAGAAAAGTGTCCAAAGCTCATCATCTAAATTT 309
QY 350 AAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCCTCAAAAAGTTAGAAAACCT 409
DB 310 AAGTGGCAACAAATTAAGAGATCTCAGCACAATAGAGCCCTCAAAAAGTTAGAAAACCT 369
QY 410 CGAGAGCTTAGACTTTTTCATCTTGGAGGTAAACCAACTGAACCTGAAAGTGTAGAAAACCT 469
DB 370 CAAGAGCTTAGACTTTTTCATCTTGGAGGTAAACCAACTGAACCTGAAAGTGTAGAAAACCT 429
QY 470 GTTCAAGCTCCTCTGCAACTACATATCTCAACGGCTGTGACCGGATGACAGGAGGC 529
DB 430 GTTCAAGCTCCTCTGCAACTACATATCTCAACGGCTGTGACCGGATGACAGGAGGC 489
QY 530 CCCTAATCTCGATGGTGGAGCTTTGGAGTGCCTGTGATGACAGGAGGAGGATGAGGA 589
DB 490 CCCGAGCTCCGATGTTGAGGCTACGTGGA-----GGATGACCGACGAGGAGATGAGGA 543
QY 590 TGAGGAGAGTATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGACGAGGATGAGGA 649
DB 544 TGAGGAGAGTATGATGAATATGCCAGCTAGTGAAGATGAAGGAGGAGGATGAGGA 603
QY 650 GGAGGAGCTCAAGGAGGAGGAGTGTGAGTGGAGACGAGGAGGAGGAGGATGAAGTTATAA 709
DB 604 GGAAGAGGGGAGGAGGAGGATGTGAGTGGAGAGGAGGAGGAGGATGAGGAGGTTACAA 663
QY 710 CAATGGAGAGGTAGATGATGAGGAGATGAAGAGAGGCTTGGTGAAGAGAAAGGGGTCA 769
DB 664 TCAGCGGGAAGTGGATGACGAGGAGAGACGAAGAAGTGTGTTGAAGAGGAGGAGTCA 723
QY 770 GAAGCGAAATAGAACTGAAGTGAAGGAGGAGACGACATGCTTAAGTGAATATCTAT 829
DB 724 GAAGCGAAACGAGACCGGAGATGAGGAGGAGGAGGAGGATGACTAAG-GAATGAACCTGT 782
QY 830 TTTGAAAATTCCTTTTGTGATTTTACTGTGTTTTTGGCCGTACCCCTCTCCCTCC 884
DB 783 TTTGGGAAATTCCTATGTGATTTGACTGTTTTTACCCATATCCCTCTCCCTCC 837

RESULT 15
ABI99657
ID ABI99657 standard; cDNA; 980 BP.

XX AC ABI99657;
XX AC ABI99657;
XX DT 07-MAR-2002 (first entry)
XX DE Mouse ischaemic condition related cdna sequence SEQ ID NO:687.
XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
XX KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX OS Mus musculus.
XX PN WO200188188-A2.

Qy	530	CCCTAACTCGGATGGTCAGGGCTTTGTGGAGTCCTCGGATGACAAGGAGGAGGATGAGGA	589
Db	490	CCCCGACTCCGATGTTGAGGGCTACGTGA-----GGATGACGACGAGGAAGATGAGGA	543
Qy	590	TGAGGAGGAGTATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGACGAGGATGAGGA	649
Db	544	TGAGGAGGAGTATGATGAATATCCCGAGCTAGTGGAAAGATGAAGAGGAGGTTGAGGA	603
Qy	650	GGAGGAACGTGAAGAGGAGGACGTGAGTGGACGAGGAGGAGAGGATGAAGGTTATAA	709
Db	604	GGAAAGAGGGGAGGAGAGGATGTGAGTGGAGGAGGAGGAGGATGAGGAAGGTTACAA	663
Qy	710	CAATGGAGAGGTAGATCAGCAAGATGAAGAAGCTTGTGTAAGAGAAAGGGGTCA	769
Db	664	TGACGGGGAAGTGGATGACGAGGAGGAGACGAGGAAGAGCTGGTGAAGAAGAGGGAGTCA	723
Qy	770	GAAGCGAAAAATAAGAACTGAAGATGAGGAGGAGAGCATGCCTAAGTGGAAATATCTAT	829
Db	724	GAAGCGAAAAACGAGAACCGGACGATGAGGCGGAGAGGATGACTAAG-GAATGAACCTGT	782
Qy	830	TTTGAAAAATTCCTTTTGTCATTTTACTGTTTTAGCCGTACCCCTCTCCCCCC	884
Db	783	TTGGGAAATTCCTATTGTGATTGACTGTTTTTACCCTATCCCTCCCTCCCTCC	837

Search completed: December 8, 2002, 21:38:04
Job time : 183.199 secs

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 21:29:48 ; Search time 38.3808 Seconds
(without alignments)
7247.256 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	825.4	91.0	1052	1 US-08-314-503A-1	Sequence 1, Appli
3	825.4	91.0	1052	1 US-08-468-066-1	Sequence 1, Appli
4	825.4	91.0	1052	2 US-08-466-717-1	Sequence 1, Appli
5	825.4	91.0	1052	1 US-08-466-743-1	Sequence 1, Appli
6	825.4	91.0	1052	5 PCT-US95-12414-1	Sequence 1, Appli
7	585	64.5	980	1 US-08-466-603-3	Sequence 3, Appli
8	585	64.5	980	1 US-08-314-503A-3	Sequence 3, Appli
9	585	64.5	980	1 US-08-468-066-3	Sequence 3, Appli
10	585	64.5	980	2 US-08-466-717-3	Sequence 3, Appli
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17	405	44.7	759	3 US-08-466-743-4	Sequence 4, Appli
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22	109.2	12.0	3489	4 US-09-298-568-1	Sequence 1, Appli
23	109.2	12.0	32207	2 US-08-770-379-20	Sequence 20, Appl
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35	80.4	8.9	390	4	US-09-197-649-7	Sequence 7, Appli
36	75.6	8.3	43795	3	US-08-742-185-101	Sequence 101, App
37	73.6	8.1	2581	4	US-09-370-838-66	Sequence 66, Appli
38	73.4	8.1	1926	4	US-09-249-585A-2	Sequence 2, Appli
39	73.4	8.1	2580	3	US-09-050-863-2	Sequence 2, Appli
40	73.4	8.1	2580	4	US-09-359-081-2	Sequence 1, Appli
c 41	73.4	8.1	5452	2	US-09-130-114-1	Sequence 1, Appli
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45	73.4	8.1	10596	1	US-07-885-971-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-08-466-603-1
; Sequence 1, Application US/08466603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnada, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,603
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-466-603-1

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Query Match          91.0%; Score 825.4; DB 1; Length 1052;
Best Local Similarity 94.4%; Pred. No. 1.7e-187;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTGCAGAGAGAGAGCGC 60
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QY 781 AAGAACTGAAGATGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 812 GAGAACTGAAGATGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 871
QY 841 CTTTTTGTGATTTTACTGTTTTAGCCGATACCCCTCTCCGCCGCCCTCTAAATCCCTGCC 900
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QY 901 CCTCGAA 907
Db 932 CCTCGAA 938

RESULT 2
US-08-314-503A-1
; Sequence 1, Application US/08314503A
; Patent No. 5734022
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; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107,47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-314-503A-1

Query Match          91.0%; Score 825.4; DB 1; Length 1052;
Best Local Similarity 94.4%; Pred. No. 1.7e-187;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTGCAGAGAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTGAATTCGGCGGGCGGGAGCCCTCTGCAGAGAGAGAGCGC 91
QY 61 GAGAGATGGAGATGGGAGAGCGGATTCATTAGAGCTGCGGAACGGGACGCCCTCTGTATG 120
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QY 121 TGAAGAAGCTTGCTCGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGGCCCTCACAG 180
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QY 781 AAGAACTGAAGATGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
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Db 872 CCTATTGTGATTTGACTGTTTTTACCCATATCCCTCTCCGCCGCCCTCTAAATCCCTGCC 931
QY 901 CCTCGAA 907
Db 932 CCTCGAA 938
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; Sequence 1, Application US/08314503A
; Patent No. 5734022

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Db 932 CCCTGAA 938

RESULT 3
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; Sequence 1, Application US/08468066
; Patent No. 5756676
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,066
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97...843
; US-08-468-066-1

Query Match 91.0%; Score 825.4; DB 1; Length 1052;
Best Local Similarity 94.4%; Pred. No. 1.7e-187;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATGATTGCTGGCTGGCGGGGAGCTCTGCGAGAGAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATGATTGCTGGCTGGCGGGGAGCTCTGCGAGAGAGAGAGCGC 91
QY 61 GAGAGATGAGATGGCGACACGATTCATTAGAGCTCGGAACGGGACGCCCTCTGATG 120
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QY 301 GCCTAGAAGTATTGGCAGAAAAAGTGTCCAAACCTCATACATCTAATTTTAAAGTGGCAACA 360
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Db 392 AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAAACTCTCAAGAGCTTAG 451
QY 421 ACCTTTTTCACCTGCGAGGTAAACCACTGAACAACTACTGAGAGAAGATGTTCAAGCTCC 480
Db 452 ACCTTTTTCACCTGCGAGGTAAACCACTGAACAACTACTGAGAGAAGATGTTCAAGCTCC 511
QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAAGAGGAGGCCCTTAAGCTCGG 540
Db 512 TCCCGCAACTCACATATCTGACGGCTATGACCGGAGGAGGAGGAGGAGGAGGAGGAGT 571
QY 541 ATGGTGAGGGCTTTGTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGATGAGGAGGAGT 600
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QY 721 TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAT 780
Db 752 TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAT 811
QY 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840

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QY 901 CCCTGAA 907
Db 932 CCCTGAA 938
RESULT 4
US-08-466-717-1
; Sequence 1, Application US/08466717
; Patent No. 5874234
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5874234el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466.717
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
US-08-466-717-1
Query Match 91.0%; Score 825.4; DB 2; Length 1052;
Best Local Similarity 94.4%; Pred. No. 1.7e-187;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
QY 1 GGGTTCGGGGTTTATTGATTGAATTGCGTGGCGGAGCCCTCTCGAGAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTGAATTGCGTGGCGGAGCCCTCTCGAGAGAGAGCGC 91
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Db 272 ACTTACCAAAAGTTAAACAAACTTTAAGAAGCTTGAACCTAAGCAGTACACAGAGTCTCAGGEG 331
QY 301 GCCTAGAACCTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 332 GCCTAGAACCTATTGGCAGAAAAGTGTCCGAACCTCAGCATCTAAATTTAAGTGGCAACA 391
QY 361 AAATTAAGAACCTCAGCACAATAAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 420
Db 392 AAATTAAGAACCTCAGCACAATAAGAGCCCTGAAAAGTTAGAAAACCTCAGAGCTTAG 451
QY 421 ACCTTTTCACTTGGCAGGTTAACCAACCTGAACAACCTACTTGAGAGAGAGATGTTCAAGCTCC 480
Db 452 ACCTTTTCACTTGGCAGGTTAACCAACCTGAAACCTTACCGAGAAAATGTGTTCAAGCTCC 511
QY 481 TCCTGCAACTCACAATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTTAACTCGG 540
Db 512 TCCTGCAACTCACAATATCTCGACGGCTATGACCCGGAGCACAAGGAGGCCCTTAACTCGG 571
QY 541 ATGGTGAGGCGCTTGTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGT 600
Db 572 ATGGTGAGGCGCTACGTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGT 631
QY 601 ATGATCAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGTG 660
Db 632 ATGATCAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGTG 691
QY 661 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 692 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 751
QY 721 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 752 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 811
QY 781 AAGAACTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 812 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 871
QY 841 CCTTTTGTGATTTTACTGTTTTTAGCGGTACCCCTCTCCCGCCACACTCTAATCTCTGCC 900
Db 872 CCTATTGTGATTTGACTGTTTTTACCCTATCCCTCTCCCGCCCTCTAATCTCTGCC 931
QY 901 CCCTGAA 907
Db 932 CCCTGAA 938
RESULT 5
US-08-466-743-1
; Sequence 1, Application US/08466743
; Patent No. 6040173
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia

Db	512	TCCGCGCAACTCACATATCTCGACGGCTATGACCCGGGACGACAAGGAGGCGCCCTGACTCGG	571
Qy	541	ATGGTGAGGCGCTTTGTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGATGAGGAGGAGT	600
Db	572	ATGCTGAGGCGCTACGTGGAGGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	631
Qy	601	ATGATGAAGATGCTCAGGTTAATGGAAGATCAGGAGGACGAGGATGAGGAGGAGGAACCTG	660
Db	632	ATGATGAAGATGCTCAGGTTAGTGGAGACGAGGAGGACGAGGATGAGGAGGAGGAGGTTG	691
Qy	661	AAGGAGGAGCGTGCAGTGGGAGACGAGGAGGAGAGGATGAAGGTTTATAACAATGGAGAGG	720
Db	692	AAGGAGGAGCGTGCAGTGGGAGAGGAGGAGGAGGATGAAGAAGGTTATAACGATGGAGAGG	751
Qy	721	TAGATGATGAGGAAGATGAGAGAGAGCTTCGTGAGAGAGAAAGGGGTGAGAAAGGAGAAAT	780
Db	752	TAGATGACGAGGAAGATGAAGAGAGAGCTTCGTGAAGAGAAAGAGGGGTGAGAAAGGAGAAAC	811
Qy	781	AAGAAACTGAAGATGAGGAGAGACGACCATGCCCTAAGTGAATTAATCTATTTTGAAAAATT	840
Db	812	GAGAACCTGAAGATGAGGGAGAGAGATGATGACTAAGTGGAAATTAACCTATTTTTGAAAAATT	871
Qy	841	CCTTTTGTGATTTTACTGTTTTTACCGCGTACCCCTCTCCCGCCCCCCTCTAATCTCCTGCC	900
Db	872	CCTATTGTGATTTGACTGTTTTTACCACATATCCCTCTCTCCCGCCCCCCTCTAATCTCCTGCC	931
Qy	901	CCCTGAA	907
Db	932	CCCTGAA	938

```

RESULT 6
PCT-US95-12414-1
: Sequence 1, Application PC/TUS9512414
: GENERAL INFORMATION:
: APPLICANT: Pasternack, Gary R.
: APPLICANT: Kuhajda, Francis P.
: TITLE OF INVENTION: Novel Mammalian Protein Associated with
: TITLE OF INVENTION: Uncontrolled Cell Division
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner & Allegretti, Ltd.
: STREET: 1001 G Street, N.W.
: CITY: Washington, D.C.
: STATE: District of Columbia
: COUNTRY: U.S.A.
: ZIP: 20001
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/12414
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/314,503
: FILING DATE: 22-SEP-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Hoscheit Esq., Dale H.
: REGISTRATION NUMBER: 19,090
: REFERENCE/DOCKET NUMBER: 1107.51507
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202 508-9153
: TELEFAX: 202 508-9299
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1052 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA

```


; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: mus sp
US-08-466-717-3

Query Match 64.5%; Score 585; DB 2; Length 980;
Best Local Similarity 83.0%; Pred. No. 2.5e-130;
Matches 693; Conservative 0; Mismatches 135; Indels 7; Gaps 2;
QY 50 AGAGAGCGCGAGAGATGGGAGATGGGAGCGGATTCATTTAGAGCTCGGGAACGGAC 109
Db 10 AGAGAGCGCGAGAGATGGGAGATGGGAGCGGATTCATTTAGAGCTCGGGAACGGAC 69
QY 110 GCCCTCTGATGTAAGAACTTTCCTGGCAACAGTCGGTTCGAATGAAGCAAACTCGA 169
Db 70 GCCCTCTGATGTAAGAACTTTCCTGGCAACAGTCGGTTCGAATGAAGCAAACTCGA 129
QY 170 AGGCCTCAGATGAATTTGAAGAACTTTCGAATGAAGCAAACTTCGAATGAAGCAAACT 229
Db 130 AGGCCTCAGATGAATTTGAAGAACTTTCGAATGAAGCAAACTTCGAATGAAGCAAACT 189
QY 230 CTCATTCGCAAACTTACCAAGTTAAACAAACTTAAAGAACTTGAATGAAGCAAACT 289
Db 190 CTCATTCGCAAACTTACCAAGTTAAACAAACTTAAAGAACTTGAATGAAGCAAACT 249
QY 290 AGCCTCAGTGGGCTTAGAAGTATTTGGCAGAAAAGTGTCCAAACCTTCAATCTAAATTT 349
Db 250 AGCCTCAGTGGGCTTAGAAGTATTTGGCAGAAAAGTGTCCAAACCTTCAATCTAAATTT 309
QY 350 AAGTGGCAACAAATTAAGAACTTCAGCAATAGAGCCCTGAAAAGTTAGAAACCT 409
Db 310 AAGTGGCAACAAATTAAGAACTTCAGCAATAGAGCCCTGAAAAGTTAGAAACCT 369
QY 410 CGAGAGCTTAGACCTTTTCACTTGGAGTAAACAACTTGAAGAACTTGAATGAAGCAAACT 469
Db 370 CGAGAGCTTAGACCTTTTCACTTGGAGTAAACAACTTGAAGAACTTGAATGAAGCAAACT 429
QY 470 GTTCAAGCTCCTCCTCAACTACATATCTCAACGGCTGTGACCCGGATGACAGGAGGC 529
Db 430 GTTCAAGCTCCTCCTCCTCAACTACATATCTCAACGGCTGTGACCCGGATGACAGGAGGC 489
QY 530 CCCTAAGCTCGATGGTGGGCTTTTGGAGTGCCTGGATGACAGGAGGAGGATGAGGA 589
Db 490 CCCCAGCTCCGATGTTGAGGGCTACGTGGA-----GGAAGCAGCAGGAGGATGAGGA 543
QY 590 TGAGGAGGATGATGATCAAGATGCTCAGGTATGGAAGATGAGGAGGAGGATGAGGA 649
Db 544 TGAGGAGGATGATGATCAAGATGCTCAGGTATGGAAGATGAGGAGGAGGATGAGGA 603
QY 650 GGAGGAACGTGAAGAGGAGCTGAGTGGAGCAGGAGGAGGAGGATGAGGATGATAA 709
Db 604 GGAAGAGGAGGAGGAGGAGGATGAGTGGAGGAGGAGGAGGAGGATGAGGAGGATGATAA 663
QY 710 CAATGGAGGATGATGATGAGGAGGATGAGGAGGAGGATGAGGAGGAGGATGAGGAT 769
Db 664 TGACGGGAGGATGATGATGAGGAGGAGGAGGAGGAGGATGAGGAGGAGGATGAGGAT 723
QY 770 GAAGCGAAATTAAGAACTTGAAGATGAGGAGGAGGAGGATGAGGATGAGGATGATAT 829
Db 724 GAAGCGAAATTAAGAACTTGAAGATGAGGAGGAGGAGGATGAGGATGAGGATGATAT 782
QY 830 TTGGAATAATCCTTTTGTGATTTTACTGTTTACTGCGTACCCCTCTCCCTCC 884
Db 783 TTGGAATAATCCTTTTGTGATTTTACTGTTTACTGCGTACCCCTCTCCCTCC 837

RESULT 11
US-08-466-743-3
; Sequence 3, Application US/08466743
; Patent No. 6040173
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.

APPLICANT: Kuhajda, Francis P.
TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,743
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: mus sp
US-08-466-743-3

Query Match 64.5%; Score 585; DB 3; Length 980;
Best Local Similarity 83.0%; Pred. No. 2.5e-130;
Matches 693; Conservative 0; Mismatches 135; Indels 7; Gaps 2;
QY 50 AGAGAGCGCGAGAGATGGGAGATGGGAGCGGATTCATTTAGAGCTCGGGAACGGAC 109
Db 10 AGAGAGCGCGAGAGATGGGAGATGGGAGCGGATTCATTTAGAGCTCGGGAACGGAC 69
QY 110 GCCCTCTGATGTAAGAACTTTCCTGGCAACAGTCGGTTCGAATGAAGCAAACTCGA 169
Db 70 GCCCTCTGATGTAAGAACTTTCCTGGCAACAGTCGGTTCGAATGAAGCAAACTCGA 129
QY 170 AGGCCTCAGATGAATTTGAAGAACTTTCGAATGAAGCAAACTTCGAATGAAGCAAACT 229
Db 130 AGGCCTCAGATGAATTTGAAGAACTTTCGAATGAAGCAAACTTCGAATGAAGCAAACT 189
QY 230 CTCATTCGCAAACTTACCAAGTTAAACAAACTTAAAGAACTTGAATGAAGCAAACT 289
Db 190 CTCATTCGCAAACTTACCAAGTTAAACAAACTTAAAGAACTTGAATGAAGCAAACT 249
QY 290 AGCCTCAGTGGGCTTAGAAGTATTTGGCAGAAAAGTGTCCAAACCTTCAATCTAAATTT 349
Db 250 AGCCTCAGTGGGCTTAGAAGTATTTGGCAGAAAAGTGTCCAAACCTTCAATCTAAATTT 309
QY 350 AAGTGGCAACAAATTAAGAACTTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 409
Db 310 AAGTGGCAACAAATTAAGAACTTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 369
QY 410 CGAGAGCTTAGACCTTTTCACTTGGAGTAAACAACTTGAAGAACTTGAATGAAGCAAACT 469
Db 370 CGAGAGCTTAGACCTTTTCACTTGGAGTAAACAACTTGAAGAACTTGAATGAAGCAAACT 429

QY 470 GTTCAAGCTCTCTGCAACTCACATATCTCAACGGGTGTGACCCCGGTGTGACCAAGGAGC 529
Db 430 GTTCAAGCTCTCTGCCAGGTCTATGTTACCTCGATGCTATGACAGGCAACAAGGAGC 489
QY 530 CCCTAACTCGGATGGTGGGGCTTTGGGAGTGCCTGGATGACAAAGGAGGAGATGAGGA 589
Db 490 CCCGACTCCGATGTTGAGGGCTACGTGGA-----GGATGACGAGGAGGAGATGAGGA 543
QY 590 TGAGGAGGATGATGAAGATGCTCAGGTAAATGGAGATGAGGAGGAGGAGGATGAGGA 649
Db 544 TGAGGAGGATGATGAATATGCCAGCTAGTGGAGATGAGGAGGAGGAGGATGAGGA 603
QY 650 GGAGGAAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 709
Db 604 GGAAGAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663
QY 710 CAATGGAGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 769
Db 664 TGAGGAGGAGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 723
QY 770 GAAGCGAAATATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 829
Db 724 GAAGCGAAATATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 782
QY 830 TTTGAAATATCTCTTTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCCC 884
Db 783 TTGGGAAATCTCTATGTGATTTGCTGTTTACCCTATCCCTCCCTCC 837

RESULT 12

PCT-US95-12414-3

; Sequence 3, Application PC/TUS9512414

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kuhnaja, Francis P.

; TITLE OF INVENTION: Novel Mammalian Protein Associated With

; TITLE OF INVENTION: Uncontrolled Cell Division

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner & Allegretti, Ltd.

; STREET: 1001 G Street, N.W.

; CITY: Washington, D.C.

; STATE: District of Columbia

; COUNTRY: U.S.A.

; ZIP: 20001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/12414

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/314,503

; FILING DATE: 22-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Hoscheit Esq., Dale H.

; REGISTRATION NUMBER: 19,090

; REFERENCE/DOCKET NUMBER: 1107.51507

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 508-9153

; TELEFAX: 202 508-9299

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 980 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: mus sp

PCT-US95-12414-3

Query Match 64.5%; Score 585; DB 5; Length 980;
Best Local Similarity 83.0%; Pred. No. 2.5e-130;
Matches 693; Conservative 0; Mismatches 135; Indels 7; Gaps 2;

QY 50 AGAGAGAGCGGAGAGATGGAGATGGCGACAGCGATTCATTATTAGAGTCGCGAAGCGGAC 109
Db 10 AGAGAGAGCGGAGAGATGGAGATGGCGAAGCGGATTCATTATTAGAGTCGCGAAGCGGAC 69
QY 110 GCCTCTGTGATGTGAAAGAACTTGTCTCGACAACTGCTCGTCAAGTGAAGTGAAGTGAAGTGA 169
Db 70 GCCTCTGTGATGTGAAAGAACTTGTCTCGTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 129
QY 170 AGGCCTCACAGATGAATTTGAAGAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 229
Db 130 AGGCCTCACAGATGAATTTGAAGAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 189
QY 230 CTCAATCGCAAACTTACCAAACTTAAACAACTTAAAGAACTTAAAGAACTTAAAGAACTTAA 289
Db 190 CTCAATCGCAAACTTACCAAACTTAAACAACTTAAAGAACTTAAAGAACTTAAAGAACTTAA 249
QY 290 AGCCTCAGTGGGCTAGAAATTTGGCAGAAAAGTGTCCAAACCTTCAACATCATACATCTAAATTT 349
Db 250 AATCTCAGGGGACTGGAAATTTGGCAGAAAAGTGTCCAAACCTTCAACATCATACATCTAAATTT 309
QY 350 AAGTGCACAAATTAAGACCTCAGCACAAATAGAGCCCTGAAACCTTGAAGTGAAGTGAAGTGAAG 409
Db 310 AAGTGCACAAATTAAGACCTCAGCACAAATAGAGCCCTGAAACCTTGAAGTGAAGTGAAGTGAAG 369
QY 410 CGAGAGCTTAGACCTTTTCACTTGGAGGTAAACCACTTAAACCACTTAAACCACTTAAACCACT 469
Db 370 CAAGAGCTTAGACCTTTTCACTTGGAGGTAAACCACTTAAACCACTTAAACCACTTAAACCACT 429
QY 470 GTTCAAGCTCTCTCGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAGGAGGAGC 529
Db 430 GTTCAAGCTCTCTCGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAGGAGGAGC 489
QY 530 CCCTAACTCGGATGGTGGGGCTTTGTGAGCTGCTGGATGACAGGAGGAGGAGGATGAGGA 589
Db 490 CCCTAACTCGGATGGTGGGGCTTTGTGAGCTGCTGGATGACAGGAGGAGGAGGATGAGGA 543
QY 590 TGAGGAGGATGATGAAGATGCTCAAGTAAATGGAAGATGAGGAGGAGGAGGAGGATGAGGA 649
Db 544 TGAGGAGGATGATGAAGATGCTCAAGTAAATGGAAGATGAGGAGGAGGAGGAGGATGAGGA 603
QY 650 GGAGGAACCTGAAGAGGAGGAGGAGTGGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 709
Db 604 GGAAGAGGAGGAGGAGGAGGAGTGGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663
QY 710 CAATGGAGGATGATGAGGAGGAGGAGTGGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 769
Db 664 TGAGGAGGAGGATGATGAGGAGGAGGAGTGGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 723
QY 770 GAAGCGAAATATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 829
Db 724 GAAGCGAAATATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 782
QY 830 TTTGAAATATCTCTTTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCCC 884
Db 783 TTGGGAAATCTCTATGTGATTTGCTGTTTACCCTATCCCTCCCTCCCTCC 837

RESULT 13

US-08-466-603-4

; Sequence 4, Application US/08466603

; Patent No. 5726018

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kuhnaja, Francis P.

; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With

; TITLE OF INVENTION: Uncontrolled Cell Division

; NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466.603
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORGANISM: Mus sp
FEATURE:
NAME/KEY: CDS
LOCATION: 3..548
US-08-466-603-4

Query Match 44.7%; Score 405; DB 1; Length 759;
Best Local Similarity 80.4%; Pred. No. 1.5e-87;
Matches 501; Conservative 0; Mismatches 115; Indels 7; Gaps 2;

QY 262 TTAAGAAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGGCCCTAGAGTATTGGCAGAAA 321
DB 4 TCAAGAAGCTTGAATTAAGCGAAACAGAACTCTCAGGGGACCTGGAAGTATTGGCAGAGA 63
QY 322 AGTGTCACAAACCTCATACATCTAAATTTAAGTGGCAACAAATTAAGAGCTTCAGCACAA 381
DB 64 AATGTCGGAACCTTAAGCATCTAAATTTAAGTGGCAACAAATTAAGAGCTTCAGCACAA 123
QY 382 TAGAGCCCTGAAAGAGTTAGAAACCTCGAGAGCTTAGACCTTTTACATTCGCGAGTAA 441
DB 124 TAGAGCCCTGAAAGAGTTAGAAATCTCAAGAGCTTAGACCTTTTAACTGTGAGGTGA 183
QY 442 CCAACCTGAACAACTACTGAGAGAGAGATGTTCAAGCTCTCTCCGCACTCACATATCTCA 501
DB 184 CCAACCTGAATGCCTACCGAGAAACGTTGTTCAAGCTCTCTCCGCACTCACATATCTCA 243
QY 502 ACGGCTGTACCCGATGACAGAGAGCCCTCACTCGGATGGTGGGCTTTGTGGAGT 561
DB 244 ATGGCTATGACAGGAGCAACAGAGGAGCCCGGACTCCGATGTTGAGGGCTACGTGA-- 301
QY 562 GCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGTAA 621
DB 302 ---GGATGACGACGAGGAGGATGAGGATGAGGAGGAGTATGATGAATATGCCAGCTAG 357
QY 622 TGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 681
DB 358 TGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
QY 682 ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 741

DB 418 AGGAGGAGGAGGATGAGGAAGTTTACAATCAGCGGGAAGTGGATGAGGAGGAAGCAAG 477
QY 742 AAGAGCTTGGTGAAGAGAAAGGGGTCAGAGCGGAAATAAGAACTGAAGATGAGGGAG 801
DB 478 AAGAAGCTGGTGAAGAGAAAGGGGAGTCAGAGCGGAAACGAGACCGGAGGAGGGCG 537
QY 802 AAGAGGATGCTTAAGTGAATATCTATTGAAAAATTCCTTTTGTGATTTACTGTTT 861
DB 538 AAGAGGATGACTAAG-GAATGAACCTGTTTGGGGAATTCCTATTGTCATTGACTGTTT 596
QY 862 TTAGCCGTACCCCTCTCCCTCC 884
DB 597 TTACCATATCCCTCCCTCC 619
RESULT 14
US-08-314-503A-4
Sequence 4, Application US/08314503A
Patent No. 5734022
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kujada, Francis P.
TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,503A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 759 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORGANISM: Mus sp
FEATURE:
NAME/KEY: CDS
LOCATION: 3..548
US-08-314-503A-4

Query Match 44.7%; Score 405; DB 1; Length 759;
Best Local Similarity 80.4%; Pred. No. 1.5e-87;
Matches 501; Conservative 0; Mismatches 115; Indels 7; Gaps 2;

QY 262 TTAAGAAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGGCCCTAGAGTATTGGCAGAAA 321
DB 4 TCAAGAAGCTTGAATTAAGCGAAACAGAACTCTCAGGGGACCTGGAAGTATTGGCAGAGA 63
QY 322 AGTGTCACAAACCTCATACATCTAAATTTAAGTGGCAACAAATTAAGAGCTTCAGCACAA 381

Db 64 AATGTCGAACCTTAAGCATCTAAATTTAAGTGGCAACAAAATAAAGATCTCAGCACAA 123
QY 382 TAGAGCCCTGAAAAGCTTAGAAAACCTCGAGAGCTTAGACCTTTTACCTTGGCAGGTAA 441
Db 124 TAGAGCCGCTGAAGAAGCTTAGAGAATCTCAAGAGCCTAGACCTGTTAACTGTGAGGTGA 183
QY 442 CCAACCTGAACTACTAGAGAGAGATGTTCAAGCTTCTCCTGCAACTCACATATCTCA 501
Db 184 CCAACCTGAACTACTAGAGAGAGATGTTCAAGCTTCTCCTGCAACTCACATATCTCA 501
QY 502 ACGGCTGTGACCCGGATGACAAAGGAGGCCCTAACTCGGATGCTGAGGGCTTTGTGGAGT 561
Db 244 ATGCTATGACAGGACAAACAGAGAGGCCCTGACCTGATGTTGAGGGCTAGCTGGA-- 301
QY 562 GCCTGGATGACAGGAGGAGATGAGATGAGGAGGAGTATGATGAAGATGCTCAGGTAA 621
Db 302 ----GGATGACGAGGAGAGATGAGATGAGGAGGAGTATGATGAATGATGCCACCTAG 357
QY 622 TGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 681
Db 358 TGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
QY 682 ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 741
Db 418 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477
QY 742 AAGAGCTTGTGAG 801
Db 478 AAGAGCTTGTGAG 801
QY 802 AAGAGCTTGTGAG 861
Db 538 AAGAGCTTGTGAG 861
QY 862 TTAGCCGTACCCCTCTCCCTCC 884
Db 597 TTACCATATCCCTCCCTCCCTCC 619

RESULT 15

US-08-468-066-4

; Sequence 4, Application US/08468066
; Patent No. 5756676
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated with
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,066
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Mus sp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..548
US-08-468-066-4

Query Match 44.7%; Score 405; DB 1; Length 759;

Best Local Similarity 80.4%; Pred. No. 1.5e-87;

Matches 501; Conservative 0; Mismatches 115; Indels 7; Gaps 2;

QY 262 TTAAGAAGCTTGAACCTAACAGCAGTACAGAGCCTCAGTGGGCTTAGAAGTATTGGCAGAAA 321
Db 4 TCAGAAGCTTGAATTAAGCGAAACAGAATCTCAGGGACCTGGAAGTATTGGCAGAGA 63
QY 322 AGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAAATTTAAAGACCTCAGCACAA 381
Db 64 AATGTCCGAACCTTAAGCATCTAAATTTAAGTGGCAACAAAATTTAAAGTCTCAGCACAA 123
QY 382 TAGAGCCCTGAAAAGTTGAAAACCTCGAGAGCTTAGACCTTTTCACTTGGCAGGTAA 441
Db 124 TAGAGCCGCTCAAGAAGTTTAGAGAATCTCAAGAGCCTTAGACCTGTTTAACTGTGAGGTGA 183
QY 442 CCAACCTGAACAACCTACTCTGAGAGAGATGTTCAAGCTTCTCCTGCAACTCACATATCTCA 501
Db 184 CCACCTGAATGCTCTACGAGAAACGTTTCAAGCTTCTCCTGCAACTCACATATCTCA 501
QY 502 ACGGCTGTGACCCGGATGACAAAGGAGGCCCTTAACTCGGATGTTGAGGGCTTTGTGGAGT 561
Db 244 ATGGCTATGACAGGCAACAAGAGAGGCCCTCCGATGTTGAGGGCTACGTGGA-- 301
QY 562 GCCTGGATGACAGGAGGAGGATGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 621
Db 302 ----GGATGACGAGGAGGAGGATGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 357
QY 622 TGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 681
Db 358 TGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 417
QY 682 ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 741
Db 418 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 477
QY 742 AAGAGCTTGTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 801
Db 478 AAGAGCTTGTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 537
QY 802 AAGAGCTTGTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 861
Db 538 AAGAGGATGACTAAG-GAATGAACCTGTTTGGGGAATTCCTATTCTGATTGACATGTTT 596
QY 862 TTAGCCGTACCCCTCTCCCTCC 884
Db 597 TTACCATATCCCTCCCTCCCTCC 619

Search completed: December 8, 2002, 23:19:39

Job time : 43.3808 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 22:43:58 ; Search time 41.4109 Seconds
(without alignments)
8540.478 Million cell updates/sec

Title: US-09-591-500-4

Perfect score: 907

Sequence: 1 ggggtcgggtttattgatt.....ctctaactcgcgccttga 907

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700950

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA.*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
1	217.8	24.0	718	10	US-09-910-943-76
2	215.4	23.7	771	10	US-09-910-943-166
3	214	23.6	748	10	US-09-910-943-132
4	188.4	20.8	763	10	US-09-910-943-622
5	124.6	13.7	557	9	US-10-046-935-2145
6	124.6	13.7	557	9	US-09-878-178-2145
7	119.8	13.2	720	9	US-10-101-487-74
8	119.8	13.2	720	9	US-10-101-487-76
9	117.4	12.9	554	9	US-10-101-487-69
10	117.4	12.9	554	9	US-10-101-487-106
11	115.6	12.7	522	9	US-10-101-487-71
12	115.6	12.7	530	9	US-10-101-487-73
13	106	11.7	575	10	US-09-864-761-20733
14	106	11.7	1969	10	US-09-864-761-3972
15	101	11.1	659158	9	US-09-771-208-20
16	91.8	10.1	423	10	US-09-864-761-18355
17	91.8	10.1	487	10	US-09-864-761-1597
18	91.4	10.1	3809	12	US-10-001-870-68
19	89.8	9.9	474	10	US-09-864-761-11284

c	20	89.6	9.9	267	10	US-09-864-761-27984	Sequence 27984, A
c	21	89.4	9.9	344	10	US-09-864-761-19694	Sequence 19694, A
c	22	89.4	9.9	700	10	US-09-864-761-17529	Sequence 17529, A
c	23	85.4	9.4	1944	10	US-09-864-761-2825	Sequence 2825, Ap
c	24	85	9.4	53226	10	US-09-818-264-3	Sequence 3, Appli
c	25	83.2	9.2	350	10	US-09-822-263-19	Sequence 19, Appl
c	26	83.2	9.2	381	10	US-09-777-564-700	Sequence 700, App
c	27	83.2	9.2	399	10	US-09-864-761-2913	Sequence 2913, Ap
c	28	82	9.0	5387	9	US-10-001-873-22	Sequence 22, Appl
c	29	81.8	9.0	583	10	US-09-864-761-20772	Sequence 20772, A
c	30	81.8	9.0	1959	10	US-09-864-761-4012	Sequence 4012, Ap
c	31	81.6	9.0	299	10	US-09-864-761-21553	Sequence 21553, A
c	32	81.6	9.0	345	10	US-09-822-263-17	Sequence 17, Appl
c	33	81.6	9.0	497	10	US-09-822-263-33	Sequence 33, Appl
c	34	81.6	9.0	1147	10	US-09-880-107-2311	Sequence 2311, Ap
c	35	80.4	8.9	390	10	US-09-790-399-7	Sequence 7, Appli
c	36	80	8.8	490	10	US-09-880-107-2261	Sequence 2261, Ap
c	37	80	8.8	497	10	US-09-822-263-35	Sequence 35, Appl
c	38	80	8.8	766	10	US-09-864-761-19608	Sequence 19608, A
c	39	79.6	8.8	327	10	US-09-864-761-28059	Sequence 28059, A
c	40	79.2	8.7	1282	9	US-10-002-344A-89	Sequence 89, Appl
c	41	78.8	8.7	4316	10	US-09-880-107-3713	Sequence 3713, Ap
c	42	78.4	8.6	251	10	US-09-864-761-19674	Sequence 19674, A
c	43	78.2	8.6	276	10	US-09-864-761-20595	Sequence 20595, A
c	44	77.8	8.6	465	10	US-09-864-761-23120	Sequence 23120, A
c	45	77.6	8.6	305	10	US-09-864-761-19262	Sequence 19262, A

ALIGNMENTS

RESULT 1

US-09-910-943-76
; Sequence 76, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/IG148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(718)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-76

Query Match 24.0%; Score 217.8; DB 10; Length 718;
Best Local Similarity 61.8%; Pred. No. 5.1e-42;
Matches 364; Conservative 0; Mismatches 222; Indels 3; Gaps 1;

QY	64	AGATGGAGATGGCGACGCGATTTCATTATAGCTCGGAAACGGGACGCCCTCTGTATGTGA	123
Db	132	ACATGGACATGAAAAGAGATTGATGCTGGAGCTCAGGAATCGGAAAGCGGCTGACGCTA	191
QY	124	AAGAATTGCTTGGACACACAGTCGGTCGAATGAAGCAAACTCGAAGGCTTCACAGATG	183
Db	192	AAGAATTGTTCTAGATAACTGCCGTTTCAGACGATGCAAAATTTATTGGACTGACCTAG	251
QY	184	AATTGAAGAACTGGATTCTTAAAGTACATCAACTAGGCGCTCACCTCAATCGCAACT	243
Db	252	AGTTTGAACCTGGAGTTTCTCAGCATGATAAATGTCACATTATTATCTGTAGCTAACT	311
QY	244	TACCAAGTTTAAACAACCTTGAAGCTTGAACCTAAGACAGTAAACAGAGCTCAGTGGGC	303
Db	312	TGCCAAGCTCCCAAGTTGAAAAGCTGGAACCTCAGTGACATCGAATCTCTGTGGAGAT	371

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QY 304 TAGAAGATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAA 363
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Db 372 TAGAGGTACTGGCAGAACGGACCCCAAAATTTGACACACCTGAACCTCAGTGGGAACAAGA 431
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 364 TTAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAGACC 423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 432 TAAAGAGATAAATACCTTAGAGCCACTTAAGAAACTACCTCATCTCATGATCTGGACC 491
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 424 TTTTCACTTGGCAGGTAACCAACCTGAACAACTACTGTAGAGAAAGATGTTCAAGCTCTCC 483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 492 TCTTTAACTGTGAGTGACCATGCTTAACAACCTACAGGAGAGTGTGTTGAATCTTCC 551
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 484 TGCAACTCATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTCAACTCGGATG 543
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 552 CTAAGCTTACCTTTTAGATGGTTTGTATGCAGATGACCAAGGAGCTCCAGATTCTGATC 611
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 544 GTGAGGCTTTGTGGAGTCCCTGGATGACAGCAAGGAGGAGTGAAGTGAAGGATG 603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 604 ATGAGATGCTCAGGTAATGGAAGATGAGGAGGACGAGGATGAGGAGGA 652
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Db 669 ATGAAGAAGAAGAATTTGAAGATGAGCTTGATGATGAGGATGAAGA 717
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RESULT 2

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US-09-910-943-166
; Sequence 166, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/1G148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 166
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(771)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-166
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Query Match 23.7%; Score 215.4; DB 10; Length 771;
Best Local Similarity 62.0%; Pred. No. 1.9e-41;
Matches 375; Conservative 0; Mismatches 223; Indels 7; Gaps 2;
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Db 153 ACATGGACATGAAAAGAGATTGATGCTGGAGCTCAGGAATCGGAAGCGCTGACGCTA 212
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 124 AAGAATTGCTTCTGACACACAGTCGGTGAATGAAGGCAAACTCGAAGGCCCTCAGAGATG 183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 213 AAGAATTGCTTCTAGATAACTGCCGTTTCAGACGATGGCAAAATATTGGACTGACCTCAG 272
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 184 AATTTGAAGAAGTGAATCTTAAGTACAATCAAGTGAAGGCCCTCACCTCAATCGCAACT 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 273 AGTTTGAAGGCTGGAGTTTCTCAGCATGATAAATGTCAACTTATTATCTGTAGCTAACT 332
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 244 TACCAAGTTAAACAACTTAAGAAGCTTGAAGCTTAAGCAGTAACAGAGCCTCAGTGGGCC 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 333 TGCCAAAGCTCCCAAGTTGAAAAGCTGGAACTCAGTGACAATCGAATCTCTGGAGAT 392
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 304 TAGAAGTATGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAA 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 393 TAGAGGTACTGGCAGAACGGACCCCAAAATTTGACACACCTGAACCTCAGTGGGAACAAGA 452
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QY 364 TTAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAGACC 423
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Db 453 TAAAGAGATAAATACCTTAGAGCCACTTAAGAAACTACCTCATCTCATGAGTCTGGACC 512
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QY 424 TTTTCACTTGGCAGGTAACCAACCTGAACAACTACTGTAGAGAAAGATGTTCAAGCTCTCC 483
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QY 544 GTGAGGCTTTGTGGAGTCCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGATG 603
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Db 690 ATGAAGAAGAAGAATTTGAAGATGAANCTTGTATGATGAGGATGAANAATGAGGAGGT 749
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Db 750 GAAAA 754
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RESULT 3

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US-09-910-943-132
; Sequence 132, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/1G148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 132
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(748)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-132
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Query Match 23.8%; Score 214; DB 10; Length 748;
Best Local Similarity 61.7%; Pred. No. 4e-41;
Matches 359; Conservative 0; Mismatches 220; Indels 3; Gaps 1;
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Db 132 ACATGGACATGAAAAGAGATTGATGCTGGAGCTCAGGAATCGGAAGCGGCTGACGCTA 191
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QY 124 AAGAATTGCTTCTGGAACAACAGTCGGTGAATGAAGGCAAACTCGAAGGCCCTCAGAGATG 183
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Db 192 AGAATTGGTCTTAGATAACTGCGGTTTCAGACGATGGCAAAATATTGGACTGACCTCAG 251
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 184 AATTTGAAGAAGTGAATCTTAAGTACAATCAACGTAGGCCCTCACCTCAATGGCAAACT 243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 252 AGTTTGAAGGCTGGAGTTTCTCAGCATGATAAATGTCAACTTATTATCTGTAGCTAACT 311
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 244 TACCAAGTTAAACAACCTTAAGAAGCTTGAAGCTTAAGCAGTAACAGAGCCTCAGTGGGCC 303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 312 TGCCAAAGCTCCCAAGTTGAAAAGCTGGAACTCAGTGACAATCGAATCTCTGGAGGAT 371
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QY 304 TAGAAGTATTTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAA 363
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Db 372 TAGAGGTACTGGCAGAACGGACCCCAAAATTTGACACACCTGAACCTCAGTGGGAACAAGA 431
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QY 364 TTAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAGACC 423
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Db 432 TAAAGAGATAAATACCTTAGAGCCACTTAAGAAATACCTCATCTCATGAGTCTGGACC 491
QY 424 TTTTCACTTGCAGGTAACCAACCTGAACAACCTACTTGAGAGAGAGATGTTCAAGCTCTCTCC 483
Db 492 TCFTTAACTGTGAGGTGACCATGCTTAACAACCTACAGGAGAGATGTTTGTGAACCTCTCC 551
QY 484 TGCACCTACATATCTCAACGGGTGTGACCCGGATGACAAAGAGAGCCCTTAACCTCGATG 543
Db 552 CTAAGCTTACCTTTTGTAGATGTTTGTGATGCAGATGACCAAGAGGCTCCAGATCTCTGATC 611
QY 544 GTGAGGCTTTGTGAGTGCCTGGATGACAAGAGAGAGATGAGGATGAGGAGGATG 603
Db 612 CAGAGG---CTGAAGATTAGAGGAAATGAGAGAGATGTTGAGGAGGATGAAGAAGATG 668
QY 604 ATGAAGATGCTCAGGTAATGGAAGATGAGGAGGACGAGGATG 645
Db 669 ATGAAGAGAAGAAGAAATTGAAGATGAGCTTGATGATGAGG 710
RESULT 4
US-09-910-943-622
; Sequence 622, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/1G148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 622
; LENGTH: 763
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(763)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-622

Query Match 20.88; Score 188.4; DB 10; Length 763;
Best Local Similarity 60.28; Pred. No. 4e-35;
Matches 342; Conservative 0; Mismatches 222; Indels 4; Gaps 2;
QY 64 AGATGGAGATGGCAGACGGGATTCATTTAGAGCTGCGGAACGGGACGCCCTCTGATGTA 123
Db 134 ACATGGACATGAAAAGAGATTGATGCTGGAGCTCAGGAATCGGAAAGCGGCTGACGCTA 193
QY 124 AAGAATCTGCTGGACAACAGTCGGTGCATGAAGGCAAACTCGAAGGCTTCACAGATG 183
Db 194 AAGAATGTTCTAGATAACTGCCGTTTCAGACGATGCGCAAAATATTGGAGTGCACCTCAG 253
QY 184 RAATTTGAAGAACTGGAATCTTAAGTACAATCAACGTAGGCTCACCTCAATCGCAAACT 243
Db 254 AGTTTGAAGCTGAGGTTTCTCAGCATGATAAATGTCAACTTATATCTGTAGCTAACT 313
QY 244 TACCAAACTTAACAACTTAAGAAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGGGCC 303
Db 314 TGCCAAAGCTCCCAAGTTGAAAAGCTGGAACCTCAGTGACAATCGAATCTCTGGAGAT 373
QY 304 TAGAAGTATGGCAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAA 363
Db 374 TAGAGGTACTGCGACAGCGGACCCCAAAATTTGACACACTGAACCTCAGTGGGACAGA 433
QY 364 TTAAGACCTCAGCACAATAGAGCCCTGAAAAGCTTAGAAAACCTCGAGAGCTTAGACC 423
Db 434 TAAAGAGATAAATACCTTAGAGCCACCTTAAGAAACTACCTCATCTCATGATGCTGGACC 493
QY 424 TTTTCACTTGCAGGTAAACCAACTGACAACCTACTTGAGAGAGATGTTCAAGCTCTCTCC 483

Db 494 TCFTTAACTGTGAGGTGACCATGCTAAACAACCTACAGGAGAGTGTTTTTTGAACCTCTCC 553
QY 484 TGCACCTACATATCTCAACGGCTGTGACCGGATGACAAGGAGGCCCTTAACCTCGGATG 543
Db 554 T-AAGCTTACCTTTTGTAGATGTTTGTATGCANATGACCAGGANGCTCCAGATTTCTGATC 612
QY 544 GTGAGGCTTTGTGAGTGCCTGGATGACAAGAGGAGGATGAGGATGAGGAGGATG 603
Db 613 CAGAG---CTGAAGAATTANAGGAAATGAGAGGATGGTGAGGAGATGAANAATG 669
QY 604 ATGAAGATGCTCAGGTAATGGAAGATGA 631
Db 670 TGAAGAAGAAGAATAATTTGGAAGATGA 697
RESULT 5
US-10-046-935-2145
; Sequence 2145, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yudi
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2145
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-2145

Query Match 13.7%; Score 124.6; DB 9; Length 557;
Best Local Similarity 57.3%; Pred. No. 2.9e-20;
Matches 248; Conservative 0; Mismatches 179; Indels 6; Gaps 1;
QY 378 ACAATAGAGCCCTGAAAAGTTAGAAAACCTCGGAGAGCTTAGACCTTTTCACTTCCGAG 437
Db 1 ACAGTAGAAGCTCTGCAAAATCTTAAAAATTTGAAAAGTCTTGACCTGTTTAACTGTGAG 60
QY 438 GTAACCAACCTGACAACTACTAGAGAGATGTTTCAAGCTCCTCTGCAACTCACATAT 497
Db 61 ATCACAACCTGGAAGATTATAGAGAAAGTATTTTGAACCTACTGAGCAATCACATAC 120
QY 498 CTCACGGCTGTGACCCGGATGACAAGAGGCGCCCTTAACCTCGGATGGTGAGGGCTTTGTG 557
Db 121 TTAGATGGATTTTCATCAGGAGGATAATGAAGCGCGGACTCTGAGAGGAGGATGATGAG 180
QY 558 GAGTGCCTGATGACAAGAGGAGGATGAGGATGAGGATGAGGAGGATGATGAGGATGAT 611
Db 181 GATGGGATGAAGATGATGAAGAGGAGGAGGAGGAGGATGAGGATGAGGATGAGGATGAT 240
QY 612 GCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGATGAGGATGAGGAT 671
Db 241 GAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGATGAGGATGAGGATGAGGATGAG 300
QY 672 GTGAGTGGAGCAGGAGGAGGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 731
Db 301 CGAGGTTTCAAGTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 732 GAAGATCAAGAGAGCTTTGTTGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 791
Db 361 GAAATTCAGGATGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 792 GATGAGGAGGAG 804
Db 421 GAGGAGGAGGAG 433

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-101-487-76

Query Match 13.2%; Score 119.8; DB 9; Length 720;
Best Local Similarity 61.3%; Pred. No. 4.3e-19;
Matches 193; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 510 GACCCGGATGACAGGAGGCCCTTAACTCGGATGGTGGAGGCTTTGTGGAGTGCTCGAT 569
DB 351 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 292
QY 570 GACAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 629
DB 291 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 232
QY 630 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
DB 231 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 172
QY 690 GAGAAGGATGAAGGTTTATAACAATCGAGAGGTAGATGATGAGGAGGAGGAGGAGGAG 749
DB 171 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 112
QY 750 GGTGAAGAGAAAGGGGTCAGAGCGAAATAAGAACTGAAGTGAAGTGAAGGAGACGAT 809
DB 111 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 52
QY 810 GCCTAAGTGAATAA 824
DB 51 GAGGAGGAGGAGGAA 37

RESULT 9

US-101-487-69
; Sequence 69, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: CDS
; LOCATION: (1)..(528)
US-101-487-69

Query Match 12.9%; Score 117.4; DB 9; Length 554;
Best Local Similarity 60.5%; Pred. No. 1.4e-18;
Matches 193; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 510 GACCCGGATGACAGGAGGCCCTTAACTCGGATGGTGGAGGCTTTGTGGAGTGCTCGAT 569
DB 229 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 289

QY 570 GACAAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGTAAATGAAGAT 629
DB 289 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 348
QY 630 GAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 589
DB 349 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 408
QY 690 GAGAAGATGAAGGTTTATACANTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 749
DB 409 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 468
QY 750 GGTGAAGAGAAAGGGTCTCAGAGCGAAATAAGAACTGAAGATGAGGAGGAGGAGGAG 809
DB 469 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 528
QY 810 GCCTAAGTGAATAAATCTA 828
DB 529 GAAGAGGAGTGTCTTCTA 547

RESULT 10

US-101-487-106
; Sequence 106, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: CDS
; LOCATION: (1)..(537)
US-101-487-106

Query Match 12.9%; Score 117.4; DB 9; Length 554;
Best Local Similarity 60.5%; Pred. No. 1.4e-18;
Matches 193; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 510 GACCCGGATGACAGGAGGCCCTTAACTCGGATGGTGGAGGCTTTGTGGAGTGCTCGAT 569
DB 229 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 288
QY 570 GACAAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGTAAATGAAGAT 629
DB 289 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 348
QY 630 GAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
DB 349 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 408
QY 690 GAGAAGATGAAGGTTTATACAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 749
DB 409 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 468

QY 750 GGTGAAGAAAGGGTTCAGAACCGAAATAAGAACTGAAGATGAGGAGAGACGAT 809
Db 469 GAAGAGGAAGAGAGGAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 528
QY 810 GCCTAAGTGGATATCTA 828
Db 529 GAAGAGGAGTAGTCTTCTA 547

RESULT 11
US-10-101-487-71
; Sequence 71, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: CDS
; LOCATION: (1)..(522)
US-10-101-487-71

Query Match 12.7%; Score 115.6; DB 9; Length 522;
Best Local Similarity 60.5%; Pred. No. 3.6e-18;
Matches 190; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 510 GACCCGGATGACAAGAGGCCCTTAACTCGGATGCTGAGGCTTTGTGGAGTGCCTGGAT 569
Db 127 GAAGAGGAAG 186
QY 570 GACAAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAATGGAAGAT 629
Db 187 GAAGAGGAG 246
QY 630 GAGGAGGAGGAGGATGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
Db 247 GAAGAGGAAG 306
QY 690 GAGAAGGATGAAGCTTATAACAATGGAGAGTATGATGAGGAGGAGGAGTGTGAGTGTGAGAGCTT 749
Db 307 GAAGAGGAAG 366
QY 750 GGTGAAGAAAGGGTTCAGAACCGAAATAAGAACTGAAGATGAGGAGAGACGAT 809
Db 367 GAAGAGGAAG 426

RESULT 12
US-10-101-487-73/c
; Sequence 73, Application US/10101487

; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-101-487-73

Query Match 12.7%; Score 115.6; DB 9; Length 530;
Best Local Similarity 60.5%; Pred. No. 3.7e-18;
Matches 190; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 510 GACCCGGATGACAAGAGGCCCTTAACTCGGATGCTGAGGCTTTGTGGAGTGCCTGGAT 569
Db 404 GAAGAGGAAG 345
QY 570 GACAAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAATGGAAGAT 629
Db 344 GAAGAGGAAG 285
QY 630 GAGGAGGAGGAGGATGAGGAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 689
Db 284 GAAGAGGAAG 225
QY 690 GAGAAGGATGAAGCTTATAACAATGGAGAGTATGATGAGGAGAGAGAGAGAGCTT 749
Db 224 GAAGAGGAAG 165
QY 750 GGTGAAGAAAGGGTTCAGAACCGAAATAAGAACTGAAGATGAGGAGAGAGACGAT 809
Db 164 GAAGAGGAAG 105
QY 810 GCCTAAGTGGATA 823
Db 104 GAAGAGGAAGAGA 91

RESULT 13
US-09-864-761-20733
; Sequence 20733, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26

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; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20733
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005822.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
; OTHER INFORMATION: NT HIT: AF185255.1, EVALUATE 4.80e+00
; OTHER INFORMATION: EST_HUMAN HIT: BE071749.1, EVALUATE 5.80e+00
;
US-09-864-761-3972
Query Match 11.7%; Score 106; DB 10; Length 575;
Best Local Similarity 61.0%; Pred. No. 6.7e-16;
Matches 172; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy 515 GGATGACAAAGGAGCCCTACTCGGATGGTGAGGGCTTTGTGGATGCGCTGGATGACAA 574
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 254 GGAGGAGAAAGAAAGAGGATCATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 575 GGAGGAGATCAGGATCAGGAGGAGTATGATGAGATGCTCAGTAAATGAGATGAGGA 634
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 314 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 635 GGACGAGGATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 694
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 374 GGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 695 GGATGAAGGTTATACAAATGAGAGAGGTAGATGATGAGAGATGATGAAGAGAGCTTGTGTA 754
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 434 GGAAGAGGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

; 755 AGAAGAAAGGGTCTCAGAAGCGAAATAAGAAACTCAAGATGA 796
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 494 AGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTGA 535

RESULT 14
US-09-864-761-3972
; Sequence 3972, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 3972
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005822.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 11
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 14
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.8
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 11
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 21:26:48 : Search time 1333.73 Seconds
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Title: US-09-591-500-4
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- EST:*
- 1: em_estba.*
 - 2: em_esthum.*
 - 3: em_estin.*
 - 4: em_estnu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_htc.*
 - 9: gb_esti.*
 - 10: gb_est2.*
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 - 21: em_gss_vrt.*
 - 22: em_gss_fun.*
 - 23: em_gss_man.*
 - 24: em_gss_mus.*
 - 25: em_gss_other.*
 - 26: em_gss_pro.*
 - 27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
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2	773.8	85.3	894	9	AL533191	AL533191
3	770.2	84.9	923	9	AL560249	AL560249
4	769.8	84.9	875	9	AL535686	AL535686
5	756.6	83.4	870	9	AL537874	AL537874
6	753.8	83.1	875	9	AL547157	AL547157

7	753.6	83.1	903	9	AL540827	AL540827
8	738	81.4	1035	14	BM904155	BM904155
9	731.2	80.6	855	9	AL543743	AL543743
10	728	80.3	992	9	AL517375	AL517375
11	716.2	79.0	834	9	AL545880	AL545880
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15	698.4	77.0	894	9	AL571434	AL571434
16	696	76.7	802	9	AL518247	AL518247
17	679.2	74.9	999	13	BM460209	BM460209
18	679	74.9	806	9	AL547462	AL547462
19	672	74.1	749	13	BI860951	BI860951
20	668.2	73.7	961	13	BM475803	BM475803
21	665.6	73.4	866	14	BQ687251	BQ687251
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23	660.2	72.8	882	14	BQ427516	BQ427516
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28	641	70.7	764	12	BG323351	BG323351
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31	616.6	68.0	710	9	AL557479	AL557479
32	613	67.6	697	9	AU123726	AU123726
33	608.8	67.1	764	10	BE561138	BE561138
34	608	67.0	683	10	BE544189	BE544189
35	606	66.8	790	10	BE409600	BE409600
36	602	66.4	850	14	BQ229967	BQ229967
37	601.4	66.3	1141	11	AK020753	AK020753
38	599.4	66.1	988	14	BQ216493	BQ216493
39	595	65.6	762	10	BE561131	BE561131
40	593.2	65.4	728	9	AU130628	AU130628
41	592	65.3	652	9	AL535685	AL535685
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43	587.6	64.8	892	13	BI254991	BI254991
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ALIGNMENTS

RESULT 1
AL518839
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

AL518839 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA011YH23 5
prime, mRNA sequence.
AL518839.1 GI:12782332
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1034)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers
i.1034
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DA011YH23"
/clone_lib="LTI_NFL011_NBC1"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 317 a 190 c 300 g 223 t 4 others
ORIGIN

Query Match 85.6%; Score 776.4; DB 9; Length 1034;
Best Local Similarity 93.4%; Pred. No. 8.5e-161;
Matches 807; Conservative 3; Mismatches 54; Indels 0; Gaps 0;

QY 44 CTGCAGAGAGAGCGCGAGAGATGGAGATGGGACGCGATTTCATTTAGAGCTGCGGAA 103
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Db 1 CTGCAGAGAGAGCGCGAGAGATGGAGATGGGACGCGATTTCATTTAGAGCTGCGGAA 60
QY 104 CGGACGCGCTCTGATGTGAAGAACTTGTCTGGACACAGTCGGTCGAATGAAGCAA 163
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Db 61 CAGGACGCGCTCTGATGTGAAGAACTTGTCTGGACACAGTCGGTCGAATGAAGCAA 120
QY 164 ACTCGAAGCGCTCACAGATGAATTTGAAGAACTGGAAATCTTAAGTACAATCAACGTAGG 223
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Db 121 ACTCGAAGCGCTCACAGATGAATTTGAAGAACTGGAATCTTAAGTACAATCAACGTAGG 180
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Db 181 COTCACCCTCAATCGCAACTTACCAAGTTAAACAATTTAAGAACTTGAACCTTAAGCAG 240
QY 284 TAACAGAGCTCAGTGGCGCTAGAGATTTGCGACAAAGTGTCCAAACCTCATACATCT 343
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Db 361 AAACCTCAGAGCTAGACCTTTTCAATTTGCGAGGTATACCACTAGCAACTACTACTAGA 420
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QY 524 GGAGCCCTTAACCTGGATGTGAGGGCTTTGTGAGTGGCTGGATGACAAAGGAGGAGGA 583
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Db 481 GGAGCCCTTAACCTGGATGTGAGGGCTTTGTGAGTGGCTGGATGAGGAGGAGGAGGA 540
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QY 704 TTATAAATCGAGAGGTAGATGATGAGGAGATGAAGAGAGCTTGGTGAAGAGAAAG 763
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QY 884 CCACACTCTAATCTCTGCCCTGAA 907
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Db 841 CACCTCCATCTCTGCCCTGAA 864

RESULT 2
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LOCUS AL533191 LTI_FL015_Brn1 Homo sapiens cDNA clone CSODN003K10 5
DEFINITION prime, mRNA sequence.
ACCESSION AL533191
VERSION AL533191.1 GI:12796684
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 894)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers

FEATURES
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/organism="Homo sapiens"
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/clone="CSODN003K10"
/clone_lib="LTI_FL015_Brn1"
/sex="male"
/tissue_type="Adult brain"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 293 a 159 c 270 g 170 t 2 others
ORIGIN

Query Match 85.3%; Score 773.8; DB 9; Length 894;
Best Local Similarity 94.2%; Pred. No. 3.2e-160;
Matches 813; Conservative 1; Mismatches 48; Indels 1; Gaps 1;

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QY 61 GAGAGATGAGATGGCAGACGCGATTTCATTAGAGCTGCGGAACGGGAGCGCCTCTGTATG 120
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Db 91 GAGAGATGAGATGGCAGACGCGATTTCATTAGAGCTGCGGAACGAGGAGCGCCTCTGTATG 150
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331 GCCTGGAAGTATTGGCAGAAAAGTGTCCGAACCTCAGCATCTAATTTAAGTGCACA 390
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361 AAATTAAGACCTCAGACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 420
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421 ACCTTTTCATCTGGAGGTAAACA-ACCTGAACAACCTACTGAGAGAGATGTTCAAGCTC 479
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Qy
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691 GAAAGGAGGAGTGTGAGTGGAGGAGGAGGAGGAGGAGGATGAAGTTTATACATGAGAG 750
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720 GTAGATGATGAGGAGATGAAGAGAGCTGTGTAAGAAGAAAGGCTCAGAACCGAAAA 779
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780 TAAGAACTGAAGATGAGGAGGAGGAGGAGGAGGATGAGTAAAGTGGAAATATCTATTTGAAAAAT 839
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811 CGAGAACCTGAAGATGAGGAGGAGGAGGATGAGTAAAGTGGAAATATCTATTTGAAAAAT 870
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840 TCCTTTTGTGATTTACTGTTTT 862
Qy
871 TCCTATTGTGATTTGACTGTTTT 893
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RESULT 3
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LOCUS
DEFINITION AL560249 LTI_FL011_BCl Homo sapiens cDNA clone CS0DG002YI23 5 prime
, mRNA sequence.
ACCESSION AL560249
VERSION AL560249.1 GI:12906528
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 923)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/clone="CS0DG002YI23"
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/note="vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-stranded cDNA was digested with Not I and cloned
into the Not I and Eco RV sites of the pCMVSPORT 6 vector.
Library was constructed by Life Technologies. Contact :

Feng Liang Life Technologies, a division of Invitrogen
9800 Medical Center Drive Rockville, Maryland 20850, USA
Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 299 a 163 c 279 g 175 t 7 others
ORIGIN
Query Match 84.9%; Score 770.2; DB 9; Length 923;
Best Local Similarity 93.5%; Pred. No. 2e-159;
Matches 807; Conservative 6; Mismatches 49; Indels 1; Gaps 1;
Qy 1 GGGTCGGGGTTTATTCATTGAATTCGGTCGGCGGGAGCCCTCTCGAGAGAGAGCGC 60
Db 62 GGGTCGGGGTTTATTCATTGAATTCGGTCGGCGGGAGCCCTCTCGAGAGAGAGCGC 121
Qy 61 CAGAGATGGAGATGGCGAGAGCGGATTCATTAGAGTCGCGGAACGGGAGCCCTCTGATG 120
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Qy 121 TGAAGAAGACTTCTCTGGACACAGTCGGTCGAATGAAGCAAACTCGAAGGCTCACAG 180
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prime, mRNA sequence.
ACCESSION  AL535686
VERSION     AL535686.1 GI:12799179
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 875)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES    Location/Qualifiers
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            /lab_host="DH10B"
            /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
            cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-stranded cDNA was digested with Not I
            and cloned into the Not I and Eco RV sites of the
            pCMVSPORT 6 vector. Library was constructed by Life
            Technologies. Contact : Feng Liang Life Technologies, a
            division of Invitrogen 9800 Medical Center Drive Rockville
            , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
            fliang@lifetech.com URL :
            http://fulllength.invitrogen.com"
BASE COUNT  291 a 156 c 267 g 160 t 1 others
ORIGIN
Query Match      84.9%; Score 769.8; DB 9; Length 875;
Best Local Similarity 94.4%; Pred. No. 2.4e-159;
Matches 798; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
QY 1 GGGTTCCGGGGTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTGCAGAGAGAGCGC 60
DB 31 GGGTTCCGGGGTTATTGATTGAATTCGGCGGGAGCCCTCTGCAGAGAGAGCGC 90
QY 61 GAGAGATGAGATGGCGAGCGGATTTCATTAGAGCTCGCGAACGGGACGCCCTCTGATG 120
DB 91 GAGAGATGAGATGGCGAGCGGATTTCATTAGAGCTCGCGAACGGGACGCCCTCTGATG 150
QY 121 TGAAGAAGACTTGCTCGACACAGTCGGTCGANTGAGCGCAACTCGAAGGCGCTCACAG 180
DB 151 TGAAGAAGACTTGCTCGACACAGTCGGTCGANTGAGCGCAACTCGAAGGCGCTCACAG 210
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QY 241 ACTTACCAAGCTTAAACAACCTTAAGAGCTTGAACCTAAGCAGTAAACAGAGCGCTCAGTGG 300
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QY 481 TCCTGCAACTCACATATCTCAAGCGCTGTGACCCGGATGACAGGAGGCCCTTAAGCTCG 540
DB 511 TCCCGCAACTCACATATCTGACGGCTATGACCGGACGACGAAGAGGCCCTGACTCGG 570
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DB 871 CCTAT 875

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LOCUS     AL537874      870 bp      mRNA      linear      EST 13-FEB-2001
DEFINITION AL537874 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF028YN19 5
prime, mRNA sequence.
ACCESSION  AL537874
VERSION     AL537874.1 GI:12801367
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 870)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES    Location/Qualifiers
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            /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
            cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-stranded cDNA was digested with Not I
            and cloned into the Not I and Eco RV sites of the
            pCMVSPORT 6 vector. Library was constructed by Life
            Technologies. Contact : Feng Liang Life Technologies, a
            division of Invitrogen 9800 Medical Center Drive Rockville
            , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
            fliang@lifetech.com URL :
            http://fulllength.invitrogen.com"
BASE COUNT  290 a 156 c 265 g 155 t 4 others

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RESULT 6	AL547157	875 bp	linear	EST 27-FEB-2001
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DEFINITION	AL547157 LTI_NFL006.PL2	875 bp	linear	EST 27-FEB-2001
ACCESSION	AL547157	875 bp	linear	EST 27-FEB-2001
VERSION	AL547157.1	875 bp	linear	EST 27-FEB-2001
KEYWORDS	EST.	875 bp	linear	EST 27-FEB-2001
SOURCE	human.	875 bp	linear	EST 27-FEB-2001
ORGANISM	Homo sapiens	875 bp	linear	EST 27-FEB-2001

Qy	1	GGTTTCGGGGTTTATTGATTCGAATTCGGCTGCGCGGGAGCCCTTCGACAGAGACGCGC	50
Db	30	GGGTTTCGGGGTTTATTGATTCGAATTCGGCGCGGGAGCCCTTCGACAGAGACGCGC	89
Qy	61	GAGAGATGGAGATGGGCAGACGGATTTCATTTAGAGCTCGGGAACGGGACGCCCTCTGATG	120
Db	90	GAGASATGGAGATGGGCAGACGGATTTCATTTAGAGCTCGGGAACAGGACGCCCTCTGATG	149
Qy	121	TGAAGAAGACTTGTCTCTGGACAAACAGTCGGTTCGAATTAAGGCAAACTCGAAGGCCCTCACAG	180
Db	150	TGAAGAAGACTTGTCTCTGGACAAACAGTCGGTTCGAATTAAGGCAAACTCGAAGGCCCTCACAG	209
Qy	181	ATGAATTTGAGAAGCTGGAATTCCTTAAGTACAACTCAACGTAGGCCCTCACCTCAATCGCAA	240
Db	210	ATGAATTTCAAGAACTGGAATTCCTTAAGTACAACTCAACGTAGGCCCTCACCTCAATCGCAA	269
Qy	241	ACTTACCAAAGTTAAACAAAACCTTAAGAAGCTTGAAGTAACTAGCAGTAAACAGAGCCTCAGTCG	300
Db	270	ACTTACCAAAGTTAAACAAAACCTTAAGAAGCTTGAAGTAACTAGCAGTAAACAGAGTCTCAGGG	329
Qy	301	GCCTAGAAGTATTGGCAGAAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA	360
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Qy	361	AAATTAAGACCTTCAGACAATATAGAGCCCTGAAAAAGTTAGAAAACCTTCGAGAGCTTAG	420
Db	390	AAATTTAAGACCTTCAGACAATATAGAGCCACTGAAAAAGTTAGAAAACCTTCAGAGCTTAG	449
Qy	421	ACCTTTTCACCTTCGAGGTTAACCAACCTCAACAACCTACTGAGAGAAAGATGTTCAAGCTCC	480
Db	450	ACCTTTTCACCTTCGAGGTTAACCAACCTGAGAGAAAGATGTTCAAGCTCC	509
Qy	481	TCCTCGAACCTCACAATATCTCAACGGCTGTGACCGCGGATGACAAGGAGGCCCTTAAGTCGS	540
Db	510	TCCCGCAACTCACAATATCTGACGGCTATGACCGGACGACAAGGAGGCCCTTGAGTCGS	569
Qy	541	ATGGTGAAGGCCTTTGTGGAGTGCCTGGATGACAAGGAGGAGGATGAGATGAGGAGGAT	600
Db	570	ATGGTGAAGGCCTACGTGGAGGCCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAT	629

FEATURES
SOURCE

1. .875
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1010YL13"
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/tissue_type="placenta"
/note="vector: pcwmsport 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcwmsport 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : <https://fulllength.invitrogen.com>"

a 157 c 267 q 161 t 2 others

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QY 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGGACGTC 660
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 630 ATGATGAAGATGCTCAGGTAGTGGGAAGACGAGGAGGACGAGGATGAGGAGGAGGAGTC 689
QY 661 AAGAGGAGACGTCAGTGGAGACGAGGAGGAGGAGGAGGATGAAGGTTATTAACATGAGGAGG 720
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Db 690 AAGAGGAGACGTCAGTGGAGAGGAGGAGGAGGAGGATCAAGAGGTTATACGATGAGGAGG 749
QY 721 TAGATGATGAGGAAGATGAAGAAGAGCTGTGGTGAAGAAGAAGGGTCAGAGCCAAAT 780
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Db 750 TAGATGAGGAGGAAGATGAAGAAGAGCTGTGGTGAAGAAGAAGGGTCAGAGCCAAAT 809
QY 781 AAGAACTGAAGATGAGGAGGAGGAGGATGCTTAAGTGAATAATCTATTTTGAATAAT 840
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 810 GAGAACTGAAGATGAGGAGGAGGAGGATGATGACTAAGTGG-ATAACCTATTTTGAATAATC 868
QY 841 CCTTT 845
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Db 869 CTATT 873

RESULT 7
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LOCUS , mRNA sequence.
DEFINITION AL540827
ACCESSION AL540827
VERSION AL540827.1 GI:12871345
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Li W.B., Gruber C., Jesse, J., and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 298 a 160 c 271 g 164 t 10 others
ORIGIN

Query Match 83.1%; Score 753.6; DB 9; Length 903;
Best Local Similarity 93.1%; Pred. No. 8.9e-156;
Matches 788; Conservative 9; Mismatches 48; Indels 1; Gaps 1;

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QY 61 GAGAGATGAGATGGGACGAGGATTCATTTAGAGCTGCGGAACGGGACGCCCTCTGATG 120
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Db 112 GARAAAGGAGAGGAGGACGAGGATTCATTTAGAGCTGCGGAACGAGCGCCCTCTGATG 171

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QY 121 TGAAGAAGACTTGCTCTGGACAACAGTCGGTCGAATGAAGCAAACTCGAAGGCCTCACAG 180
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QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACAATCAACGTAGGCCTCACCTCAATGCCAA 240
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 ATGAATTTGAAGAACTGGAATTTCTTAAGTACAATCAACGTAGGCCTCACCTCAATGCCAA 291
QY 241 ACTTACCAAGTTAAACAACTTAAGAACTTGAACCTTAACAGCTTAACAGAGCCTCAGTGG 300
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Db 772 TAGATGAGGAGGAGGATGAAGAGAGCTTGGTTGAAGAAGAAGGGGTGAGAGCGGAAA 831
QY 780 TAAGAAGCTCAAGATGAGGAGGAGGAGGAGGATGAAGGTTATTAACATGGAGAGG 839
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QY 840 TCCTTT 845
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VERSION BM904155.1 GI:19354489
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SOURCE human.
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgi.cni.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt

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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12133 row: d column: 11
High quality sequence stop: 674.
Location/Qualifiers
1..1035

FEATURES
source

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/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
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Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
325 a 204 c 301 g 205 t

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Qy	541	ATGCTGAGGGCTTTGTGGAGTGCCTGGATGACAAAGAGGAGGATGAGGATGAGGAGGAGT	600
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DEFINITION			
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AL543743			
VERSION			
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE			
1 (bases 1 to 855)			
AUTHORS			
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.			
TITLE			
Full-length cDNA libraries and normalization			
JOURNAL			
Unpublished (2001)			
COMMENT			
Contact: Genoscope			
Genoscope - Centre National de Sequencage			
Bp 191 91006 EVRY cedex - France			
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.			
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enriched, double-stranded cDNA was digested with Not I and			
cloned into the Not I and Eco RV sites of the pCMVSPORT 6			
vector. Library was normalized. Library was constructed by			
Life Technologies. Contact : Feng Liang Life Technologies,			
a Division of Invitrogen 9800 Medical Center Drive			
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371			
Email : fliang@lifetech.com URL :			
http://fulllength.invitrogen.com"			
BASE COUNT 280 a 151 c 265 g 152 t 7 others			
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Query Match 80.6%; Score 731.2; DB 9; Length 855;			
Best Local Similarity 94.0%; Pred. No. 7.7e-151;			
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Qy	121	TGAAGAAGCTTGTCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGGCGCTCACAG	180
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Db 220 ATGATTTGAAGAACTGGAATTTTAAGTACAATCAACGTAGGCTCACCTCAATCGCAA 279
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Db 580 ATGCTGAGGGGTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGT 639
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RESULT 10
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DEFINITION AL517375 prime, mRNA sequence.
ACCESSION AL517375
VERSION AL517375.1 GI:12780868
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 992)
Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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FEATURES
source

/note="Organ: brain; Vector: pCMWSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMWSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life technologies. Contact : Feng Liang Life technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 301 a 174 c 289 g 217 t 11 others
ORIGIN

Query Match 80.3%; Score 728; DB 9; Length 992;
Best Local Similarity 91.9%; Pred. No. 3.8e-150;
Matches 772; Conservative 7; Mismatches 59; Indels 2; Gaps 1;

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Db 481 GGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGTATGATGA 540
Qy 608 AGATGCTCAGGTAAATCGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 667
Db 541 AGATGCTCAGGTAAATCGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
Qy 668 GGACGTGAGTGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 727
Db 601 GGACGTGAGTGGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy 728 TGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAATTAAGAAGAC 787
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Qy 788 TGAAGATGAGGAGGAGAGAGATGCTTAAAGTGAAGTAAATCTATTTTGAAGAAATTCCTTTG 847
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RESULT 11
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VERSION
KEYWORDS
SOURCE EST.
AL545880.1 GI:12878473
human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 834)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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/db_xref="taxon:9606"
/clone="CS0D1023YE09"
/clone_lib="LTI_NFL006.PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 272 a 153 c 257 g 148 t 4 others
ORIGIN
Query Match 79.0%; Score 716.2; DB 9; Length 834;
Best Local Similarity 94.1%; Pred. No. 1.5e-147;
Matches 739; Conservative 4; Mismatches 42; Indels 0; Gaps 0;
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Qy 121 TGAAGAACCTTGTCCTGGACAACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCTCACAG 180
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Qy 181 ATGAATTGAAGAACTGGAATTCCTTAAGTACATCAATCAACGTAGGCCCTACCTCAATCGCAA 240
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Qy 241 ACTTACCAAGTTAAACAACCTTAAAGTACATCAATCAACGTAGGCCCTACCTAGTGG 300
Db 285 ACTTACCAAGTTAAACAACCTTAAAGTACATCAATCAACGTAGGCCCTACCTAGTGG 344
Qy 301 GCCTAGAAGTATGGCAGAAAAGTGTCCTCAACCTCATACATCTAAATTTAAAGTGGCAACA 360
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Db 705 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 764
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Qy 721 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
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Qy 781 AAGAA 785
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RESULT 12
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LOCUS
DEFINITION AL535863 LTI_FL013_FBrnl Homo sapiens cDNA clone CS0DF013YJ23 5
prime, mRNA sequence.
ACCESSION AL535863
VERSION AL535863.1 GI:12799356
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 853)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/clone_lib="LTI_FL013_FBrnl"
/dev_stage="pooled tissue from post conception fetuses (20
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/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 283 a 147 c 254 g 164 t 5 others
ORIGIN
Query Match 79.0%; Score 716.2; DB 9; Length 853;
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Best Local Similarity 92.08; Pred. No. 1.5e-147; Matches 785; Conservative 4; Mismatches 57; Indels 7; Gaps 3;									
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Db	61	CAGACGGATTCATTATAGAGCTGCGGAACAGGAGCGCCCTCTGATGTGAAGAACTTGTCT	120						
Qy	137	GCACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCTCACAGATGAATTTGAAGAACT	196						
Db	121	GCACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCTCACAGATGAATTTGAAGAACT	180						
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Db	181	GGAATTCCTTAAGTACAATCAACGTAGCGCTCACCTCAATCGCAAACTTACCAAGTTAA	240						
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Qy	317	AGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACAAATTTAAGACCTCAG	376						
Db	301	AGAAAAGTGTCCGAACCTCAGCATCTAAATTTAAGTGGCAACAAATTTAAGACCTCAG	360						
Qy	377	CACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTACACTTTTCACTTGGCA	436						
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Qy	437	GGTAACCAACCTGAACAACTACTGAGAGAAGATGTTCAAGCTCCTCGCAACTCACATA	496						
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Qy	497	TCTCAAGCGCTGTACCGGATGACAGGAGGCGCCCTAACCTCGGATGGTGAGGCT----	552						
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Qy	553	TTGTGGAGTGCCTGGATGACAAG-GAGGAGGATGAGG--ATGAGGAGGAGTATGATGAAG	609						
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Qy	610	ATGCTCAGGTAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGGACGTTGAAGAGGAGG	669						
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RESULT 13
BQ232856
LOCUS BQ232856
DEFINITION AGENCOURT_7567365 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6060491
5', mRNA linear EST 02-MAY-2002
ACCESSION BQ232856
VERSION BQ232856.1
KEYWORDS EST. GI:20414256
SOURCE human.

ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 895)	
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue procurement: DCTD/DTF/Gazdar cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM13328 row: n column: 12 High quality sequence stop: 676.	
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	/lab_host="DH10B (phage-resistant)"	
	/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."	
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Qy 780 TAAGAA-ACTGAAGATGA-GGGAGAGACGATGCTTAAGTGG----AATAATCTATTGTTG 833
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LOCUS BM543218
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5', mRNA sequence.
ACCESSION BM543218
VERSION BM543218.1 GI:18773420
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1066)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M12327 row: b column: 18
High quality sequence stop: 628.
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Site:2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Best Local Similarity 92.4%; Pred. No. 2.6e-145;
Matches 787; Conservative 0; Mismatches 60; Indels 5; Gaps 4;
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Qy 360 AAAATTAAGAGCTCAGCACAATAGAGCCCTCAAAAAGTTAGAAAACCTCGAGAGCTTA 419
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Db 421 CTCCTCAACTCATATATCTCAACGGCTGTGACCCGGATGACAAGAGGCCCTCACTCG 480
Qy 540 GATGTTGAGGGCTTTGTCGAGTGCCTGGATGACAAGGAGGAGGATGAGGAGGAG 599
Db 481 GATGTTGAGGGCTTACGTGGAGGCTGGATGATGAGGAGGAGGATGAGGAGGAG 540
Qy 600 TATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 659
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Qy 660 GAAGAGGAGAGCTGAGTGGAGACGAGGAGGAGGAGGATGAGGATGAGGAGGAGGAG 719
Db 601 GAAGAGGAGAGCTGAGTGGAGAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAG 660
Qy 720 GTAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGTCAAGAGCGAAA 779
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Qy 780 TAGAAACTGAAG-ATGAGGAGGAGGAGGAGGATGCTTAAGTGGATTA-TCTATTTTGA 837
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Qy 896 CTGCCCCCTGAA 907
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RESULT 15
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prime, mRNA sequence.
ACCESSION AL571434
VERSION AL571434.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
```

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 177 a 266 c 165 g 279 t 7 others
ORIGIN

Query Match 77.0%; Score 698.4; DB 9; Length 894;
Best Local Similarity 92.3%; Pred. No. 1.3e-143;
Matches 742; Conservative 4; Mismatches 55; Indels 3; Gaps 1;

QY 107 GAGCGCCCTCTGATGTGAAGAAGTTCCTCGACACAGTCGGTGAATGAAGCAAACT 166
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Db 891 GAGCGCCCTCTGATGTGAAGAAGTTCCTCGACACAGTCGGTGAATGAAGCAAACT 832
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Db 711 CAGAGCTCAGGGGCCCTGGAAGTATTGGCAGAAAAGTGTCCGAACTCAGGCATCTAAA 652
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QY 647 GGAGGAGGAACGTGAAGAGGAGGAGGCTGAGTGGAGACGAGGAGGAGGAGGATGAAGGTTA 706
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Db 351 GGAGGAGGAAGGTGAAGAGGAGGAGGCTGAGTGGAGGAGGAGGAGGATGAAGAGGTTA 292
QY 707 TAACAATGGAGAGGTAGATGATGAGGAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGG 766
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: December 8, 2002, 14:53:12 ; Search time 9582 seconds
(without alignments)
17570.417 Million cell updates/sec
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :					GenEmbl :				
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6:	gb_pat.*	7:	gb_ph.*	8:	gb_pl.*	9:	gb_pr.*	10:	gb_ro.*
11:	gb_sts.*	12:	gb_sy.*	13:	gb_un.*	14:	gb_vi.*	15:	em_ba.*
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36:	em_htg_mam.*	37:	em_htg_vrt.*	38:	em_sy.*	39:	em_htgo_hum.*	40:	em_htgo_mus.*
41:	em_htgo_other.*								

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	5785	100.0	5785	9	AF008216	AF008216 Homo sapi
c	4531.6	78.3	202847	9	AC079240	AC079240 Homo sapi
c	3193.4	55.2	70449	9	AC105250	AC105250 Homo sapi
4	917.6	15.9	1136	9	BC007200	BC007200 Homo sapi
5	867.8	15.0	1052	6	AR009985	AR009985 Sequence 1
6	867.8	15.0	1052	6	I91514	I91514 Sequence 1
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c	794.8	13.7	162482	9	AC022740	AC022740 Homo sapi
c	794.4	13.7	164945	9	AC089987	AC089987 Homo sapi
c	793.2	13.7	149015	9	AC107992	AC107992 Homo sapi
c	793.2	13.7	186886	2	AC016297	AC016297 Homo sapi
13	791	13.7	916	9	HSPHAP1	X75090 H. sapiens m
14	764.4	13.2	925	9	AF025584	AF025584 Homo sapi
15	689	11.9	1017	10	RATLANP	D32209 Rat mRNA fo
16	659.2	11.4	904	9	HSU71084	U71084 Homo sapien
17	649.6	11.2	980	6	AR009986	AR009986 Sequence
18	649.6	11.2	980	6	AX305936	AX305936 Sequence
19	649.6	11.2	980	6	I91515	I91515 Sequence 3
20	649.6	11.2	980	6	I96075	I96075 Sequence 3
21	649.6	11.2	980	10	MMU73478	U73478 Mus muscula
22	640.4	11.1	750	9	HSU60823	U60823 Human poten
23	581	10.0	1656	9	AY007110	AY007110 Homo sapi
24	573.4	9.9	863	10	AF022957	AF022957 Mus muscu
25	569	9.8	771	9	BC000608	BC000608 Homo sapi
26	518.4	9.0	101819	2	AC129809	AC129809 Rattus no
27	518.4	9.0	170170	2	AC106610	AC106610 Rattus no
28	508	8.8	759	6	AR009987	AR009987 Sequence 4
29	508	8.8	759	6	I91516	I91516 Sequence 4
30	508	8.8	759	6	I96076	I96076 Sequence 4
31	444.8	7.7	79457	2	AC098396	AC098396 Rattus no
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32	297.8	5.1	1011	9	HSPHAP12A	Y07569 H. sapiens m
33	297.8	5.1	1035	9	BC013003	BC013003 Homo sapi
34	297.8	5.1	1371	9	BC019658	BC019658 Homo sapi
35	297.8	5.1	1371	9	HSAPRIL	Y07969 H. sapiens m
36	297.8	5.1	1475	9	HSU70439	U70439 Human silve
37	297.8	5.1	3980	9	BC000476	BC000476 Homo sapi
38	297.8	5.1	198926	10	AL683843	AL683843 Mouse DNA
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39	292.8	5.1	1988	9	AB047872	AB047872 Macaca fa
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41	284.4	4.9	200445	2	AC105137	AC105137 Homo sapi
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42	272.8	4.7	1225	10	BC003489	BC003489 Mus muscu
43	264.6	4.6	1397	10	BC003489	BC003489 Mus muscu
44	264.6	4.6	1408	10	BC005628	BC005628 Mus muscu
45	264.6	4.6	1408	10	BC005628	BC005628 Mus muscu

ALIGNMENTS

RESULT 1	AF008216	5785 bp	DNA	linear	PRI 05-FEB-1999
LOCUS	AF008216	Homo sapiens candidate tumor suppressor pp32r1 (PP32R1) gene,			
DEFINITION	AF008216	complete cds.			
ACCESSION	AF008216				
VERSION	AF008216.1	GI:2738512			
KEYWORDS					
SOURCE		Homo sapiens.			
ORGANISM		Homo sapiens			
		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE		1 (bases 1 to 5785)			
AUTHORS		Kadkol,S.S., Brody,J.R., Pevsner,J., Bai,J. and Pasternack,G.R.			
TITLE		Modulation of oncogenic potential by alternative gene use in human			

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RESULT 2


```

AC079240/c
LOCUS       AC079240               202847 bp    DNA    linear    PRI 09-JAN-2002
DEFINITION  Homo sapiens BAC clone RP11-808H17 from 4, complete sequence.
ACCESSION   AC079240
VERSION     AC079240.6  GI:15431275
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens.
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 202847)
    Sultston,J.E. and Waterston,R.
    Toward a complete human genome sequence
    Genome Res. 8 (11), 1097-1108 (1998)
    99063792
    PUBMED   9847074
  2 (bases 1 to 202847)
    Tomlinson,C., Kozlowski,A., Phillips,A., Dixon,R. and Spalding,L.
    The sequence of Homo sapiens BAC clone RP11-808H17
    Unpublished (2001)
  3 (bases 1 to 202847)
    Waterston,R.H.
    Direct Submission
    Submitted (24-AUG-2000) Genome Sequencing Center, Washington
    University School of Medicine, 4444 Forest Park Parkway, St. Louis,
    MO 63108, USA
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    Waterston,R.H.
    Direct Submission
    Submitted (05-SEP-2001) Genome Sequencing Center, Washington
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    MO 63108, USA
  5 (bases 1 to 202847)
    Waterston,R.
    Direct Submission
    Submitted (09-JAN-2002) Department of Genetics, Washington
    University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
    On Sep 5, 2001 this sequence version replaced gi:15145274.
    ----- Genome Center
    Center: Washington University Genome Sequencing Center
    Center code: WUGSC
    Web site: http://genome.wustl.edu/gsc
    Contact: sapiens@watson.wustl.edu
    ----- Summary Statistics
    -----
    Center project name: H_NH0808H17
    -----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-39C10; the clone sequenced
to the right is RP11-277J14. Actual start of this clone is at base
position 1 of RP11-808H17; actual end is at base position 202847 of
RP11-808H17.

FEATURES             Location/Qualifiers
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Qy	61	CTTTTCTTATGTAACCTCATCAACACATAGCAATAAGTTTGGCATGTTTCTTCCCT	120				
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Qy	121	ATCAGTTGCAAGTTCAGCAGAGCTGATATTTTCAATTTCAATTCGCTACTAGCCCTA	180				
Db	4502	ATCAGTTGCAAGTTCAGCAGAGCTGATATTTTCAATTTCAATTCGCTACTAGCCCTA	4443				
Qy	181	GAGCCTGACATAGTTTCTGGCTGTGAATGCTCAATAAATATTTGTTAATGAGTAGAAA	240				

Db	3362	TG	GCTCTTTCATTCTCCCTCGAATGCTCTCCACTCCAGATCCTTACTAGATCTTTAGCTCAG	3303
QY	1311	TC	ATCACCCCTGCAGGAAGATCTTCCAACCATTCACCTGCGATACACCTATGGCTGCTGCC	1370
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[illegible]

Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-360H22, 2000 bp overlap;
the clone sequenced to the right is RP11-808H17, 2000 bp overlap.
Actual start of this clone is at base position 97207 of
RP11-360H22; actual end is at base position 22714 of RP11-808H17.

The sequence of AC011026 has been incorporated into AC105250.

FEATURES

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QY 4811 AGGTTAACCAACCTGAAGACTTACGGAAGAAACGTTCAAGCTTCTCTGCAACTCACAT 4870

Db	68229	AGGTAACCAACCTGAACGACTACGGAGAAACCGTGTTCAGCTTCCTCGCAACTCACAT	68170	VERSION KEYWORDS SOURCE ORGANISM	BC007200.1 GI:13938167 MGC. Homo sapiens. Homo sapiens
Qy	4871	ATCTCGACAGCTGTTACTTGGGACCAACAAGGAGGCCCTTACTCAGATATTGAGGACCACG	4930	REFERENCE AUTHORS TITLE JOURNAL	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1136) Strausberg,R. Direct Submission Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov
Db	68169	ATCTCGACAGCTGTTACTGGAACCAACAAGGAGGCCCTTACTCAGATATTGAGGACCACG	68110		Tissue procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
Qy	4931	TGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATGCTC	4990	REMARK COMMENT	Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McTeavy, Steven Ness, Pawan Pandoh, Anna-Lilisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
Db	68109	TGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATGCTC	68050		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 18 Row: j Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5453879. Location/Qualifiers 1..1136 /organism="Homo sapiens" /db_xref="LocusID:8125" /db_xref="taxon:9606" /clone="MGC:12667 IMAGE:3677623" /tissue_type="Lymph, Burkitt lymphoma" /clone_lib="NIH_MGC-8" /lab_host="DH10B-R" /note="Vector: pOTB7" 134..883 /codon_start=1 /product="putative human HLA class II associated protein I" /protein_id="AAH07200.1" /db_xref="GI:13938168" /translation="MEMGRRIHLELRNRTPSDVKELVLNDSRNECKLGLTDFEEL EPLSTINGVLTSTIANLPKLNKLELSDNRVSGVLEVLAEKCPNTHLNLGNKIKD LSTLEPKLLEKSLDFNCEVTNLNRYENFKLLPQLTYLDGYDRDDKKAQPSDA EGYVEKLDDEEDEDYEDAQVVEDEDEDEDEDEDEDEDEDEDEDEDEDEDE VDDDEDEELCEERGGOKRKRPEDECEDD"
Qy	4991	AGGTAGTGAAGATGAGGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	5050		BASE COUNT 369 a 207 c 337 g 223 t
Db	68049	AGGTAGTGAAGATGAGGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	67990	ORIGIN	
Qy	5051	GTGAGGCGGACGAGGAGGATGAAGAAGTTATACGATGAGGAGGATAGATGCGGAGGAG	5110	Query Match	15.9%; Score 917.6; DB 9; Length 1136;
Db	67989	GTGAGGCGGACGAGGAGGATGAAGAAGTTATACGATGAGGAGGATAGATGCGGAGGAG	67930	Best Local Similarity	91.3%; Pred. No. 1.9e-152;
Qy	5111	ATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGCAAAATGAGAACCTGAAGATG	5170	Matches 1013; Conservative	0; Mismatches 79; Indels 18; Gaps 3;
Db	67929	ATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGCAAAATGAGAACCTGAAGATG	67870	Qy 4327	TTGGGGCTCGAGAACCGAGCGAGCTGGTTGAGTCTTCAAGTCTTAAACGTCGCGCGC 4386
Qy	5171	AGGAGAAGATGATGACTAGTATAGATAACCTATTTTGAATAATTCCTATTCTGATTTGA	5230	Db 8	TGGGGCTCGAGAACCGAGCGAGCTGGTTGAGCTTCAAGTCTTAAACGTCGCGCGC 67
Db	67869	AGGAGAAGATGATGACTAGTATAGATAACCTATTTTGAATAATTCCTATTCTGATTTGA	67810	Qy 4387	TGGGTCGAGGTTTATTGATTTCGGCTGGCAGCAGAGCCCTCTCAGACAGAGCG 4446
Qy	5231	CTGTTTTTACCCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	5290	Db 68	TGGGTCGCGGTTTATTGATTTCGGCTGGCAGCAGAGCCCTCTCAGACAGAGCG 127
Db	67809	CTGTTTTTACCCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	67750	Qy 4447	CGAGAGATGGAGATGGGACGAGGATTCATTTCAGAGCTGGCGAAGCGCCCTCTGAT 4506
Qy	5291	GATTGTAACATTGCTGTGGGAATGACAGCGGAAAAGTGACTGGGGGTTGTGGAGGAGG	5350		
Db	67749	GATTGTAACATTGCTGTGGGAATGACAGCGGAAAAGTGACTGGGGGTTGTGGAGGAGG	67690		
Qy	5351	GAGGCGAGGAGGCGGTGGACTAAAATACTATTTTACTGCCAAATAAATAATATTTCTGA	5410		
Db	67689	GAGGCGAGGAGGCGGTGGACTAAAATACTATTTTACTGCCAAATAAATAATATTTCTGA	67630		
Qy	5411	AATATTAACTGGGATAGCTAGCTTTGATGAATGATTAATTAATTTCTCTCTCTCTTT	5470		
Db	67629	AATATTAACTGGGATAGCTAGCTTTGATGAATGATTAATTAATTTCTCTCTCTCTTT	67570		
Qy	5471	TTATTTTTTACACATCTATCTTTTAAAGTATAGTACCTTTTGTAGTCCAAAGAAAGGCAC	5530		
Db	67569	TTATTTTTTACACATCTATCTTTTAAAGTATAGTACCTTTTGTAGTCCAAAGAAAGGCAC	67510		
Qy	5531	TACAATCCACTTATTATGCTGCTACTGTGTTCAAGTAAATAAGCTCCAGGATTTAAC	5590		
Db	67509	TACAATCCACTTATTATGCTGCTACTGTGTTCAAGTAAATAAGCTCCAGGATTTAAC	67450		
Qy	5591	AAAAGAGGAAGAAATATTACAATGAAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	5650		
Db	67449	AAAAGAGGAAGAAATATTACAATGAAATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	67390		
Qy	5651	GTAATCTATTGTTAAAGCAAAATCTATTTTAAATTTTAAATGAAATATTTTGC	5710		
Db	67389	GTAATCTATTGTTAAAGCAAAATCTATTTTAAATTTTAAATGAAATATTTTGC	67330		
Qy	5711	TAAAGCAAAATTTTGGAAAAATAAATAATGCACCTTATATCTGATTTTATTATTAATAACA	5770		
Db	67329	TAAAGCAAAATTTTGGAAAAATAAATAATGCACCTTATATCTGATTTTATTATTAATAACA	67270		
Qy	5771	ATGATTTTAAAGCTT 5785			
Db	67269	ATGATTTTAAAGCTT 67255			
RESULT 4					
BC007200					
LOCUS					
DEFINITION					
ACCESSION					

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Db 128 CGAGAGATGGAGTGGCAGACGGATTATTTAGAGCTGCGGAACGAGCGCCCTCTGAT 187
QY 4507 GTGAAGAAGTTCGCCCTGGACACAGTCCGTCGATGAGGCAAACTGGAAGCCCTCACA 4566
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QY 4567 GATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCA 4626
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QY 4627 GACTTACCAAAAGTTAAAGT---TGAGAAAGCTTGAACTA-----AGAGTCFCAGGG 4674
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QY 4675 GGCCTGGAAGTATGGCAGAAAAGTTCACAAACCTCAGCATCTATATTAAGTGGCAAC 4734
Db 368 GGCCTGGAAGTATGGCAGAAAAGTTCGGAACCTCAGCATCTAAATTTAAGTGGCAAC 427
QY 4735 AAAATTTAAAGACTCAGCACAATAGAGCCACTGAACAGTTTAAAAAGCTCAAGAGCTTA 4794
Db 428 AAAATTTAAAGACTCAGCACAATAGAGCCACTGAANAAGTTAAGAACTCAAGAGCTTA 487
QY 4795 GACCTTTTCAATTCGAGGTAAACCAACCTGAACGACTACGGAGAAAACGTTGTTCAAGCTT 4854
Db 488 GACCTTTTCAATTCGAGGTAAACCAACCTGAACGACTACCGAGAAAATGTTGTTCAAGCTC 547
QY 4855 CTCCTGCAACTCACATATCTCGACAGCTGTACTGGGACCAAGAGGCCCTTACTTCA 4914
Db 548 CTCCTGCAACTCACATATCTCGACAGCTGTACTGGGACCAAGAGGCCCTTACTTCA 607
QY 4915 GATATTGAGGACCACTGGAGGCGCTTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAG 4974
Db 608 GATGCTGAGGCGCTACCTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 667
QY 4975 TATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 5034
Db 668 TATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGATGAACGAT 727
QY 5035 GAAGAGGAGGAGTGTAGTGGAGGGACGAGGAGGATGAAGAAGTTTATAACCATGGAGAG 5094
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QY 5095 GTAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAAA 5154
Db 788 GTAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAAA 847
QY 5155 TGAGAACCTGAAGATGAGGAGGAGGATGATGACTAGTAGATACCTTATTTTGAANAAT 5214
Db 848 CGAGAACCTGAAGATGAGGAGGAGGATGATGACTAGTAGATACCTTATTTTGAANAAT 907
QY 5215 TCCTATTGTGATTGACTGTTTATCCCATATCCCTC-----CCCCCTCCCAATCCCTGC 5268
Db 908 TCCTATTGTGATTGACTGTTTATCCCATATCCCTC-----CCCCCTCCCAATCCCTGC 967
QY 5269 CCCCTGAAACTTACTTTTTTCTGATTGTAAACATGCTGTGGGAATGAGACGGGAAAAAGTG 5328
Db 968 CCCCTGAAACTTACTTTTTTCTGATTGTAAACGTTGCTGTGGGAACGAGGAGGGAAGATG 1027
QY 5329 TACTGGGGTGTGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5388
Db 1028 TACTGGGGTGTGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1087
QY 5389 GCCAAATAAATAATTTTGAATAATTA 5418
Db 1088 GCCACTTTTAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1117

RESULT 5
AR009985
LOCUS AR009985 1052 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 1 from patent US 5756676.
ACCESSION AR009985

AR009985.1 GI:3968790
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack,G.R.
TITLE Mammalian protein associated with uncontrolled cell division
JOURNAL Patent: US 5756676-A 1 26-MAY-1998;
FEATURES Location/Qualifiers
source 1..1052
BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN
Query Match 15.0%; Score 867.8; DB 6; Length 1052;
Best Local Similarity 91.8%; Pred. No. 1.2e-143;
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;
QY 4357 GAGTCTTCAAAGTCTCTAAAACGTCGCGCCGTGGGTTCGAGGTTTATTTGATTGAATTCGGC 4416
Db 1 GAATTCCTCCAAAGTCTCTAAAACGTCGCGCCGTGGGTTCGCGGTTTATTGATTGAATTCGCG 60
QY 4417 TGGCAGCAGAGCCCTCTCGACACAGAGAGCGCGAGAGATGGAGATGGCCACACGGATTTCAT 4476
Db 61 CGCGCGCGGAGCCCTCTCGAGAGAGAGCGCGAGATGGAGATGGCGCAGCGGATTCAT 120
QY 4477 TCAGAGCTGGGGAACACGCGCCCTCTGATGTGAAGAAGCTTGCCTTGGACACAGTCGG 4536
Db 121 TTAGAGCTGGGGAACACGAGCGCCCTCTGATGTGAAGAAGCTTGTCTTGGACACAGTCGG 180
QY 4537 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAAGCTTGAATTTCTTAAAGT 4596
Db 181 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAAGCTTGAATTTCTTAAAGT 240
QY 4597 AAAATCAACGGAGCCCTCACCTCAATCTCAGACTTACCAAGTTA---AAGTTCAGAAAG 4653
Db 241 ACAATCAACGTAAGCCCTCACCTCAATCGAAACCTTACCAAGTTTAAACAACTTAAAGAG 300
QY 4654 CTTGAACCTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCA 4704
Db 301 CTTGAACCTAAGCGATAACAGAGTCTCAGGGGCGCTAGAAGTATTGGCAGAAAAAGTGTCCG 360
QY 4705 AACCTCAGCATCTATATTAAAGTGGCAACAAATTTAAAGCTCAGCACAATAGAGCCA 4764
Db 361 AACCTCAGCATCTATAATTTAAAGTGGCAACAAAAATTAAAGACCTCAGCACAATAGAGCCA 420
QY 4765 CTGAACAGATTAGAAAAACCTCAAGAGCTTAGACCTTTTCAATTTCGAGAGTAAACCAACTG 4824
Db 421 CTGAACAGATTAGAAAAACCTCAAGAGCTTAGACCTTTTCAATTTCGAGAGTAAACCAACTG 480
QY 4825 AACGACTACGGAGAAAAAGTGTTCAAAGCTTCTCTGCAACTCACAATCTCGACAGCTGT 4884
Db 481 AACGACTACCGAGAAAAATGTGTTCAAGCTCTCTCCGCAACTCACAATCTCGACAGCTAT 540
QY 4885 TACTGGGACACAGAGGAGGCGCCCTTACTCAGATATTGAGGACCACTGAGGAGGCGCTGGAT 4944
Db 541 GACCGGACACAGAGGAGGCGCCCTGACTCGGATCTGAGGCTACGTTGAGGAGGCGCTGGAT 600
QY 4945 GACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAAAGAT 5004
Db 601 GATGAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAAAGAT 660
QY 5005 GAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5064
Db 661 GAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 5065 GAGGATGAAGAAGGTTATAACGATGGAGAGTACATGGCAGGAGGAGATGAAGAAGCTT 5124
Db 721 GAGGATGAAGAAGGTTATAACGATGGAGAGGATGATGACGAGGAGGAGATGAAGAAGCTT 780
QY 5125 GGTGAAGAAGAAAGGGGTCAAGAAGCAAAATGAGAACTGGAAGATGAGGAGGAGGAGATGAT 5184
Db 5125 GGTGAAGAAGAAAGGGGTCAAGAAGCAAAATGAGAACTGGAAGATGAGGAGGAGGAGATGAT 5184

Db 781 GGTGAAGAAAGAGGGGTCTAGAACGCGAAACGAGAACTGAAGATGAGGGAGAAAGATGAT 840

QY 5185 GACTAAGTAGAATAACCTATTATTTGAAAAATTCCTATTCTGATTGACTGTTTATACCCAT 5244

Db 841 GACTAAGTGAATAACCTATTATTTGAAAAATTCCTATTCTGATTGACTGTTTATACCCAT 900

QY 5245 ATCCCT-----CCGCCCTCCAATCCCTGCCCCCTGAAACTTACTTTTTCTGATTGTAA 5298

Db 901 ATCCCTCTCCGCCCTCTAATCCTGCCCCCTGAAACTTACTTTTTCTGATTGTAA 960

QY 5299 CATTGCTGTGGGAATGAGACGGGAAAGTGTACTGGGGTGTGAGGGAGGGAGGCAG 5358

Db 961 GTTGCTGTGGGACGAGAGGGGAGAGTGTACTGGGGTGTGCGGGGGA--GGATGCGG 1019

QY 5359 GAGCGGTGGACTAAATACTATTTTACTGCC 5391

Db 1020 GTGGGGTGGATTAATACTATTTTACTGCC 1052

RESULT 6

LOCUS 191514

DEFINITION Sequence 1 from patent US 5726018.

ACCESSION 191514

VERSION 191514.1 GI:3935984

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1052)

AUTHORS Pasternack,G.R.

TITLE Nucleic acid based assays to detect a novel mammalian protein associated with uncontrolled cell division

JOURNAL Patent: US 5726018-A 1 10-MAR-1998;

FEATURES Location/Qualifiers

source 1..1052

BASE COUNT 326 a 196 c 316 g 214 t

ORIGIN

Query Match 15.0%; Score 867.8; DB 6; Length 1052;

Best Local Similarity 91.8%; Pred. No. 1.2e-143;

Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTCAAAGTCTTAAACGTCGCGCTTGGGTTCGAGGTTTATTGATTGAATTCGGC 4416

Db 1 GAATTCCTCAAGTCTTAAACGTCGCGCTTGGGTTCGAGGTTTATTGATTGAATTCGGC 60

QY 4417 TGGCAGAGAGCCCTCTCAGACAGAGAGCGCGAGAGATGGAGACGAGATTCAT 4476

Db 61 CGCGCGGGAGCCCTCTCAGAGAGAGAGCGCGAGAGATGGAGACGAGATTCAT 120

QY 4477 TCAGAGTCGGGACAGGGGCCCTCTGATGTGAAGAACTTCGCCCTGGACACAGTCGG 4536

Db 121 TTAGAGTGGGAAACAGAGCGCCCTCTGATGTGAAGAACTTCTCTCGACACAGTCGG 180

QY 4537 TCGAATGAAGCAAACTCGAAGCCCTCACAGATGAATTTCAAGAACCTGGAATCTTAAGT 4596

Db 181 TCGAATGAAGCAAACTCGAAGCCCTCACAGATGAATTTCAAGAACCTGGAATCTTAAGT 240

QY 4597 AAAATCAACGGAGCCCTACCTCAATCTCAGACTTACCAAAGTTA---AAGTTGAGAAAG 4653

Db 241 ACAATCAACGTAGCCCTCAGCTCAATCGCAAACTTACCAAAGTTAAACAACCTTAAGAAG 300

QY 4654 CTTCGAACTA-----AGAGTCTAGGGGCCCTGGAAGTATGCGAGAAAAGTGTCCA 4704

Db 301 CTGAACTAAGCGATAACAGAGTCTCAGGGGCCCTAGAAGTATGCGAGAAAAGTGTCCG 360

QY 4705 AACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCA 4764

Db 361 AACCTCAGCATCTAATTTAAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCA 420

QY 4765 CTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCAACCTG 4824

Db 421 CTGAAAGATTGAAACCTCTAGAGCTTAGACCTTTCAATTGCGAGGTAAACCACTG 480

QY 4825 AAGCACTACGGAGAAACGTGTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGT 4884

Db 481 AAGCACTACCGAGAAATGTGTTCAAGCTCTCCGCCAACTCACATATCTCGACGCTAT 540

QY 4885 TACTGGGACCACAGAGAGGCCCTTACTCAGATATTGAGGACCACCTGGAGGSCCTGGAT 4944

Db 541 GACCGGACACAAAGAGGCCCTGACTCGATGCTGAGGGCTACGTGGAGGCCCTGGAT 600

QY 4945 GACGAGGAGGAGGTGAGCATGAGGAGGAGTAGATGAAGATGCTCAGCTAGTGGAGAT 5004

Db 601 GATGAGGAGGAGGATCAGGATGAGGAGGAGTAGATGAAGATGCTCAGCTAGTGGAGAC 560

QY 5005 GAGGAGGGCAGGAGGAGGAGGAGGAGTAGAGGAGGAGGAGCTGAGTGGAGGGGACGAG 5064

Db 661 GAGGAGGACGAGGATGAGGAGGAGGAGGAGTGAAGAGGAGGAGCTGAGTGGAGAGGAGG 720

QY 5065 GAGGATGAAGAGGTTTATACGATGGAGGAGTAGATGGCGAGGAAGATGAAGAAGCTT 5124

Db 721 GAGGATGAAGAGGTTTATACGATGGAGGAGTAGATGACGAGGAAGATGAAGAAGCTT 780

QY 5125 GGTGAAGAAAGAGGGTCTAGAAGCGGAAATGAGAACCTGAAGATCAGGAGAGATGAT 5184

Db 781 GGTGAAGAAAGAGGGTCTAGAAGCGGAAACGAGAACCTGAAGATGAGGAGAGATGAT 840

QY 5185 GACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTTGATTGACTGTTTTTACCCAT 5244

Db 841 GACTAAGTGAATAACCTATTTTGAAAAATTCCTATTGTTGATTGACTGTTTTTACCCAT 900

QY 5245 ATCCCT-----CCCCCTCCAATCCTCGCCCTGAAACTTACTTTTTCTGATTGTAA 5298

Db 901 ATCCCTCTCCGCCCTCTAATCCTCGCCCTGAAACTTACTTTTTCTGATTGTAA 960

QY 5299 CATTGCTGTGGAAATGAGACGGGAAAGTGTACTGGGGTGTGAGGAGGAGGAGGCAG 5358

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QY 5359 GAGCGGTGGACTTAAATACTATTTTACTGCC 5391

Db 1020 GTGGGGTGGATTAATACTATTTTACTGCC 1052

RESULT 7

LOCUS 196074

DEFINITION Sequence 1 from patent US 5734022.

ACCESSION 196074

VERSION 196074.1 GI:3940544

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1052)

AUTHORS Pasternack,G.R.

TITLE Antibodies to a novel mammalian protein associated with uncontrolled cell division

JOURNAL Patent: US 5734022-A 1 31-MAR-1998;

FEATURES Location/Qualifiers

source 1..1052

BASE COUNT 326 a 196 c 316 g 214 t

ORIGIN

Query Match 15.0%; Score 867.8; DB 6; Length 1052;

Best Local Similarity 91.8%; Pred. No. 1.2e-143;

Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTCAAAGTCTTAAACGTCGCGCTTGGGTTCGAGGTTTATTGATTGAATTCGGC 4416

Db 1 GAATTCCTCAAGTCTTAAACGTCGCGCTTGGGTTCGAGGTTTATTGATTGAATTCGGC 60

Qy	4825	AACGACTACGGAGAAACGTGTTCAAGCTTCTCCTGCAACTCACATATCTCGACAGCTGT	4884
Db	481	AACGACTACCCGAGAAAAATGTCTCAAGCTCCTCCGCAACTCACATATCTCGACGGCTAT	540
Qy	4885	TACTTGGGACCACAAGGAGGCCCTTACTACGATATTGAGGACACAGTGAGGGGCTGTGAT	4944
Db	541	GACCGGACGACAGAAGGAGGCCCTGACTCGGATGCTGAGGCTACGTGGAGGGCTGTGAT	600
Qy	4945	GACGAGGAGGAGGTGAGCATGAGGAGGATGATGAAGATGCTCAGGTAGTGGAGAT	5004
Db	601	GATCAGGAGGAGTATGAGGATGAGGAGGATGATGAAGATGCTCAGGTAGTGGAGAT	660
Qy	5005	GAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	5064
Db	661	GAGGAGGACGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	720
Qy	5065	GAGGATGAAGAAGCTTATAAGGATGAGAGGTACATGCGGAGGAGATGANGAAGACGCTT	5124
Db	721	GAGGATGAAGAAGCTTATAAGGATGAGAGGTACATGCGGAGGAGATGANGAAGACGCTT	780
Qy	5125	GGTGAAGAAGAAAGGGGTGAGAAGCGAAAATGAGAACCTCAAGATGAGGGAGAGAAGATGAT	5184
Db	781	GGTGAAGAAGAAAGGGGTGAGAAGCGAAAACGAGAACCTCAAGATGAGGGAGAGAAGATGAT	840
Qy	5185	GACTAAGTAGAATAAACCCTATTTCGAAAATTCCTATTGCTGATTTGACCTGTTTTACCCAT	5244
Db	841	GACTAAGTGGAAATAACCTATTTCGAAAATTCCTATTGCTGATTTGACCTGTTTTACCCAT	900
Qy	5245	ATCCCCCT-----CCCCCTCCAATCTCGCCCCCTGAAACTTACTTTTCTGATTTGTA	5298
Db	901	ATCCCCCTCCCCCCCCCTCTAATCTGCCCCCTGAACTTATTTTCTGATTTGTA	960
Qy	5299	CATTGCTGTGGGAATGAGACGGGAAAAAGTGTACTTGGGGGTGTGCGAGGAGGAGGCAG	5358
Db	961	CGTTGCTGTGGGAACGAGAGGGGAAGAGTGTACTTGGGGGTGTGCGGGGGA--GGATGCGG	1019
Qy	5359	GAGSCGTGTGACTAAATACTATTTTACTGCC	5391
Db	1020	GTGGGGTGGAAATAACTATTTTACTGCC	1052
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RESULT 9			
AC022740/c			
LOCUS			
DEFINITION			
AC022740 Homo sapiens chromosome 15, clone RP11-617D22, complete sequence.			
ACCESSION			
VERSION			
AC022740.4 GI:13786480			
KEYWORDS			
HTG.			
SOURCE			
Homo sapiens.			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE			
AUTHORS			
TITLE			
Birren,B., Linton,L., Nusbaum,C. and Lander,E.			
JOURNAL			
Homo sapiens chromosome 15, clone Rpl1-617D22			
REFERENCE			
2 (bases 1 to 162482)			
AUTHORS			
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,			
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bada,F.,			
Boguslavsky,L., Boukhalter,B., Brown,A., Burkett,G., Castle,A.,			
Choeple,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P.,			
DeAtellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,			
Ferreira,P., FlitzHugh,W., Forrest,C., Gage,D., Galagan,J.,			
Gardyna,S., Grant,G., Hagos,B., Hesford,A., Horton,L.,			
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,			
Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K.,			
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,			
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,			
Norman,C.H., O'Connor,T., O'Donnell,P., Oliviar,T.M., Peterson,K.,			
Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,			
Roy,A., Santos,R., Severi,P., Spencer,B., Stange-Thomann,N.,			
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,			

Miner, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, N.M., Neal, D., Neilson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogulu, M., Okunolu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoshitari, N., Sisson, I., Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Teifrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Zhou, J., Zorrilla, S., Kucherlapati, R., Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 164945)
Worley, K.C.
Direct Submission
Submitted (07-FEB-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 164945)
Worley, K.C.
Direct Submission
Submitted (01-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 164945)
Worley, K.C.
Direct Submission
Submitted (05-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 164945)
Worley, K.C.
Direct Submission
Submitted (29-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 164945)
Worley, K.C.
Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
7 (bases 1 to 164945)
Worley, K.C.
Direct Submission
Submitted (07-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jun 1, 2001 this sequence version replaced g1:14150337.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email qc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons

flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT.

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DEFINITION Homo sapiens chromosome 15, clone RP11-150L8, complete sequence.
ACCESSION AC107992
VERSION AC107992.3 GI:19683511
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149015)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-150L8
Unpublished
2 (bases 1 to 149015)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Linderblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihoval,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 149015)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,
Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Linderblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihoval,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 149015)

TITLE

JOURNAL
REFERENCE
AUTHORS
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Linderblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihoval,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 149015)

Landers,T., Lehoczy,J., Levine,R., Linderblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihoval,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 149015)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Linderblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L.,
Mihoval,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
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Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
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Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
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Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (27-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 22, 2002 this sequence version replaced gi:18677521.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project information
Center project name: L24554
Center clone name: 150_L_8

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QY 4447 CGAGAGATGGAGATGGCGACAGCGGATTTCATTAGAGCTGCGGAACAGCGGCGCTCTGAT 4506
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Db 86098 GGCGTGAAGCATTTGGCAGAAAGTGTCCGAACTCACGATCTAAATTTATGTGCGCAAC 86039
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QY 4915 GATATTGAGGACCACTGAGGGGCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAG 4974
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RESULT 12
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LOCUS
DEFINITION Homo sapiens clone RP11-82L14, WORKING DRAFT SEQUENCE, 15 unordered
pieces.
ACCESSION AC016297
VERSION AC016297.4 GI:15022083
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 186886)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Bozulavkiy,L., Boukhgaltier,B.,
Brown,A., Castie,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domino,M., Doneilan,L., Doyle,M.,
Ferrelle,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galaad,J., Gardyna,S., Grant,G., Hagos,B., Hearford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tefaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 26, 2001 this sequence version replaced gi:7139678.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4280
Center clone name: 82-L14
----- Summary Statistics
Sequencing vector: M13; M77815; 96% of reads
Sequencing vector: Plasmid; n/a; 4% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 179979 bases at least Q40
Consensus quality: 183319 bases at least Q30
Consensus quality: 184541 bases at least Q20
Insert size: 185000; agarose-fp
Insert size: 185486; sum-of-contigs
Quality coverage: 5.3 in Q20 bases; agarose-fp
Quality coverage: 5.3 in Q20 bas.
* NOTE: This is a 'working draft' sequence. It currently

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* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 28840: contig of 28840 bp in length
* 28841 28940: gap of 100 bp
* 28941 30179: contig of 1239 bp in length
* 30180 30279: gap of 100 bp
* 30280 33993: contig of 3714 bp in length
* 33994 34093: gap of 100 bp
* 34094 37562: contig of 3469 bp in length
* 37563 37662: gap of 100 bp
* 37663 41176: contig of 3514 bp in length
* 41177 41276: gap of 100 bp
* 41277 76172: contig of 34896 bp in length
* 76173 76272: gap of 100 bp
* 76273 83570: contig of 7298 bp in length
* 83571 83670: gap of 100 bp
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* 92375 92474: gap of 100 bp
* 92475 100960: contig of 8486 bp in length
* 100961 101060: gap of 100 bp
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* 110545 110644: gap of 100 bp
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* 124450 124549: gap of 100 bp
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Best Local Similarity 87.8%; Pred. No. 2.6e-130;
Matches 960; Conservative 0; Mismatches 93; Indels 41; Gaps 7;
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QY 5392 AAATAAATAATAT 5405
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RESULT 13
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LOCUS H.sapiens mRNA for HLA-DR associated protein I (PHAPI).
DEFINITION X75090
ACCESSION X75090
VERSION 1 GI:403006
KEYWORDS HLA-DR associated protein I; PHAPI.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS Kratzin,H.D.
TITLE Direct Submission
JOURNAL Submitted (20-SEP-1993) H.D. Kratzin, Max Planck Inst. for
Experimental Med., Dept. for Immunochimistry, Hermann-Rein-str. 3,
37075 Goettingen, FRG
REFERENCE 2 (bases 1 to 916)
AUTHORS Vaesen,M., Barnikol-Watanabe,S., Gotz,H., Awni,L.A., Cole,T.,
Zimmermann,B., Kratzin,H.D. and Hilschmann,N.
TITLE Purification and characterization of two putative HLA class II
associated proteins: PHAPI and PHAPII
JOURNAL Biol. Chem. Hoppe-Seyler 375 (2), 113-126 (1994)
MEDLINE 94250340
PUBMED 8192856
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Best Local Similarity 93.2%; Pred. No. 4.5e-130;
Matches 853; Conservative 0; Mismatches 50; Indels 12; Gaps 2;
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QY 4470 GATTCATTGAGCTGCGGAACAGGGCCCTCTGATGTGAAGAACTTGCCCTGGACAA 4529
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QY 4530 CAGTCGGTCGAATGAAGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAATT 4589
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QY 4590 CTTAAGTAAATCAACGAGAGCCCTCACTCAATCTCAGACTTACCAAGTTA---AAGTT 4646
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RESULT 14
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DEFINITION Homo sapiens cerebellar leucine rich acidic nuclear protein (LANP)
ACCESSION AF025684
VERSION AF025684.1 GI:2589220
KEYWORDS mRNA, linear, PRI 19-DEC-1997
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 925)
AUTHORS Matilla,A., Koshy,B.T., Cummings,C.J., Isobe,T., Orr,H.T. and Zoghbi,H.Y.

TITLE The cerebellar leucine-rich acidic nuclear protein interacts with ataxin-1
JOURNAL Nature 389 (6654), 974-978 (1997)
MEDLINE 98013170
PUBMED 9353121
REFERENCE 2 (bases 1 to 925)
AUTHORS Matilla,A. and Zoghbi,H.Y.
DIRECT SUBMISSION
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1997) Molecular and Human Genetics, and Pediatrics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Query Match 13.2%; Score 764.4; DB 9; Length 925;
Best Local Similarity 92.8%; Pred. No. 2.3e-125;
Matches 838; Conservative 0; Mismatches 52; Indels 13; Gaps 3;
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RESULT 15
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LOCUS
DEFINITION Rat mRNA for leucine-rich acidic nuclear protein, complete cds.
ACCESSION D32209
VERSION 1
KEYWORDS leucine-rich acidic nuclear protein; leucine-rich repeat; nuclear factor.
SOURCE Rattus norvegicus (strain Wistar) (library: library of M.Taoka)
postnatal days 7 brain cDNA to mRNA, clone PRN-8.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 1017)
Matsuoka,K., Taoka,M., Satozawa,N., Nakayama,H., Ichimura,T.,
Takahashi,N., Yamakuni,T., Song,S.Y. and Isohe,T.
A nuclear factor containing the leucine-rich repeats expressed in
murine cerebellar neurons
Proc. Natl. Acad. Sci. U.S.A. 91 (21), 9670-9674 (1994)
JOURNAL 95024022
MEDLINE 2 (bases 1 to 1017)
REFERENCE Direct Submission
AUTHORS Matsuoka,K.
JOURNAL Submitted (18-JUL-1994) Kunie Matsuoka, Mitsubishi Kasei Institute
of Life Science, 11 Minami-Oya, Machida, Tokyo 194, Japan
(Tel:0427-24-6288, Fax:0427-24-6316)
COMMENT Submitted (18-Jul-1994) to DDBJ by:
Kunie Matsuoka
Mitsubishi Kasei
Institute of Life Science
11 Minami-Oya, Machida
Tokyo 194
Japan
Phone: 0427-24-6288
Fax: 0427-24-1252.
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ORIGIN

Query Match 11.9%; Score 689; DB 10; Length 1017;
Best Local Similarity 83.3%; Pred. No. 4.8e-112;
Matches 850; Conservative 0; Mismatches 150; Indels 21; Gaps 5;

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QY 4540 AATGAAGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAATTTCTTAAGTAA 4599
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Search completed: December 8, 2002, 18:46:26
Job time : 12839 secs

XX
PT
phosphoprotein 32 (pp32) related genomic sequences

Applicant's name

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RESULT 2

AAA88236
ID AAA88236 standard; DNA; 5785 BP.
XX AAA88236;
XX
DT 15-DEC-2000 (first entry)
XX
DE Human placenta variant pp32rl genomic DNA sequence.
XX
KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200045852-A1.
XX
PD 10-AUG-2000.
XX
PF 03-FEB-2000; 2000WO-US02656.
XX
PR 03-FEB-1999; 99US-0118667.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Pasternack GR, Bai J;
XX WPI; 2000-514896/46.
DR

XX Treatment of cancer comprising restoration of pp32 function in
PT malignant cells -
XX
PS Example 3; Fig 2; 90pp; English.
XX
CC The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human placenta variant pp32r1 genomic DNA sequence from
CC an example of the present invention.
XX
SQ Sequence 5785 BP; 1755 A; 1087 G; 1162 C; 1781 T; 0 other;

Query Match 100.0%; Score 5785; DB 21; Length 5785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	2461	TCTTCT	2520	Db	3541	TATCTTCTCTCAGTGTGTTTTCCACAAAATCCCATAGCCCTGTGAAAAGATTTGTTTAGGG	3600
Db	2461	TCTTCT	2520	QY	3601	AAATATATTTTAAATATAGCATATTTTGTCAATGTGGGACATAGGACTAGTACCTGCTG	3660
QY	2521	GTGTGTGTGTGACAGAGTCCCTCTGTACCCAGGCTGGAGTGTAGTGGAGTATCTCC	2580	Db	3601	AAATATATTTTAAATATAGCATATTTTGTCAATGTGGGACATAGGACTAGTACCTGCTG	3660
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QY	2701	TACCATTTTGGCCAGGCTGTCTTCAACTCCTGACCTCAGGTGATCTGCCCTGGCTTG	2760	Db	3781	ATGCCACTCAAAATTTTATTCCTCTACCACTTGGCTATCTAAACCTAGTTAGATCTTTG	3840
Db	2701	TACCATTTTGGCCAGGCTGTCTTCAACTCCTGACCTCAGGTGATCTGCCCTGGCTTG	2760	QY	3841	GTTTTAGGTATAATCTGACAGACAGATCAACCAAGATCACATTCGTGAGTCAGAAAGTGG	3900
QY	2761	TTCCAAAGTGTGGGATACAGCGCTGAGCCACCTGCTGCTGTAGAAAGTTTGATTTTG	2820	Db	3841	GTTTTAGGTATAATCTGACAGACAGATCAACCAAGATCACATTCGTGAGTCAGAAAGTGG	3900
Db	2761	TTCCAAAGTGTGGGATACAGCGCTGAGCCACCTGCTGCTGTAGAAAGTTTGATTTTG	2820	QY	3901	AAAATTCATTAATTCATGATGATACCAATAAAAGATAGATTTAGCTTTTACAGGATGTTT	3960
QY	2821	ATGTCAGTGTGTAGATGAATTTGTGGGAAGCAAAACAAAGATAGATTTCAATGACAGTGA	2880	Db	3901	AAAATTCATTAATTCATGATGATACCAATAAAAGATAGATTTAGCTTTTACAGGATGTTT	3960
Db	2821	ATGTCAGTGTGTAGATGAATTTGTGGGAAGCAAAACAAAGATAGATTTCAATGACAGTGA	2880	QY	3961	TTGGCATTTTATTTCTTTCATTTTGGGGGAGATCTCACCAGAAATATGCTTTTCATGTTTCA	4020
QY	2881	AAAGTTTATTTGTAAGCTATATAAAGAAAATGTTGAAGCTTTCAATTCATTAGTGGC	2940				

Db 3961 TTGCAATTTTATCTTTTCATTTGAGGGAGATCTCACAAAAATATGCTCTTCATGGTTCA 4020
Qy 4021 TTGCTGTAATTAATTTCTGTCATGCATATCTTCAGGTTACTTTAAACCTAGTCTATAGAT 4080
Db 4021 TTGCTGTAATTAATTTCTGTCATGCATATCTTCAGGTTACTTTAAACCTAGTCTATAGAT 4080
Qy 4081 TCAAGAGATATCCCGTGTGTCAGTCTCTAAAGTAAAGAAAGAAATGGGTACTTGTGAAGGC 4140
Db 4081 TCAAGAGATATCCCGTGTGTCAGTCTCTAAAGTAAAGAAAGAAATGGGTACTTGTGAAGGC 4140
Qy 4141 TGATTCACAGTAAGTAGTGTAGAGGGAGTCCCTTGTGTAATCAAAATATCAACGTGA 4200
Db 4141 TGATTCACAGTAAGTAGTGTAGAGGGAGTCCCTTGTGTAATCAAAATATCAACGTGA 4200
Qy 4201 GCATCAGATAAGATTTTCTTTAGTCCACACACACCTACCTCTTACTAGGAGATCCATAT 4260
Db 4201 GCATCAGATAAGATTTTCTTTAGTCCACACACACCTACCTCTTACTAGGAGATCCATAT 4260
Qy 4261 ACTTGAATAATTTGTTCTGTTGACCCAGGTTACTTATCAGTCCCTTTATTAATAATTTTG 4320
Db 4261 ACTTGAATAATTTGTTCTGTTGACCCAGGTTACTTATCAGTCCCTTTATTAATAATTTTG 4320
Qy 4321 TAAATATTTGGGCTCGAGAACCGGAGCGAGCTGGTTGAGTCTCAAAAGTCCCTAAACGTG 4380
Db 4321 TAAATATTTGGGCTCGAGAACCGGAGCGAGCTGGTTGAGTCTCAAAAGTCCCTAAACGTG 4380
Qy 4381 CGGCGTGGGTTTCGAGGTTTATTCATTTGAATTCGGCTGGCAGCAGAGCCCTTCGACAGAC 4440
Db 4381 CGGCGTGGGTTTCGAGGTTTATTCATTTGAATTCGGCTGGCAGCAGAGCCCTTCGACAGAC 4440
Qy 4441 AGAGCGGAGAGATGGAGATGGGAGCGGATTCATTTCAGAGCTGCGGAAACAGGGCGCCC 4500
Db 4441 AGAGCGGAGAGATGGAGATGGGAGCGGATTCATTTCAGAGCTGCGGAAACAGGGCGCCC 4500
Qy 4501 TCTGATGTGAAGAACTTGCCTCGGACACAGCTCGTGCATGAAGCAAACTCGAAGCC 4560
Db 4501 TCTGATGTGAAGAACTTGCCTCGGACACAGCTCGTGCATGAAGCAAACTCGAAGCC 4560
Qy 4561 CTCACAGATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCA 4620
Db 4561 CTCACAGATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCA 4620
Qy 4621 ATCTCAGACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGGGCGCTG 4680
Db 4621 ATCTCAGACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGGGCGCTG 4680
Qy 4681 GAAGTATTTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTAAAGTGCACACAAAT 4740
Db 4681 GAAGTATTTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTAAAGTGCACACAAAT 4740
Qy 4741 AAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTT 4800
Db 4741 AAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTT 4800
Qy 4801 TTCAATTTGCGAGGTAAACACCTGAACGACTACGGAGAAAACGTTTCAAGCTTCTCCTG 4860
Db 4801 TTCAATTTGCGAGGTAAACACCTGAACGACTACGGAGAAAACGTTTCAAGCTTCTCCTG 4860
Qy 4861 CAACCTCACAATCTCGACAGCTGTTACTGGGACCAACAGGAGGCGCCCTTACTCAGATATT 4920
Db 4861 CAACCTCACAATCTCGACAGCTGTTACTGGGACCAACAGGAGGCGCCCTTACTCAGATATT 4920
Qy 4921 GAGGACCACCTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGAT 4980
Db 4921 GAGGACCACCTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGAT 4980
Qy 4981 GAAGATCCTCAGGTAGTGGAGAGTGAAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040
Db 4981 GAAGATCCTCAGGTAGTGGAGAGTGAAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040
Qy 5041 GAGGACCTGAGTGGAGGGGACGAGGAGGATCAAGAGGTTTAAACGATGGAGAGGTAGAT 5100
Db 5041 GAGGACCTGAGTGGAGGGGACGAGGAGGATCAAGAGGTTTAAACGATGGAGAGGTAGAT 5100

Qy 5101 GGCAGGAAGATGAAGAAGAGCTTGTGTGAAGAAGAAGGGGTGAGAGCGAAATAGAGAA 5160
Db 5101 GGCAGGAAGATGAAGAAGAGCTTGTGTGAAGAAGAAGGGGTGAGAGCGAAATAGAGAA 5160
Qy 5161 CCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAACCTATTTTGAAAATTCCTAT 5220
Db 5161 CCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAACCTATTTTGAAAATTCCTAT 5220
Qy 5221 TGTGATTTGACTGTTTTTACCCATATCCCTCCCTCCCAATCTCTGCCCTGAAACAT 5280
Db 5221 TGTGATTTGACTGTTTTTACCCATATCCCTCCCTCCCAATCTCTGCCCTGAAACAT 5280
Qy 5281 ACTTTTTTCTGATTTAAACATTCCTCTGGAATGACACGGGAAAGTGTACTGGGGTTG 5340
Db 5281 ACTTTTTTCTGATTTAAACATTCCTCTGGAATGACACGGGAAAGTGTACTGGGGTTG 5340
Qy 5341 TGGAGGAGGAGGCGGAGGCGGTGGACTAAATTAATTTTACTGCCAAATAAAT 5400
Db 5341 TGGAGGAGGAGGCGGAGGCGGTGGACTAAATTAATTTTACTGCCAAATAAAT 5400
Qy 5401 AATATTTGTAATTAATTAACCTGGGATAGCTTAGAATGATTACTATTATTTCT 5460
Db 5401 AATATTTGTAATTAATTAACCTGGGATAGCTTAGAATGATTACTATTATTTCT 5460
Qy 5461 CTCTCTCTTTTTTATTTTTTACACATCTATTCTTTTAAAGTATAGTCTTTAGTCCAAG 5520
Db 5461 CTCTCTCTTTTTTATTTTTTACACATCTATTCTTTTAAAGTATAGTCTTTAGTCCAAG 5520
Qy 5521 GAAAGGCACTCAATCCACTTATTAACTGCTTACTGCTCAAGTAAATAAGCTCC 5580
Db 5521 GAAAGGCACTCAATCCACTTATTAACTGCTTACTGCTCAAGTAAATAAGCTCC 5580
Qy 5581 AGAATTTACAAAAGAGGAGAAATAATTTACAATGAAATGTTGCTTAAATAATTTAA 5640
Db 5581 AGAATTTACAAAAGAGGAGAAATAATTTACAATGAAATGTTGCTTAAATAATTTAA 5640
Qy 5641 ACAATTTACAGTAAATGATTTGTTAAAGCAAAATCTTATTTTAAATAATTTTAAAGA 5700
Db 5641 ACAATTTACAGTAAATGATTTGTTAAAGCAAAATCTTATTTTAAATAATTTTAAAGA 5700
Qy 5701 AATAATTTGCTTAAAGCAAAATTTTGGAAAATAAATGCACCTTTATCTGATTTTAT 5760
Db 5701 AATAATTTGCTTAAAGCAAAATTTTGGAAAATAAATGCACCTTTATCTGATTTTAT 5760
Qy 5761 TATTAACAATGATTTATAAGCTT 5785
Db 5761 TATTAACAATGATTTATAAGCTT 5785

RESULT 3
AAA88237
ID AAA88237 standard; DNA; 1035 bp.
XX AAA88237;
XX AC
XX XX
DT 15-DEC-2000 (first entry)
XX Human variant pp32rl nucleotide sequence.
XX Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.
XX Homo sapiens.
OS
XX WO200045852-A1.
PN
XX 10-AUG-2000.
PD
XX 03-FEB-2000; 2000WO-US02656.
PF
XX 03-FEB-1999; 99US-0118667.
PR

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XX (UYJO ) UNIV JOHNS HOPKINS.
PA Pasternack GR, Bai J;
XX P-PSDB; AAB20655.
DR WPI; 2000-514896/46.
DR P-PSDB; AAB20655.
XX
PT Treatment of cancer comprising restoration of pp32 function in
PT malignant cells -
XX
PS Example 3; Fig 3; 90pp; English.
XX
CC The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human variant pp32r1 nucleotide sequence from
CC an example of the present invention.
XX
SQ Sequence 1035 BP; 322 A; 189 C; 308 G; 216 T; 0 other;
```

Query Match 17.9%; Score 1035; DB 21; Length 1035;
Best Local Similarity 100.0%; Pred. No. 7.9e-150;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 4357 GAGTCTTCAAAAGTCTAAACGCTGGCGCGTTCGAGGTTTATTGATTGAATTCGGC 4416
DB 1 GAGTCTTCAAAAGTCTAAACGCTGGCGCGTTCGAGGTTTATTGATTGAATTCGGC 60
QY 4417 TGGCAGCAGAGCCTCTGCAGACAGAGCGCGGAGAGTGGAGATGGCAGCGGATTTCAT 4476
DB 61 TGGCAGCAGAGCCTCTGCAGACAGAGCGCGGAGAGTGGAGATGGCAGCGGATTTCAT 120
QY 4477 TCAGAGCTCGGAAACAGGCGCCCTCTGATGTGAAGAACTTGCCTCGACAACTAGTCGG 4536
DB 121 TCAGAGCTCGGAAACAGGCGCCCTCTGATGTGAAGAACTTGCCTCGACAACTAGTCGG 180
QY 4537 TCGAATGAGGCAAACTCGAAGCCCTCAGAGATGAATTTGAAGAACTGGAATTCCTTAAGT 4596
DB 181 TCGAATGAGGCAAACTCGAAGCCCTCAGAGATGAATTTGAAGAACTGGAATTCCTTAAGT 240
QY 4597 AAAATCAAGCGAGGCGCTCACCTCAATCTCAGACTTACCAAGTTAAAGTTGAGAAAGCTT 4656
DB 241 AAAATCAAGCGAGGCGCTCACCTCAATCTCAGACTTACCAAGTTAAAGTTGAGAAAGCTT 300
QY 4657 GAACTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCAACTCAGCAT 4716
DB 301 GAACTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCAACTCAGCAT 360
QY 4717 CTATATTAAAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTA 4776
DB 361 CTATATTAAAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTA 420
QY 4777 GAAAACCTCAAGAGCTTAGACCTTTTCAATTGGAGGTAAACCAACCTGAACGACTACGGA 4836
DB 421 GAAAACCTCAAGAGCTTAGACCTTTTCAATTGGAGGTAAACCAACCTGAACGACTACGGA 480
QY 4837 GAAAACGTGTTCAAGCTTCTCTGCAACTCAGATATCTGACAGCTGTTTACTGGACAC 4896
DB 481 GAAAACGTGTTCAAGCTTCTCTGCAACTCAGATATCTGACAGCTGTTTACTGGACAC 540
QY 4897 AAGGAGGCGCCCTTACTCAGATATTGAGGACACGCTGGAGGCGCTGATGACGAGGAG 4956
DB 541 AAGGAGGCGCCCTTACTCAGATATTGAGGACACGCTGGAGGCGCTGATGACGAGGAG 600
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QY 4957 GGTGAGCATGAGGAGGATGATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGCGCAG 5016
DB 601 GGTGAGCATGAGGAGGATGATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGCGCAG 660
QY 5017 GAGGAGGAGGAGGAGGATGAAGAGGAGGAGGCTGAGTGGAGGAGGAGGAGGATGAAGAA 5076
DB 661 GAGGAGGAGGAGGAGGATGAAGAGGAGGAGGCTGAGTGGAGGAGGAGGAGGATGAAGAA 720
QY 5077 GGTATTAACCATGAGAGGTAGATGCGAGGAAGATGAAGAAGAGCTTGTGTAAGAAGAA 5136
DB 721 GGTATTAACCATGAGAGGTAGATGCGAGGAAGATGAAGAAGAGCTTGTGTAAGAAGAA 780
QY 5137 AGGGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5196
DB 781 AGGGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 5197 TAACCTATTGTAAGAAATTCCTATTGATGATTTGACTGTTTACCCATATCCCTCCCC 5256
DB 841 TAACCTATTGTAAGAAATTCCTATTGATGATTTGACTGTTTACCCATATCCCTCCCC 900
QY 5257 CTCCAATCTGCGCCCTGAAACTTACTTTTCTGATTTGTAACATTTGCTGTGGAATGAG 5316
DB 901 CTCCAATCTGCGCCCTGAAACTTACTTTTCTGATTTGTAACATTTGCTGTGGAATGAG 960
QY 5317 ACGGGAAGAGTGTACTGGGGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5376
DB 961 ACGGGAAGAGTGTACTGGGGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
QY 5377 ACTATTTTACTGCC 5391
DB 1021 ACTATTTTACTGCC 1035
RESULT 4
AA81537
ID AA81537 standard; DNA; 889 BP.
XX
AC AA81537;
XX AC
XX AC
DT 26-AUG-1999 (first entry)
XX
DE Genomic sequence of phosphoprotein 32 variant pp32r2.
XX
KW Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;
KW prostatic adenocarcinoma; antineoplastic activity;
KW transformation suppression; malignant potential; neuroendocrine;
KW neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.
XX
OS Homo sapiens.
XX
PN WO9929906-A2.
XX
PD 17-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US26433.
XX
PR 12-DEC-1997; 97US-0069677.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
PI Brody JR, Kadkol SS, Kochevar GJ, Pasternack GR;
XX WPI; 1999-385626/32.
XX
PT Phosphoprotein 32 (pp32) related genomic sequences
XX
PS Claim 1; Fig 5; 65pp; English.
XX
CC The present sequence represents the genomic sequence of phosphoprotein
CC 32 (pp32) variant pp32r2. The pp32r1 and pp32r2 sequences are associated
CC with cancer in prostate, especially prostatic adenocarcinomas. Normal
CC pp32 exerts antineoplastic activity through suppression of
CC transformation. Cancer-associated pp32 variants augment, rather than
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CC inhibit, transformation. Determining the presence of a gene encoding
CC residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a
CC diagnostic method for predicting malignant potential of neuroendocrine,
XX neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.
SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

```
Query Match      15.4%; Score 889; DB 20; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCTCTGCAGACAGAGAGCGC 4447
DB 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCTCTGCAGACAGAGAGCGC 60

QY 4448 GAGAGATGGAGTGGCAGACGGATTTCATTTCAGAGCTCGCGAACAGAGCGGCCCTCTGATG 4507
DB 61 GAGAGATGGAGTGGCAGACGGATTTCATTTCAGAGCTCGCGAACAGAGCGGCCCTCTGATG 120

QY 4508 TGAAGAAGACTTGGCTGGACAACTGCGTGCATGAAGGCAAACTCGAAGCCCTCAG 4567
DB 121 TGAAGAAGACTTGGCTGGACAACTGCGTGCATGAAGGCAAACTCGAAGCCCTCAG 180

QY 4568 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 4627
DB 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240

QY 4628 ACTTACCAAGTTAAAGTTGAGAAGCTTGAATTAAGTAAATCAACGGAGGCTCGAAGTAT 4687
DB 241 ACTTACCAAGTTAAAGTTGAGAAGCTTGAATTAAGTAAATCAACGGAGGCTCGAAGTAT 300

QY 4688 TGGCAGAAAGTGTCCAACTCAGCATCTATATTTAAGTGGCAACAAATTAAGAAC 4747
DB 301 TGGCAGAAAGTGTCCAACTCAGCATCTATATTTAAGTGGCAACAAATTAAGAAC 360

QY 4748 TCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 4807
DB 361 TCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420

QY 4808 GCGAGGTAAACCACTGAACGACTACGAGAAACAGTTCCTCAAGCTCA 4867
DB 421 GCGAGGTAAACCACTGAACGACTACGAGAAACAGTTCCTCAAGCTCA 480

QY 4868 CATATCTCGACAGCTGTACTGGACACACAGAGAGGCCCTTACTAGATATTGAGGACC 4927
DB 481 CATATCTCGACAGCTGTACTGGACACACAGAGAGGCCCTTACTAGATATTGAGGACC 540

QY 4928 ACGTGGAGGGCTCGATGACGAGGAGGCTGAGCATGAGGAGGTATGATCAAGATG 4987
DB 541 ACGTGGAGGGCTCGATGACGAGGAGGCTGAGCATGAGGAGGTATGATCAAGATG 600

QY 4988 CTCAGGTAGTGGAGATGAGGAGGGCGAGGAGGAGGAGGAGGTGAAGAGGAGGACG 5047
DB 601 CTCAGGTAGTGGAGATGAGGAGGGCGAGGAGGAGGAGGAGGTGAAGAGGAGGACG 660

QY 5048 TGAGTGGAGGGGACGAGGAGTGAACAGGTATTAACAGTGGAGAGGTAGATGGCGAGG 5107
DB 661 TGAGTGGAGGGGACGAGGAGTGAACAGGTATTAACAGTGGAGAGGTAGATGGCGAGG 720

QY 5108 AAGATGAAGAAGAGCTTGGTGAAGAAAGAGGGCTCAGAACGCAAAATGAGAACCTGAAG 5167
DB 721 AAGATGAAGAAGAGCTTGGTGAAGAAAGAGGGCTCAGAACGCAAAATGAGAACCTGAAG 780

QY 5168 ATGAGGAGAGATGATGACTAAGTAACTATTTTGAAGAAATTCCTATTGTGATT 5227
DB 781 ATGAGGAGAGATGATGACTAAGTAACTATTTTGAAGAAATTCCTATTGTGATT 840

QY 5228 TGACTGTTTTTACCCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 5276
DB 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT 889
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RESULT 5

AAA88239
ID AAA88239 standard; DNA; 889 BP.
XX
AC AAA88239;
XX
DT 15-DEC-2000 (first entry)
XX
DE Human variant pp32r2 genomic DNA sequence.
XX
KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200045852-A1.
XX
PD 10-AUG-2000.
XX
PF 03-FEB-2000; 2000WO-US02656.
XX
PR 03-FEB-1999; 99US-0118667.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
PA
PI Pasternack GR, Bai J;
XX
XX WPI; 2000-514896/46.
XX
PT Treatment of cancer comprising restoration of pp32 function in
XX malignant cells -
XX
PS Example 5; Fig 5; 90pp; English.
XX
CC The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human variant pp32r2 genomic DNA sequence from
CC an example of the present invention.
XX
SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 15.4%; Score 889; DB 21; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCTCTGCAGACAGAGAGCGC 4447
DB 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCTCTGCAGACAGAGAGCGC 60
QY 4448 GAGAGATGGAGTGGCAGACGGATTTCATTTCAGAGCTCGCGAACAGAGGGGCCCTCTGATG 4507
DB 61 GAGAGATGGAGTGGCAGACGGATTTCATTTCAGAGCTCGCGAACAGAGGGGCCCTCTGATG 120
QY 4508 TGAAGAAGCTTGGCTGGACAACTGCGTGCATGAAGGCAAACTCGAAGCCCTCAG 4567
DB 121 TGAAGAAGCTTGGCTGGACAACTGCGTGCATGAAGGCAAACTCGAAGCCCTCAG 180
QY 4568 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 4627
DB 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240
QY 4628 ACTTACCAAGTTAAAGTTGAGAAGCTTGAATTAAGTAACTAGAGTCTCAGGGGGCTCGAAGTAT 4687
DB 241 ACTTACCAAGTTAAAGTTGAGAAGCTTGAATTAAGTAACTAGAGTCTCAGGGGGCTCGAAGTAT 300

QY 4688 TGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGACC 4747
Db |||||||
QY 301 TGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGACC 360
Db |||||||
QY 4748 TCAGCACAAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 4807
Db |||||||
QY 361 TCAGCACAAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420
Db |||||||
QY 4808 GCGAGTTACCAACCTGAAAGACTACGGAGAAAACGTTCAAGCTTCTCTGCAACTCA 4867
Db |||||||
QY 421 GCGAGTTACCAACCTGAAAGACTACGGAGAAAACGTTCAAGCTTCTCTGCAACTCA 480
Db |||||||
QY 4868 CATATCTCACAGCTCTTACTGGGACCAAGAGGCCCTTACTCAGATATTGAGGACC 4927
Db |||||||
QY 481 CATATCTCACAGCTCTTACTGGGACCAAGAGGCCCTTACTCAGATATTGAGGACC 540
Db |||||||
QY 4928 ACCTGAGGGCCCTGGATGACGAGGAGGGTGAAGTGAAGAGGAGTATGATGAAGATG 4987
Db |||||||
QY 541 ACCTGAGGGCCCTGGATGACGAGGAGGGTGAAGTGAAGAGGAGTATGATGAAGATG 600
Db |||||||
QY 4988 CTCAGTAGTGAAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
Db |||||||
QY 601 CTCAGTAGTGAAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db |||||||
QY 5048 TGAGTGGAGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGATGGCGAGG 5107
Db |||||||
QY 661 TGAGTGGAGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGATGGCGAGG 720
Db |||||||
QY 5108 AAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAAGCGAAATGAGAACCTGAAG 5167
Db |||||||
QY 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAAGCGAAATGAGAACCTGAAG 780
Db |||||||
QY 5168 ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTTTGAABAATCCTATTCTGATT 5227
Db |||||||
QY 781 ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTTTGAABAATCCTATTCTGATT 840
Db |||||||
QY 5228 TGACTGTTTTTACCCTATATCCCTCCCTCCCTCCCAATCTCCCTCCCTGAA 5276
Db |||||||
QY 841 TGACTGTTTTTACCCTATATCCCTCCCTCCCTCCCAATCTCCCTCCCTGAA 889
Db |||||||
RESULT 6
AAS76389
ID AAS76389 standard; cdna; 1155 BP.
AC AAS76389;
XX
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #12193.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN W0200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PA Drmanac RT, Liu C, Tang YT;
XX
PI WPI; 2001-639362/73.
DR P-PSDB; ABG12202.
XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 12193; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1155 BP; 340 A; 219 C; 347 G; 249 T; 0 other;

Query Match 15.3%; Score 883; DB 23; Length 1155;
Best Local Similarity 91.7%; Pred. No. 1.5e-126;
Matches 984; Conservative 0; Mismatches 70; Indels 19; Gaps 4;

QY 4332 GCTCGAGAACCGGAGCGAGCTGGTGTGAGCTTCAAGCTCTAAACCTGCGCGCGTGGT 4391
Db 1 GCTCGAGAACCGGAGCGAGCTGGTGTGAGCTTCAAGCTCTAAACCTGCGCGCGTGGT 60
QY 4392 TCGAGGTTTATTGATTGAATTCGGCTGGCAGGAGAGCTCTGCGACAGAGAGCGGAGA 4451
Db 61 TCGGGGTTTATTGATTGAATTCGGCGCGGGAGCTCTGCGAGAGAGAGCGGAGA 120
QY 4452 GATGAGATGGCGAGAGATTCATTGAGCTCGGGAACAGGCGCCCTCTGATGTGAA 4511
Db 121 GATGAGATGGCGAGAGATTCATTGAGCTCGGGAACAGGCGCCCTCTGATGTGAA 180
QY 4512 AGAAGTTGCCCTGGACACAGCTCGGTGGAATGAAGGAACTCGAAGCCCTCACAGATGA 4571
Db 181 AGAAGTTGCCCTGGACACAGCTCGGTGGAATGAAGGAACTCGAAGCCCTCACAGATGA 240
QY 4572 ATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAGACTT 4631
Db 241 ATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAGACTT 300
QY 4632 ACCAAAGTTAAAGT---TGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGGCGCT 4679
Db 301 ACCAAAGTTAAACAACTTAAGAAAGCTTGAACCTAAGCGATTAACAGAGTCTCAGGGGCGCT 360
QY 4680 GGAAGTATGGCAGAAAAGTGTCCAAACCTCAAGC-CATCTATATTTAAGTGGCAACAAA 4738
Db 361 GGAAGTATGGCAGAAAAGTGTCCGAACTTCCGCACTTAATTTAAGTGGCAACAAA 420
QY 4739 TTAAAGAGCTCAGCACAAATAGAGCCACTGAAACAGTTTGAAGAACTCTAAGAGCTTAGACC 4798
Db 421 TTAAAGAGCTCAGCACAAATAGAGCCACTGAAAGAAATTTAGAAAGCTCTAAGAGCTTAGACC 480
QY 4799 TTTTCAATTTGGAGGTAAACCACTGAAGAGTACCGAGAGAAAAGCTGTTCAAGCTTCTCC 4858
Db 481 TTTTCAATTTGGAGGTAAACCACTGAAGAGTACCGAGAGAAAATGTGTTCAAGCTTCTCC 540
QY 4859 TGCAACTCACATATCTCGACAGCTGTTACTGGGACCAAGGAGGCGCCCTTACTCAGATA 4918
Db |||||||

Db	781	GGTGAAGAAGAGGGT	CAGAACGAAACAGAACCTGAAGATGAGGAGAGATGAT	840
Qy	5185	GACTAAGTAGAATAACCTATTTTGA	AAATTCCTATTTGTTGATTTGACTGTTTACCCTAT	5244
Db	841	GACTAAGTGGAAATACCTATTTTGA	AAATTCCTATTTGTTGATTTGACTGTTTACCCTAT	900
Qy	5245	ATCCCTCT-----CC	CCCTCTCAATCTGCCCCCTGAACTTACTTTTCTGATTGTAA	5298
Db	901	ATCCCTCTCTCCCCCCCCCTCTAATCTGCCCCCTGAACTTATTTTCTGATTGTAA	960	
Qy	5299	CATTGCTGTGGGAATGAGACGGGAA	AGTGTACTTGGGGTTGTGGAGGGAGGGAGGCAG	5358
Db	961	CGTTCGCTGTGGACGAGAGGGGA	AGTGTACTTGGGGTTGCGGGGGA-GGATGGCGG	1019
Qy	5359	GAGCGGTGGACTAAAATACTATTTTACTGCC	5391	
Db	1020	GTGGGGGTGGAAATAAAATACTATTTTACTGCC	1052	
RESULT 8				
AAx81536				
ID	AAx81536 standard; DNA; 1052 BP.			
XX	AC	AAx81536;		
XX	XX			
XX	DT	26-AUG-1999 (first entry)		
XX	XX			
DE	Nucleotide sequence of normal human phosphoprotein 32 (pp32).			
XX	XX			
KW	Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;			
KW	prostatic adenocarcinoma; antineoplastic activity;			
KW	transformation suppression; malignant potential; neuroendocrine;			
KW	neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.			
XX	XX			
OS	Homo sapiens.			
XX	XX			
PN	W09929906-A2.			
XX	XX			
PD	17-JUN-1999.			
XX	XX			
PF	11-DEC-1998; 98WO-US26433.			
XX	XX			
PR	12-DEC-1997; 97US-0069677.			
XX	XX			
PA	(UYJO) UNIV JOHNS HOPKINS.			
XX	XX			
PI	Brody JR, Kadkol SS, Kocheavar GJ, Pasternack GR;			
XX	XX			
DR	WPI; 1999-385626/32.			
XX	XX			
PT	Phosphoprotein 32 (pp32) related genomic sequences			
XX	XX			
PS	Example 2; Fig 3; 65pp; English.			
XX	XX			
CC	The present sequence represents a human phosphoprotein 32 (pp32) nucleotide sequence. The specification describes pp32 variants, designated pp32r1 and pp32r2. The pp32r1 and pp32r2 sequences are associated with cancer in prostate, especially prostatic adenocarcinomas. Normal pp32 exerts antineoplastic activity through suppression of CC transformation. Cancer-associated pp32 variants augment, rather than inhibit, transformation. Determining the presence of a gene encoding CC residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a CC diagnostic method for predicting malignant potential of neuroendocrine, CC neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.			
XX	XX			
SQ	Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;			
Query Match 15.0%; Score 867.8; DB 20; Length 1052;				
Best Local Similarity 91.8%; Pred. No. 3.1e-124;				
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;				
Qy	4357	GAGTCTTCAAAAGTCTTAAACGTCGCGCGCTGAGGTTTATTTGATTTGATTCGCGC	4416	

Db	1	GAATTC	CCCAAGTCTCTAAACCGCGCGCGCTGGTTCGGGGTTTATTGATTGAATTC	60
Qy	4417	TGCGCAGAGAGCCCTCTGC	ACAGAGAGCGCGAGATGAGATGGCAGCGGATTCAT	4476
Db	61	CGCGCGGAGAGCCCTCTGC	AGAGAGAGCGCGAGATGAGATGGCAGCGGATTCAT	120
Qy	4477	TCAGAGCTCGGGAACAGGCG	CCCTCTGATGTGTAAAGAACTTGCCTTGACAACTGCG	4536
Db	121	TTAGAGCTCGGGAACAGGAG	CGCCCTCTGATGTGTAAAGAACTTGTCTTGACAACTGCG	180
Qy	4537	TCGAATGAAGGCAAACTCGA	AGCCCTCACAGATGAATTTGAAGAACTGGAATTC	4596
Db	181	TCGAATGAAGGCAAACTCGA	AGCCCTCACAGATGAATTTGAAGAACTGGAATTC	240
Qy	4597	AAATCAACGAGGAGCCCTCA	CTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAG	4653
Db	241	ACAATCAACGTAGGCTCACC	TCAATCGCAAACTTACCAAAAGTTAACAACAACTTAAGAG	300
Qy	4654	CTTGAACCTA-----AG	AGTCTCAGGGGCTCGAAAGTATTTGGCAGAAAAAGTGTCCA	4704
Db	301	CTTGAACCTAAGCGATAAC	AGAGTCTCAGGGGCTTAGAAGTATTGGCAGAAAAAGTGTCCG	360
Qy	4705	AACCTCAGCGATCTATATTA	AGTGGCAACAAATTAAGAGCCCTCAGCACAATAGAGCCA	4764
Db	361	AACCTCAGCGATCTAATAAT	TTAAGTGGCAACAAATTAAGAGCCCTCAGCACAATAGAGCCA	420
Qy	4765	CTGAACAGTTAGAAAACCTC	AAAGAGCTTAGACCTTTTCAATTCGAGAGTTAACCAACCTG	4824
Db	421	CTGAACAGTTAGAAAACCTC	AAAGAGCTTAGACCTTTTCAATTCGAGAGTTAACCAACCTG	480
Qy	4825	AACGACTACGGAAGAAACG	TGTTCAAGCTTCTCTGCAACTCACAATCTCGACACGCTGT	4884
Db	481	AACGACTACGGAAGAAATG	TTCCTCAAGCTTCTCTGCAACTCACAATCTCGACACGCTAT	540
Qy	4885	TACTGGACACAAAGGAGCG	CCCTTACTCAGATATTTAGGACCCAGCTGGAGGCGCTGGAT	4944
Db	541	GACCGGAGACAAAGGAGCG	CCCTTACTCAGATATTTAGGAGCCCTGAGTGGAGGCGCTGGAT	600
Qy	4945	GACGAGGAGGAGGTGAGCA	TGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAGAT	5004
Db	601	GATGAGGAGGAGGTGAGCA	TGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAGAT	660
Qy	5005	GAGGAGGCGAGGAGGAGG	AGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG	5064
Db	661	GAGGAGGCGAGGAGGAGG	AGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG	720
Qy	5065	GAGGATGAAGAAGGTTATA	ACGATGGAGAGGTAGATGGCGAGGAAGATGAAGAAGAGCTT	5124
Db	721	GAGGATGAAGAAGGTTATA	ACGATGGAGAGGTAGATGGCGAGGAAGATGAAGAAGAGCTT	780
Qy	5125	GGTGAAGAAGGAGGAGG	GTCAAGCGGAAATGAGAACTTGAAGATGAGGAGGAGGAGATGAT	5184
Db	781	GGTGAAGAAGGAGGAGG	GTCAAGCGGAAATGAGAACTTGAAGATGAGGAGGAGGAGATGAT	840
Qy	5185	GACTAAGTAGAATAACCTAT	TTTGAAGAAATTCCTATTTGATTTGACTGTTTACCCTAT	5244
Db	841	GACTAAGTAGAATAACCTAT	TTTGAAGAAATTCCTATTTGATTTGACTGTTTACCCTAT	900
Qy	5245	ATCCCTCT-----CC	CCCTCTCAATCTGCGCCCTGAAACTTACTTTTCTGATTGTAA	5298
Db	901	ATCCCTCTCT	CCCCCTCTAATCTGAGTATCTGCCCTGAAACTTATTTTCTGATTGTAA	960
Qy	5299	CATTGCTGTGGGAATGACAC	GGGAAAGTGTACTTGGGGTTGTGGAGGGAGGAGGAGGAG	5358
Db	961	CGTTCGCTGTGGGAACGAG	AGGAAAGTGTACTTGGGGTTGTGGGGGGA-GGATGGCGG	1019
Qy	5359	GAGGCGGTGGACTAAAATAC	TATTTTACTGCC	5391
Db	1020	GTGGGGGTGGAAATAAAATAC	TATTTTACTGCC	1052
RESULT 9				
AAA88238				

AAA88238 standard; DNA; 1052 BP.
AC AAA88238;
XX
DT 15-DEC-2000 (first entry)
XX
DE Human pp32 nucleotide sequence.
XX
KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200045852-A1.
XX
PD 10-AUG-2000.
XX
PF 03-FEB-2000; 2000WO-US02656.
XX
PR 03-FEB-1999; 99US-0118667.
XX
PA (UJYO) UNIV JOHNS HOPKINS.
XX
PI Pasternack CR, Bai J;
XX
XX WPI; 2000-514896/46.
DR P-PSDB; AAB20656.
XX
DR
XX
PT Treatment of cancer comprising restoration of pp32 function in
PT malignant cells -
XX
PS Example 3; Fig 3; 90pp; English.
XX
CC The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human pp32r1 nucleotide sequence from an example of
CC the present invention.
XX
XX Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;
XX
Query Match 15.0%; Score 867.8; DB 21; Length 1052;
Best Local Similarity 91.8%; Pred. No. 3.1e-124;
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;
QY 4357 GAGTCTTCARAAGTCCTAAAACGTGCGGCCGTGGTTCGAGGTTATTGATTGAATTCGGC 4416
Db 1 GAATTCCTCAAGTCTCTCAAGACGCGCGCGCGTGGGTTCGGGTTTATTGATTGAATTCGCG 60
QY 4417 TGGCAGCAGAGCCCTCTGCAGACAGAGCGCGAGAGATGGAGATGGCAGCGGATTCAT 4476
Db 61 CGGCGCGGAGCCCTCTGCAGAGAGAGCGCGGAGATGGAGATGGCAGCGGATTCAT 120
QY 4477 TCAGAGCTCGGACAGCGGCCCTCTGATGTGAAAGAACTTCGCCCTGGACACACATCGG 4536
Db 121 TTAGAGCTCGGAAACAGCGCCCTCTGATGTGAAGAACTTCCTCTGGACACATCGG 180
QY 4537 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAAATTCCTTAAGT 4596
Db 181 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAAATTCCTTAAGT 240
QY 4597 AAAATCAACGGAGCCCTCACCTCAATCTCAGACTTACCAAGTTA--AGTTGAGAAAG 4653
Db 241 ACAATCAACGTAGGCCCTCACCTCAATCGCAAACTTACCAAGTTAAACAACTTAAGAAG 300

QY 4654 CTTGAACATA-----AGAGTCTCAGGGGCGCTCGAAGTATTGGCAGAAAAGTGTCCA 4704
Db 301 CTTGAACATAAGCGATAACAGAGTCTCAGGGGCGCTAGAAGTATTGGCAGAAAAGTGTCCG 360
QY 4705 AACCTCAGCATCTATATTAAAGTGGCAACAATAAAGACCTCAGCACAATAGAGCCA 4764
Db 361 AACCTCAGCATCTAAATTTAAGTGGCAACAATAAAGACCTCAGCACAATAGAGCCA 420
QY 4765 CTGAACAGTTAGAAAACCTCAAGAGCTTACAGCTTTTCAATTTGCGAGGTAAACCACTG 4824
Db 421 CTGAACAGTTAGAAAACCTCAAGAGCTTACAGCTTTTCAATTTGCGAGGTAAACCACTG 480
QY 4825 AACGACTACGGAGAAAACGTGTTCAAGCTTCTCCTCCAACTCACATATCTCGACAGCTGT 4884
Db 481 AACGACTACCGAGAAAATGTGTTCAAGCTCTCCCGCAACTCACATATCTCGACGCTAT 540
QY 4885 TACTGGGACCACAAAGGAGGCCCTTACTCAGATATTAGAGACCACGCTGAGGGCCCTGGAT 4944
Db 541 GACCGGAGCAGCAAGAGGCCCTGACTCGGATCTGAGGGCTACGTGAGGGCCCTGGAT 600
QY 4945 GACGAGGAGGGGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGCTAGTGAAGAT 5004
Db 601 GATGAGGAGGAGTGAAGATGAGGAGGAGTATGATGAAGATGCTCAGCTAGTGAAGAT 660
QY 5005 GAGGAGGCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5064
Db 661 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 5065 GAGGATGAAGAAGGTTATAACGATGAGAGGTAGATGGCGAGGAGATCAAGAAGAGCTT 5124
Db 721 GAGGATGAAGAAGGTTATAACGATGAGAGGTAGATGGCGAGGAGATGAAGAAGAGCTT 780
QY 5125 GGTGAAGAAAAGGGGTGAGAAAGCGAAAATGAGAACCTGAAGATGAGGAGGAGGAGATGAT 5184
Db 781 GGTGAAGAAAAGGGGTGAGAAAGCGAAAACGAGAACCTGAAGATGAGGAGGAGGAGATGAT 840
QY 5185 GACTAGTAGAATAACCTATTGTTGAAAATTCCTATTGATGATGATGATGATGATGATGAT 5244
Db 841 GACTAGTAGAATAACCTATTGTTGAAAATTCCTATTGATGATGATGATGATGATGATGAT 900
QY 5245 ATCCCTCT-----CCCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 5298
Db 901 ATCCCTCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 960
QY 5299 CATTCGTGTGGAATGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5358
Db 961 CGTTCGTGTGGAATGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1019
QY 5359 GAGGCGGTGGACTAAAATACTATTTTACTGCG 5391
Db 1020 GTGGGGGTGGAATAAATACTATTTTACTGCG 1052
RESULT 10
ABK84424
ID ABK84424 standard; cDNA; 1052 BP.
XX
AC ABK84424;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #995.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
XX granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens.

XX WO200228999-A2.

XX 11-APR-2002.

XX 03-OCT-2001; 2001WO-US30821.

XX 03-OCT-2000; 2000US-237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

XX Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -

XX Claim 1; SEQ ID No 995; 114pp; English.

XX The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;

CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis, renal
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection, and
CC parasitic infection, protozoal infection, fungal infection, and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;

Query Match 15.0%; Score 867.8; DB 24; Length 1052;

Best Local Similarity 91.8%; Pred. No. 3.1e-124;

Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGCTCTTAAAGTCCATAACGTCGGCGGTTCGAGGTTTATGATTAATTCGC 4416

Db 1 GAAATCCCAAGTCCATAACGTCGGCGGTTCGAGGTTTATGATTAATTCGC 60

QY 4417 TGGCAGCAGAGCCTCTGCAGACAGAGCGCGAGAGATGAGATGGCAGCGGATTCAT 4476

Db 61 CGGCGGGAGGCTCTGCAGAGAGAGCGCGAGAGATGAGATGGCAGCGGATTCAT 120

QY 4477 TCAGAGCTGCGGAACAGGCGCCCTCTGATGTGAAGAAGTCTGCCCTGGACAAACATCGG 4536
Db 121 TTAGAGCTGCGGAACAGGCGCCCTCTGATGTGAAGAAGTCTGCCCTGGACAAACATCGG 180
QY 4537 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAAGTCTTAACT 4596
Db 181 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAAGTCTTAACT 240
QY 4597 AAAATCAACGAGGCGCTCACCTCAATCTCAGACTTACCAAAGTTA---AAGTTGAGAAAG 4653
Db 241 ARAATCAACGAGGCGCTCACCTCAATCGCAAACTTACCAAGTTAAACRAACTTAAGAAG 300
QY 4654 CTTGAACATA-----AGAGTCTCAGGCGGCTCGAAGTATTGGCAGAAAAAGTCTCCG 360
Db 301 CTTGAACATAAGGATTAACAGAGTCTCAGGCGGCTCGAAGTATTGGCAGAAAAAGTCTCCG 360
QY 4705 AACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCA 4764
Db 361 AACCTCAGCATCTAAATTTAAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCA 420
QY 4765 CTGAACACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCAACCTG 4824
Db 421 CTGAACACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCAACCTG 480
QY 4825 AACGACTACGCGAGAAAACGTTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGT 4884
Db 481 AACGACTACGCGAGAAAATGTGTTCAAGCTCTCTCCGCAACTCACATATCTCGACAGCTAT 540
QY 4885 TACTGGACACACAGGAGGCGCCCTTACTCAGATATTAAGACCAACCTGAGGAGGCGCTTGGAT 4944
Db 541 GACCGGACACACAGGAGGCGCCCTTACTCAGATATTAAGACCAACCTGAGGAGGCGCTTGGAT 600
QY 4945 GACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATCAAGATGCTCAGGTAGTGAAGAT 5004
Db 601 GATGAGGAGGAGGTGAGCATGAGGAGGAGTATGATCAAGATGCTCAGGTAGTGAAGAT 660
QY 5005 GAGGAGGCGGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAG 5064
Db 661 GAGGAGGCGGAGGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 5065 GAGGATCAAGAGGTTTAAAGTGGAGGAGTATGATCGGAGGAGGAGGAGGAGGAGGAGGAG 5124
Db 721 GAGGATCAAGAGGTTTAAAGTGGAGGAGTATGATCGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 5125 GGTCAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5184
Db 781 GGTCAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 5185 GACTAAGTAGAATTAACCTATTTTGAAGAAATTCCTATTTGATTTGATTTTACCCTAT 5244
Db 841 GACTAAGTAGAATTAACCTATTTTGAAGAAATTCCTATTTGATTTGATTTTACCCTAT 900
QY 5245 ATCCCTCT-----CCCCCTCCATCTCCCTCCCTGAACTTACTTTTCTGATTTCTAA 5298
Db 901 ATCCCTCTCCCTCCCTCCCTCTAATCTCCCTCCCTGAACTTACTTTTCTGATTTCTAA 960
QY 5299 CATTCGCTGTGGGAATGAGACGGGAAAAGTGTACTCTGGGGTGTGGAGGAGGAGGAGGAG 5358
Db 961 CTTGCTGTGGGAATGAGACGGGAAAAGTGTACTCTGGGGTGTGGAGGAGGAGGAGGAGGAG 1019
QY 5359 GAGCGGTGGACTAAATACTATTTTACTGCC 5391
Db 1020 GTGGGGGTGGAATAAAATACTATTTTACTGCC 1052

RESULT 11

AAV71743

ID AAV71743 standard; cdna; 916 BP.

XX

AC AAV71743;

XX

DT 15-MAR-1999 (first entry)

Db	181	CAGTCGGTCGAATCAAGGCAAACTCGAAGGCCCTCACAGATGAATTTGAAGAACTCGGAATT	240
Qy	4590	CTTAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTT	4648
Db	241	CTTAAGTACAATCAACGTAGGCCCTCACCTCAATTCGCAAACTTACCAAAAGTTTAAACAACT	300
Qy	4647	GAGAAAGCTTGAACTA-----AGAGTCTCAGGGGCCCTGGGAAGTATTGGCAGAAAA	4697
Db	301	TAAGAAGCTTGAACCTAAGCGATTAACAGAGTCTCAGGGGCCCTGGGAAGTATTGGCAGAAAA	360
Qy	4598	GTGTCCAAACCTCAGCGATCTATATTTAAAGTGGCAACAAAATTAAGACCTCAGCACAAAT	4757
Db	361	GTGTCCGAACCTCAGCGATCTAAATTTAAGTGGCAACAAAATTAAGACCTCAGCACAAAT	420
Qy	4758	AGACCCACTGAACAGTTAGAAAACCTCAAGAGCTTACAGCTTTTCAATTTGGAGGTTAAC	4817
Db	421	AGACCCACTGAAAAGTTAGAAAACCTCAAGAGCTTACAGCTTTTCAATTTGGAGGTTAAC	480
Qy	4818	CAACCTGAACGACTACGGAGAAAACTGTTCAAGCTTCTCCCTGCAACTCACATATCTCGA	4877
Db	481	CAACCTGAACGACTACCGAGAAAATGTGTCAAGCTCTCCCGCAACTCACATATCTCGA	540
Qy	4878	CAGCTGTTACTTGGGACACAAAGAGGCCCTTACTCAGATATTGAGGACCAAGTGGAGGG	4937
Db	541	CGGCTATGACGGGACGACAAAGAGGCCCTGACTCGGATGCTGAGGGCTACGTGGAGGG	600
Qy	4938	CCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAGT	4997
Db	601	CCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGT	660
Qy	4998	GGAAGATGAGGAGGGCGGAGGAGGAGGAGGAAGGTGAAGAGGAGGACGTGAGTGGAGG	5057
Db	661	GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGGTGAAGAGGAGGACGTGAGTGGAGA	720
Qy	5058	GGACGAGGAGGATGAAGAAGTTTATAACGATGGAGGTAGATGCGGAGGAAGATGAAGA	5117
Db	721	GGAGGAGGAGGATGAAGAAGTTTATAACGATGGAGGTAGATGCGGAGGAAGATGAAGA	780
Qy	5118	AGAGCTTGGTGAAGAAAGAGGGGTCAGAAAGCGAAATGAGAACTGAAGATGAGGGAGA	5177
Db	781	AGAGCTTGGTGAAGAAAGAGGGGTCAGAAAGCGAAATGAGAACTGAAGATGAGGGAGA	840
Qy	5178	AGATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGATTTGACTGTGTTT	5237
Db	841	AGATGATGACTAAGTGGATACCTATTTTGAAAAATTCCTATTGATTTGACTGTGTTT	900
Qy	5238	TACCCATATCCCTC 5252	
Db	901	TACCCATATCCCTC 915	
RESULT 12			
AAA88240			
ID	AAA88240 standard; DNA; 906 BP.		
XX	AAA88240;		
AC			
XX			
DT	15-DEC-2000 (first entry)		
XX			
DE	Human prostatic adenocarcinoma consensus pp32 nucleotide sequence.		
XX			
KW	Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;		
KW	acidic protein rich in leucine; chromosome 15q25; tumour suppressor;		
KW	malignant; cytostatic; gene therapy; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200045852-A1.		
XX			
PD	10-AUG-2000.		
XX			
PF	03-FEB-2000; 2000WO-US02656.		
XX			

Query Match		11.2%;	Score 649.6;	DB 17;	Length 980;
Best Local Similarity		83.0%;	Pred. No. 8e-91;		
Matches 807;		Conservative	0;	Mismatches 144;	Indels 21; Gaps 5;
Qy	4437	ACAGAGAGCGGAGAGATGGAGATGGCGACAGCGGATTCATTACAGAGCTGCGGAACAGGCG	4496		
Db	10	AGAGAGAGCGGAGAGATGGAGATGGCAACAGGATTTATTAGAGCTGCGGAACAGGAC	69		
Qy	4497	GCCCTCTGATGTGAAGAACTTGCCTGGACACACAGTCGTCGAATGAAGGCAAACTCGA	4556		
Db	70	GCCCTCTGATGTGAAGAGCTGGTCCCTGGATAACTGTAACTCAATTAAGCGCAAAATCGA	129		
Qy	4557	AGCCCTCACAGATGAATTTGAAGAACTTGAAGTAAATCAACGAGGCGCTCAC	4616		
Db	130	AGGCTCACGGATGAGTTTGAGAACTTGAATTCCTAAGTACAATCAACGTAGGCTCAC	189		
Qy	4617	CTCAATCTCAGACTTACCAAGTTA- - - AAGTTGAGAAAGCTTGAAC- - - - - AG	4664		
Db	190	CTCAATTTCCAACCTTACCAAGTTTAAACAAACTCAAGAAGCTTGAATTAAGCGAAACAG	249		
Qy	4665	AGTCAGGGGCTGGAAGTATTTGGCAGAAAAGTGTCCAAACCTCACGCATCTATATT	4724		
Db	250	AATCTCAGGGACCTGGAAGTATTTGGCAGAGAAATGTCCGAACCTTAAGCATCTAAATTT	309		
Qy	4725	AAGTGGCAACAAATTAAGACCTTCAGCAATAGAGCCACTGAAACAGTTAGAAACCT	4784		
Db	310	AAGTGGCAACAAATAAAGATCTCAGCAATAGAGCCGCTGAAGAAGTTAGAGATCT	369		
Qy	4785	CAAGAGCTTAGACCTTTTCAATTCGAGGTTAACCAACCTCAAGGACTACGAGAAACGT	4844		
Db	370	CAAGAGCTTAGACCTTTTAACTGTGAGGTGACCAACCTGAATGCCTACCGAAGAACT	429		
Qy	4845	GTTCAAAGCTTCTCTGCAACTCACAATCTCGACAGCTGTTACTGGACACAAAGAGGC	4904		
Db	430	GTTCAAAGCTTCTGCCACAGTCTATGTACCTCGATGCGTATGACAGGGGACAAAGAGGC	489		
Qy	4905	CCCTTACTCAGATATTGAGGACCACTGGAGGCGCTGGATGACGAGGAGGCTGAGCA	4964		
Db	490	CCCGACTCCGATCTTGAGGCTACGTGGA- - - - - GGATGACGACGAGGAAGATGAGGA	543		
Qy	4965	TGAGGAGGATGATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGA	5024		
Db	544	TGAGGAGGATGATGATGAATATGCCAGCTAGTGGAGATGAAGAGATGAAGAGGTTGAGGA	603		
Qy	5025	GGAGGAGGTGAAGAGACGCTGAGTCAGGGGACGAGGAGGATGAAGAGGTTATAA	5084		
Db	604	GGAGGAGGAGGAGAGAGATGTGATGGAGAGGAGGAGGATGAGGAAGGTTTACAA	663		
Qy	5085	CGATGAGAGGTAGATGGCGAGGAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGTCA	5144		
Db	664	TGACGGGAAGTGGATGACGAGGAGACGACGAAGAGAGCTGGTGAAGAGAGGGAGTCA	723		
Qy	5145	GAAGCGAAATGAGAACTTCAAGATGAGGAGGAGAGATGACTAAGTAACTAT	5204		
Db	724	GAAGCGAAATGAGAACTTCAAGATGAGGAGGAGAGATGACTAAGGA-ATGAACCTGT	782		
Qy	5205	TTTGAAAAATCTATGTGATTTGACTGTTTACCATATCCCTCCCTCCCTCAACT	5264		
Db	783	TTGGGGAATTCCTATGTGATTTGACTGTTTACCATATCCCTCCCTCCCTTATTC	842		
Qy	5265	CTGCCCCCTGAAACTTACTTTTCTGATTTGATTAACATTTGCTGTGGGAATGAGACGGAAA	5324		
Db	843	CTGCCCCCTGAAACTTATTTTCTGATTTGATTAACATTTGCTGTGGGAAGGAGGGAAA	902		
Qy	5325	AGTGTACTGGGGTTG- - - TGGAGGGAGGGAGGCGAGGCGGTGGACTAAAATACTATT	5382		
Db	903	AGTGTACTGGGGTTGATGGGGGTGGGGGTGGGGGTGGGGGTGGGATTAATACTATT	962		
Qy	5383	TTTACTGCCAAA	5394		
Db	963	TTTACTGCCACA	974		

RESULT 14
ABI99657
ID ABI99657 standard; cDNA; 980 BP.
XX
AC ABI99657;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:687.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX
OS Mus musculus.
XX
PN WO200188188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP04192.
XX
PR 18-MAY-2000; 2000JP-0145977.
XX
PA (UYN-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR WPI; 2002-034733/04.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
XX genes -
PS Claim 2; Page 1714-1716; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding
CC the protein sequences in AB57020 to AB57374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC used as an indicator when screening for ischaemic condition-improving
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
CC represent PCR primers for a mouse ischaemic condition related sequence,
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 980 BP; 312 A; 169 C; 302 G; 197 T; 0 other;

Query Match		11.2%;	Score 649.6;	DB 24;	Length 980;
Best Local Similarity		83.0%;	Pred. No. 8e-91;		
Matches 807;		Conservative	0;	Mismatches 144;	Indels 21; Gaps 5;
Qy	4437	ACAGAGAGCGGAGAGATGGAGATGGCGACAGCGGATTCATTACAGAGCTGCGGAACAGGCG	4496		
Db	10	AGAGAGAGCGGAGAGATGGAGATGGCAACAGGATTTATTAGAGCTGCGGAACAGGAC	69		
Qy	4497	GCCCTCTGATGTGAAGAACTTGCCTGGACACACAGTCGTCGAATGAAGGCAAACTCGA	4556		
Db	70	GCCCTCTGATGTGAAGAGCTGGTCCCTGGATAACTGTAACTCAATTAAGCGCAAAATCGA	129		
Qy	4557	AGCCCTCACAGATGAATTTGAAGAACTTGAAGTAAATCAACGAGGCGCTCAC	4616		
Db	130	AGGCTCACGGATGAGTTTGAAAGAACTGGAATTCCTAAGTACAATCAACGTAGGCTCAC	189		
Qy	4617	CTCAATCTCAGACTTACCAAGTTA- - - AAGTTGAGAAAGCTTGAAC- - - - - AG	4664		

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Db 190 CTCCATTTCACACTTACCAAGATTAAACAAACTCAAGAAAGCTTGAATTAAAGCGAAAAACAG 249
Qy 4665 AGTCTCAGGGGCGCTGGAAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCCATCTATATTTT 4724
Db 250 AATCTCAGGGGACCTGGAAAGTATTGGCAGAGAAATGTCGGAACCTTAAGCATCTAAATTT 309
Qy 4725 AAGTGGCAACAAAATTAAAGACCTCAGCACAAATAGAGCCACTGAACACAGTTAGAAAACCT 4784
Db 310 AAGTGGCAACAAAATAAAGATCTCAGCACAAATAGAGCGCTGAAGAAGTTAGAGAAATCT 369
Qy 4785 CAAGAGCTTAGACCTTTCAATTGGCAGGTACCAACCTGAACGACTACGAGGAAACGT 4844
Db 370 CAAGAGCTTAGACCTGTTTAACTGTGAGGTGACCAACCTGAATGCCCTACCGAGAAAACGT 429
Qy 4845 GTTCAAGCTTCTCCTGCAACTCACATATCTCACAGCTGTTTACTGGGACCAACAAGGAGGC 4904
Db 430 GTTCAAGCTTCTGCCCCAGGTCATCTACTCGATGGCTATGACAGGGACACAAGGAGGC 489
Qy 4905 CCCTTACTCAGATATTGAGGACCACTGGAGGGCTTGATGACGAGGAGGAGGTGAGCA 4964
Db 490 CCCCAGCTCCGATGTTGAGGGCTACGTGA-----GGATGACGACGAGGAGGAATGAGGA 543
Qy 4965 TCAGGAGGAGTATGATGAGATGCTCAGGTAGTGAAGATGAGGAGCGGAGGAGGAGGA 5024
Db 544 TGAGGAGGAGTATGATGATGATATGCCCAGCTAGTGGAAATGAAGAGGAGGTTGAGGA 603
Qy 5025 GGAGGAAGGTGAAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATAA 5084
Db 604 GGAAGAGGGGAGGAAGAGGATGTCAGTGGAGAGGAGGAGGATGAGGAAGGTTACAA 663
Qy 5085 CGATGAGAGGTAGATGGCGGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCA 5144
Db 664 TGACGGGGAAGTGGATGACGAGGAAGACGAGAGAAGCTGGTGAAGAAGAAAGGAGTCA 723
Qy 5145 GAAGCGAATCAGACACCTGAAGATGAGGAGGAGGAGATGATGACTAAGTAGAATACCTAT 5204
Db 724 GAAGCGAATCAGACACCTGAAGATGAGGAGGAGGAGGATGACTAAGTAGAATACCTAT 782
Qy 5205 TTTGAAAAATTCCTATTGTGATTGACTGTTTTTACCATATCCCTCCCTCCCTCAATC 5264
Db 783 TTGGGGAATTCCTATTGTGATTGACTGTTTTTACCATATCCCTCCCTCCCTATTC 842
Qy 5265 CTGCCCCCTGAACCTACTTTTTCTGATTGTAACATTTGCTGTGGGAATGACAGGGGAAA 5324
Db 843 CTGCCCCCTGAACCTACTTTTTCTGATTGTAACATTTGCTGTGGGAATGACAGGGGAAA 902
Qy 5325 AGTGACTGGGGTTG--TGGAGGGGAGGCGGAGGAGGCGTGGACTAAAATACTATT 5382
Db 903 AGTGACTGGGGTTGATGAGGGGTTGGGGTGGGGGAGGGGTTGGAATAAATACTATT 962
Qy 5383 TTTACTGCCAAA 5394
Db 963 TTTACTGCCACA 974

RESULT 15
AAAI5294
ID AAI5294 standard; cDNA; 750 BP.
XX
AC AAI5294;
XX
XX
DT 04-SEP-2000 (first entry)
XX
DE cDNA encoding a protein phosphatase 2A inhibitor.
XX
KW Syndecan-4; angiogenesis; proteoglycan; protein kinase C;
KW delta-isoenzyme; alpha isoenzyme; protein phosphatase; infarction;
KW endothelial cell proliferation; endothelial cell migration; anoxia;
KW myocardial infarction; chronic myocardial ischemia; heart tissue; ss.
OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
```

```
FT CDS 1..750
FT /*tag= a
XX WO200027416-A1.
XX
XX 18-MAY-2000.
XX
XX 10-NOV-1999; 99WO-US26647.
XX
XX 12-NOV-1998; 98US-0190976.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX Simons M, Horowitz A;
XX
XX WPI: 2000-376307/32.
XX
XX P-PSDB; AAY93262.
XX
XX Stimulating angiogenesis, useful particularly for treating cardiac
XX anoxia and infarction, by preventing phosphorylation of specific
XX residue in syndecan-4, present in endothelial cells -
XX
XX Disclosure; Page 35; 73pp; English.
XX
XX The present sequence encodes a protein phosphatase 2A inhibitor. The
XX protein phosphatase 1 is used in the method of the invention. The
XX specification describes a method for stimulating angiogenesis within
XX variable cells, tissues, or organs in situ. The method comprises
XX treating target endothelial cells such that Ser183, in the
XX intracellular cytoplasmic domain of syndecan-4 proteoglycan, is
XX present in non-phosphorylated form in at least some syndecan-4 molecules.
XX The cells are treated with an inhibitor of syndecan-4 protein kinase C
XX (PKC) delta-isoenzyme, an agent that increases intracellular activity of
XX the PKC delta-isoenzyme, or an agent that activates at least one of
XX protein phosphatases 1 or 2A. Keeping Ser183 in the non-phosphorylated
XX form results in activation of protein kinase C alpha isoenzyme, which is
XX essential for endothelial cell proliferation and migration in situ.
XX Syndecan-4 participates in intracellular signalling through
XX oligomerisation of its cytoplasmic tail and this process does not
XX occur if Ser183 is phosphorylated. The method can be used in vivo or
XX in vitro, to stimulate angiogenesis in cells or tissues which are
XX defective or have suffered anoxia or infarction, particularly myocardial
XX infarction, or chronic myocardial ischemia of heart tissue, and to
XX study mechanisms involved in control of angiogenesis.
XX
XX Sequence 750 BP; 260 A; 130 C; 229 G; 131 T; 0 other;
XX
XX Query Match 11.1%; Score 640.4; DB 21; Length 750;
XX Best Local Similarity 92.9%; Pred. No. 2e-89;
XX Matches 697; Conservative 0; Mismatches 41; Indels 12; Gaps 2;
Qy 4453 ATGGAGATGGCGACGACGATTTCATTCAGAGCTGCGGAACAGGGCGCCCTCTGATGTGAA 4512
Db 1 ATGGAGATGGCGACGACGATTTCATTCAGAGCTGCGGAACAGGACGCCCTCTGATGTGAA 60
Qy 4513 GAACCTGCCCTGGACAACACAGTCGGTCAATGAAGGCAAACTCGAACCCCTCAGATGAA 4572
Db 61 GAACCTTCTGGACAACAGTCGGTCAATGAAGGCAAACTCGAACCCCTCAGATGAA 120
Qy 4573 TTTGAAGAACTGGAAATCTTAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAGACTTA 4632
Db 121 TTTGAAGAACTGGAAATCTTAAGTAAATCAACGTAGGCCCTCACCTCAATTCGCAACTTA 180
Qy 4633 CCAAGTTA---AAGTTGAGAAAAGCTTTGAACATA-----AGAGTCTCAGGGGCGCTG 4680
Db 181 CCAAGTTAACAACACTTAAGAACTTGAAGCTTGAAGCGATAACAGAGTCTCAGGGGCGCTG 240
Qy 4681 GAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTAACTAGTGCACACAAATTT 4740
Db 241 GAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATAAATTTAAGTGCGACACAAATTT 300
Qy 4741 AAAGACCTCAGCAACATAGAGCCACTGAAACAGTGTAGAAAACCTCAAGAGCTTAGACCTT 4800
Db
```


Db	301	AAAGACCTCAGCACAAATAGACCCACTGAAAAAGTTAGAAAAACCTCAAGAGCCTTAGACCTT	360
Qy	4801	TTCRAATTCGAGGTAACCAACCTGAACGACTACGGAGAAAACGTTCAAGCTTCTCCTG	4860
Db	361	TTCRAATTCGAGGTAACCAACCTGAACGACTACGGAGAAAATGTTCAAGCTCCTCCCG	420
Qy	4861	CAACTCACATATCTCGACAGCTGTTACTGGGACCACAAAGGAGGCCCTTACTCAGATATT	4920
Db	421	CAACTCACATATCTCGACGGCTATGACCGGACGACAAAGGAGGCCCTGACTCGGATGCT	480
Qy	4921	GAGGACCACTGGAGGGCCTGGATCACCAGGAGGAGGCTGAGCATGAGGAGGATATGAT	4980
Db	481	GAGGGCTACGTGGAGGGCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGATATGAT	540
Qy	4981	GAAGATGCTCAGGTAGTGGAAAGATGAGGAGGGCCGAGGAGGAGGAGGAGGTTGAAGAG	5040
Db	541	GAAGATGCTCAGGTAGTGGAAAGACGAGGAGGAGGAGGATGAGGAGGAGGAGGTTGAAGAG	600
Qy	5041	GAGGACGTGAGTGGAGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGAT	5100
Db	601	GAGGACGTGAGTGGAGGAGGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGAT	660
Qy	5101	GGCGAGGAGATGAGAGAGACCTTGGTGAAGAAAGGGTCAGAAGCGAAATGAGAA	5160
Db	661	GACGAGGAAGATGAAGAAGCTTGGTGAAGAGAAAGGGTCAGAAGCGAAACGAGAA	720
Qy	5161	CCTGAAGATGAGGAGAGATGATGACTAA	5190
Db	721	CCTGAAGATGAGGAGAGATGATGACTAA	750

Search completed: December 8, 2002, 15:13:19
Job time : 799 secs

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 14:59:02 ; Search time 123 Seconds
(without alignments)
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Title: US-09-591-500-1
Perfect score: 5785
Sequence: 1 aagcttctcgtactctctaa.....aaacaatgatttaagctt 5785

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	867.8	15.0	1052	1	US-08-466-603-1
2	867.8	15.0	1052	1	US-08-314-503A-1
3	867.8	15.0	1052	1	US-08-468-066-1
4	867.8	15.0	1052	2	US-08-466-717-1
5	867.8	15.0	1052	3	US-08-466-743-1
6	867.8	15.0	1052	5	PCT-US95-12414-1
7	649.6	11.2	980	1	US-08-466-603-3
8	649.6	11.2	980	1	US-08-314-503A-3
9	649.6	11.2	980	1	US-08-468-066-3
10	649.6	11.2	980	2	US-08-466-717-3
11	649.6	11.2	980	3	US-08-466-743-3
12	649.6	11.2	980	5	PCT-US95-12414-3
13	508	8.6	759	1	US-08-466-603-4
14	508	8.8	759	1	US-08-314-503A-4
15	508	8.8	759	1	US-08-468-066-4
16	508	8.8	759	2	US-08-466-717-4
17	508	8.8	759	3	US-08-466-743-4
18	508	8.8	759	5	PCT-US95-12414-4
19	326	5.6	387	4	US-09-018-584A-5
20	296.4	5.1	966	2	US-08-766-738-2
21	296.4	5.1	966	4	US-09-262-610-2
22	233	4.0	14636	4	US-09-173-914-6
23	232.6	4.0	162450	4	US-09-345-882-1
24	228.4	3.9	70000	4	US-09-851-896-3
25	228.4	3.9	84495	4	US-09-797-906-3
26	227.4	3.9	99500	4	US-09-798-096-10
27	226.6	3.9	713	4	US-08-943-607-23

28	226.6	3.9	713	4	US-08-943-607-24
29	226.6	3.9	6063	1	US-08-195-744-4
30	226.6	3.9	6063	2	US-08-788-279-4
31	226.6	3.9	59065	4	US-09-813-817-3
32	226.6	3.9	59065	4	US-09-978-197-3
33	226	3.9	28001	4	US-09-819-993-3
34	225	3.9	713	4	US-08-943-607-25
35	225	3.9	713	4	US-08-943-607-26
36	224.2	3.9	152331	3	US-09-128-155-16
37	223.4	3.9	5408	1	US-08-471-058-20
38	223.4	3.9	5408	3	US-08-471-057-20
39	223.2	3.9	111282	4	US-09-754-250-3
40	223	3.9	26664	4	US-09-564-805-28
41	221.8	3.8	87350	3	US-08-781-891-79
42	221.8	3.8	87543	2	US-09-791-211-3
43	221.4	3.8	2886	2	US-08-687-080-55
44	221.4	3.8	6330	4	US-09-880-427-2
45	221.4	3.8	6330	4	US-09-306-538B-2

ALIGNMENTS

RESULT 1
US-08-466-603-1
; Sequence 1, Application US/08466603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,603
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
US-08-466-603-1

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Query Match 15.0%; Score 867.8; DB 1; Length 1052;
Best Local Similarity 91.8%; Pred. No. 1.7e-169;
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTCAAAAGTCTTAAACGTCGGCGGCTGAGGTTTATTCGAGGTTTATTCGATTCGATTCGCGC 4416
DB 1 GAATTCCTCCAAAGTCTTAAACCGCGCGCGCTGGGTTTCGGGTTTATTCGATTCGATTCGCGC 60

QY 4417 TGGCAGCAGAGGCTCTGCACAGACGAGCGCGGAGAGATGGAGATGGCGAGCGGATTCAT 4476
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QY 4477 TCAGAGCTCGGAACAGCGCGCCCTCTGATGTGAAGAACTTGGCCCTGGACAAACAGTCGG 4536
DB 121 TTAGAGCTCGGAACAGCGCGCCCTCTGATGTGAAGAACTTGTCTCGACAAACAGTCGG 180

QY 4537 TCGAATGAAGGCAAACTCAAGCCCTCAGAGATGAATTTGAAGAACTTGAATTCCTTAAGT 4596
DB 181 TCGAATGAAGGCAAACTCAAGCCCTCAGAGATGAATTTGAAGAACTTGAATTCCTTAAGT 240

QY 4597 AAAATCAACGGAGGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAG 4653
DB 241 ACATCAACGCTAGGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAG 300

QY 4654 CTGAACTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAGTGTCCA 4704
DB 301 CTGAACTAAGCGATAACAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAGTGTCCG 360

QY 4705 AACCTCAGCATCTATATTAGTGGCAACAAAATTAAGACCTCAGCACATAGAGCCA 4764
DB 361 AACCTCAGCATCTATATTAGTGGCAACAAAATTAAGACCTCAGCACATAGAGCCA 420

QY 4765 CTGAACAGTGTAGAAACCTCAAGAGCTTAGACCTTTCAATTCGAGGTACCAACCTG 4824
DB 421 CTGAACAGTGTAGAAACCTCAAGAGCTTAGACCTTTCAATTCGAGGTACCAACCTG 480

QY 4825 AAGGACTACGGAGAAACGTTGTTCAAGCTTCTCCTGCAACTCACATATCTGCACAGCTGT 4884
DB 481 AAGGACTACGGAGAAACGTTGTTCAAGCTTCTCCTGCAACTCACATATCTGCACAGCTAT 540

QY 4885 TACTGGACCAACAGAGCGCCCTTACTCAGATATGAGGACCACTGGAGGCGCTGGAT 4944
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DB 601 GATGAGGAGGAGGATGAGCATGAGGAGGATGATGAAGATGCTCAGGTAGTGAAGAT 660

QY 5005 GAGGAGGCGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGCTGAGTGGAGGAGGAG 5064
DB 661 GAGGAGGCGAGGATGAGGAGGAGGAGGAGTGAAGAGGAGGAGCTGAGTGGAGGAGGAG 720

QY 5065 GAGGATGAAGAAGGTTATACGATGAGAGGTAGATGGCGAGGAGAGTCAAGAGAGCTT 5124
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QY 5125 GGTGAAGAAGAAGGCTCAGAAAGGCTGAGAACTTGAAGATGAGGAGGAGGAGATGAT 5184
DB 781 GGTGAAGAAGAAGGCTCAGAAAGGCTGAGAACTTGAAGATGAGGAGGAGGAGATGAT 840

QY 5185 GACTAAGTGAATAACCTATTTTGAAGAAATTCCTATTTGATGATTTGACTGTTTTTACCCT 5244
DB 841 GACTAAGTGAATAACCTATTTTGAAGAAATTCCTATTTGATGATTTGACTGTTTTTACCCT 900

QY 5245 ATCCCT-----CCCCCTCAATCTCCCTCCCTGAAACTTACTTTTTTCGATGTGAA 5298
DB 901 ATCCCTCTCCCTCCCTCAATCTCCCTCCCTGAAACTTACTTTTTTCGATGTGAA 960

QY 5299 CATTCGTGTGGGAATGAGACGGGAAAGTGTACTGGGGGTTGTGGAGGAGGAGGGGAG 5358
DB 961 CATTCGTGTGGGAATGAGACGGGAAAGTGTACTGGGGGTTGTGGAGGAGGAGGGGAG 1019

QY 5359 GAGGCGGTGGACTAAAATACTATTTTACTGCC 5391
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DB 1020 GTGGGGTGAATAAAATACTATTTTACTGCC 1052

RESULT 2
US-08-314-503A-1
; Sequence 1, Application US/08314503A
; Patent No. 5734022
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated with
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-314-503A-1

Query Match 15.0%; Score 867.8; DB 1; Length 1052;
Best Local Similarity 91.8%; Pred. No. 1.7e-169;
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTCAAAAGTCTTAAACGTCGGCGGCTGAGGTTTATTCGAGGTTTATTCGATTCGCGC 4416
DB 1 GAATTCCTCCAAAGTCTTAAACCGCGCGCTGGGTTTCGGGTTTATTCGATTCGATTCGCGC 60

QY 4417 TGGCAGCAGAGGCTCTGCACAGACGAGCGCGGAGAGATGGAGATGGCGAGCGGATTCAT 4476
DB 61 CGCGCGGAGGCTCTGCACAGACGAGCGCGGAGAGATGGAGATGGCGAGCGGATTCAT 120

QY 4477 TCAGAGCTCGGAACAGCGCGCCCTCTGATGTGAAGAACTTGGCCCTGGACAAACAGTCGG 4536
DB 121 TTAGAGCTCGGAACAGCGCGCCCTCTGATGTGAAGAACTTGTCTCGACAAACAGTCGG 180

QY 4537 TCGAATGAAGGCAAACTCAAGCCCTCAGAGATGAATTTGAAGAACTTGAATTCCTTAAGT 4596
DB 181 TCGAATGAAGGCAAACTCAAGCCCTCAGAGATGAATTTGAAGAACTTGAATTCCTTAAGT 240

QY 4597 AAAATCAACGGAGGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAG 4653
DB 241 ACATCAACGCTAGGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAG 300
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Db 241 ACAATCAACGATAGGCGCTCACCTCAATACGCAAACTTACCAAAAGTTAAACAACTTAAGAAG 300
QY 4654 CTTGAACHTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCA 4704
Db 301 CTTGAACHTAAGCGATACAGAGTCTCAGGGGCGCTAGAAGTATTGGCAGAAAAGTGTCCG 360
QY 4705 AACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGAACCTTCAGCAACAATAGAGCCA 4764
Db 361 AACCTCAGCATCTAAATTTAAGTGGCAACAAATTAAGAACCTTCAGCAACAATAGAGCCA 420
QY 4765 CTGAACAGATTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAACCAACCTG 4824
Db 421 CTGAACAGATTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAACCAACCTG 480
QY 4825 AACGACTACGGAGAAAACGTTCTCAAGCTTCTCCTGCAACTCACATATCTCGACAGCTGT 4884
Db 481 AACGACTACGGAGAAAACGTTCTCAAGCTTCTCCTGCAACTCACATATCTCGACAGCTGT 540
QY 4885 TACTGGGACCAAGAGGCGCCCTTACTCAGATATTGAGGACCACTGGAGGCGCTGGAT 4944
Db 541 GACCGGACGACAAAGAGGCGCCCTGACTCGATGCTGAGGCTACGTTGAGGCGCTGGAT 600
QY 4945 GACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGTGTAGTGAAGAT 5004
Db 601 GATGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGTGTAGTGAAGAT 660
QY 5005 GAGGAGGCGGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 5064
Db 661 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 5065 GAGGATCAACAGGTTATACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5124
Db 721 GAGGATCAACAGGTTATACGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 5125 GGTGAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5184
Db 781 GGTGAACAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 5185 GACTAAGTAGAATAACCTATTTTGAATAATTCCTATTGATTTGATTTTACTGATTTTACCCAT 5244
Db 841 GACTAAGTAGAATAACCTATTTTGAATAATTCCTATTGATTTGATTTTACTGATTTTACCCAT 900
QY 5245 ATCCCTCT-----CCCCCTCCAACTCGTGGCCCTGAAACTTACTTTTCTGATTTGATAA 5298
Db 901 ATCCCTCTCCCTCCCTCCCTCTAATCCTGCCCCCTGAAACTTACTTTTCTGATTTGATAA 960
QY 5299 CATTTGTTGGGAATGAGACGGGAAAGTGTACTGGGGTTTGGAGGAGGAGGAGGAGGAG 5358
Db 961 CGTTGTTGTTGGGAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1019
QY 5359 GAGGCGGTGAGCAATAACTATTTTACTGCG 5391
Db 1020 GTGGGGGTGGAATAAAATACTATTTTACTGCC 1052

RESULT 3

US-08-468-066-1
; Sequence 1, Application US/08468066
; Patent No. 5756676
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnajda, Francis P.
; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,066
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107,47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-468-066-1

Query Match 15.0%; Score 867.8; DB 1; Length 1052;
Best Local Similarity 91.8%; Pred. No. 1.7e-169;
Matches 967; Conservative 0; Mismatches 67; Indels 19; Gaps 4;

QY 4357 GAGTCTTCAAACTCTATAAACGTCGGCGCTGGGTTCCAGGTTTATGATTCAAATTCGCG 4416
Db 1 GAATTCCTCCAACTCTATAAACGTCGGCGCTGGGTTTATGATTCAAATTCGCG 60
QY 4417 TGGCAGGAGAGCCTCTGCGAGCAGAGAGCGCGAGAGATGGAGATGGCAGACGGATTTCAT 4476
Db 61 CGCGCGGGAGGCTCTGCGAGAGAGAGCGCGAGAGATGGAGATGGCAGACGGATTTCAT 120
QY 4477 TCAGAGCTCGGAAACAGCGGCCCTCTCTGATGTGAAGAACTTCGCCCTGGACAAACAGTCGG 4536
Db 121 TTAGAGCTCGGAAACAGCGGCCCTCTCTGATGTGAAGAACTTCGCCCTGGACAAACAGTCGG 180
QY 4537 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAATTCCTTAAGT 4596
Db 181 TCGAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAATTCCTTAAGT 240
QY 4597 AAAATCAACGAGGCGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAG 4653
Db 241 ACAATCAACGAGGCGCTCACCTCAATCGCAAACTTACCAAAAGTTAACAACAACTTAAGAAG 300
QY 4654 CTTGAACHTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCA 4704
Db 301 CTTGAACHTAAGCGATACAGAGTCTCAGGGGCGCTAGAAGTATTGGCAGAAAAGTGTCCG 360
QY 4705 AACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGAACCTTCAGCAACAATAGAGCCA 4764
Db 361 AACCTCAGCATCTAAATTTAAGTGGCAACAAATTAAGAACCTTCAGCAACAATAGAGCCA 420
QY 4765 CTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAACCAACCTG 4824
Db 421 CTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTCGAGGTAACCAACCTG 480
QY 4825 AACGACTACGGAGAAAACGTTCTCCTGCAACTCACATATCTCGACAGCTGT 4884
Db 481 AACGACTACGGAGAAAACGTTCTCCTGCAACTCACATATCTCGACAGCTGT 540
QY 4885 TACTGGGACCAAGAGGCGCCCTTACTCAGATATTGAGGACCACTGGAGGCGCTGGAT 4944

[illegible]

RESULT 4	
US-08-466-717-1	
; Sequence 1, Application US/08466717	
; Patent No. 5874234	
; GENERAL INFORMATION:	
; APPLICANT: Pasternack, Gary R.	
; APPLICANT: Kuhajda, Francis P.	
; TITLE OF INVENTION: No. 5874234el Mammalian Protein Associated With	
; TITLE OF INVENTION: Uncontrolled Cell Division	
; NUMBER OF SEQUENCES: 9	
; CORRESPONDENCE ADDRESS:	
; ADDRESSEE: Banner, Birch, McKie & Beckett	
; STREET: 1001 G Street, N.W.	
; CITY: Washington, D.C.	
; STATE: District of Columbia	
; COUNTRY: U.S.A.	
; ZIP: 20001	
; COMPUTER READABLE FORM:	
; MEDIUM TYPE: Floppy disk	
; COMPUTER: IBM PC compatible	
; OPERATING SYSTEM: PC-DOS/MS-DOS	
; SOFTWARE: PatentIn Release #1.0, Version #1.25	
; CURRENT APPLICATION DATA:	
; APPLICATION NUMBER: US/08/466,717	
; FILING DATE: 06-JUN-1995	
; CLASSIFICATION: 435	
; PRIOR APPLICATION DATA:	
; APPLICATION NUMBER: US 08/314,503	
; FILING DATE:	
; ATTORNEY/AGENT INFORMATION:	
; NAME: Posorske Esq., Laurence H.	
; REGISTRATION NUMBER: 34,698	
; REFERENCE/DOCKET NUMBER: 1107.47218	
; TELECOMMUNICATION INFORMATION:	
; TELEPHONE: 202 508-9153	
; TELEFAX: 202 508-9299	
; INFORMATION FOR SEQ ID NO: 1:	

QY 4654 CTTGAACTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTTGTCCA 4704
|||||
Db 301 CTTGAACTTAAGCGATAACAGAGTCTCAGGGGCGCTAGAAGTATTGGCAGAAAAGTTGCCG 360
QY 4705 AACCTCACGCATCTATATTAAAGTGGCAACAATAAATAAGAACCTTCAGCAACATAAGAGCCA 4764
|||||
Db 361 AACCTCACGCATCTAAATTTAAGTGGCAACAATAAATAAGAACCTTCAGCAACATAAGAGCCA 420
QY 4765 CTGAAACAGTTAGAAAAACCTCAAGAGCTTAGACCCTTTTCAATTCCGAGGTTAACCAACTG 4824
|||||
Db 421 CTGAAAAAGTTAGAAAAACCTCAAGAGCTTAGACCCTTTTCAATTCCGAGGTTAACCAACTG 480
QY 4825 AAGCACTACGGAGAAAAACGTTCTCAAGCTTCTCCTGCAACTCACATATCTCGACAGCTGT 4884
|||||
Db 481 AACGACTACCGAGAAAAATGTGTTCAAGCTCTCCCGCAACTCACATATCTCGACGGCTAT 540
QY 4885 TACTGGACCACAAGGAGGCCCTTACTTCAGATATTGAGGACCACGCTGGAGGGCGCTGGAT 4944
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Db 541 GACCGGAGCAGCAAGAGGGCCCCCTGACTCGGATGCTGAGGCTACGTGGAGGGCGCTGGAT 600
QY 4945 GACGAGGAGGAGGGTGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAAAGAT 5004
|||||
Db 601 GATGAGGAGGAGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGGAAAGAC 660
QY 5005 GAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5064
|||||
Db 661 GAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 5065 GAGGATGAAGAAGGTTATAACGATCGAGAGGTAGTAGTCCGAGGAGAGATGAAGAAGAGCTT 5124
|||||
Db 721 GAGGATGAAGAAGGTTATAACGATCGAGAGGTAGTAGTACGAGGAGAGATGAAGAAGAGCTT 780
QY 5125 GGTGAAGAAGAAGGGGTGAGAAAGCGAAAAATCAGAACTCAGAACTGAGGAGGAGAAAGATGAT 5184
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Db 781 GGTGAAGAAGAAGGGGTGAGAAAGCGAAAAACGAGAACTCAGAACTGAGATGAGGAGGAGAGATGAT 840


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; Sequence 1, Application PC/TUS9512414
;
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: Novel Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
;
; NUMBER OF SEQUENCES: 9
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12414
; FILING DATE:
; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoescheit Esq., Dale H.
; REGISTRATION NUMBER: 19,090
; REFERENCE/DOCKET NUMBER: 1107.51507
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
;
; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
;
; CDS-12414-1

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Query Match 15.0%; Score 867.8; DB 5; Length 1052;
Best Local Similarity 91.8%; Pred. No. 1.7e-169;
Matches 967; Conservative 0; Mismatches 67; Indels 19;

Qy	4357	GAGTCTTCAAAGTCTCTAAACGCTGGCGCGTGGTTCACAGTATTGATGATTAATTCGGC	4416
Db	1	GAATTCCTCAAAGTCTCTAAACGCTGGCGCGTGGTTCACAGTATTGATGATTAATTCGGC	60
Qy	4417	TGSCACGAGAGCCTCTGCACAGACAGAGCGCGAGAGATGAGATGGCGACACGGAATTCAT	4476
Db	61	CGCGCGGGAGCCTCTGCACAGACAGAGCGCGAGAGATGAGATGGCGACACGGAATTCAT	120
Qy	4477	TCAGAGCTGCGGAACAGGCGCCCTCTGATGTGAAGAACTTGCCTTGGACACAGTCGG	4536
Db	121	TTAGAGCTGCGGAACAGGCGCCCTCTGATGTGAAGAACTTGTCTTGGACACAGTCGG	180
Qy	4537	TCGAAAGGCAAACTCGAAGCCCTCAGATGAATTTGAAGAACTTCTTAAAT	4596
Db	181	TCGAATGAAGCAAACTCGAAGCCCTCAGATGAATTTGAAGAACTTCTTAAAT	240
Qy	4597	AAATCAACGAGCGCTCAGCTCAATCTCAGACTTACCAAAGTTA -- AAGTTCGAAAG	4653
Db	241	ACATCAACGCTAGCGCTCAGCTCAATTCGCAAACTTACCAAAGTTTAAACAACCTTAAGAG	300
Qy	4654	CTTTGAACATA ----- TAGAGTCTCAGGGCGCCTGGGAAGTATTGGCAAGAAAGTGTCCA	4704

Dh	301	CTTTGAAC	TAAAGCGAT	AACAGAGCT	CTCAGGGGCC	TAGAAAGT	TATGGCAG	AAAGTGTCCG	360	
Qy	4705	AACTC	CACGCATCT	ATATTTAA	TAGTGGCA	CAAAAATTA	AAAGACCT	CAGCAACA	TAGAGCCA	4764
Dh	361	AACTC	CACGCATCT	AAATTTAA	TAGTGGCA	CAAAAATTA	AAAGACCT	CAGCAACA	TAGAGCCA	420
Qy	4765	CTGAA	CACAGTTAG	AAACCTC	TAAGAGCT	TTAGACCTTTT	TCAATTT	CGGAGGTTA	ACCACCTG	4824
Dh	421	CTGAAA	AAAGTTAG	AAACCTC	TAAGAGCT	TTAGACCTTTT	TCAATTT	CGGAGGTTA	ACCACCTG	480
Qy	4825	AACGACT	ACGGAGAA	ACGTGTT	TCAAGCTT	CTCTCG	CAACTCACAT	ATCTCG	CACAGCTGT	4884
Dh	481	AACGACT	ACGGAGAA	ATGTGTT	CAAGCTCT	CTCCGCA	CAACTCACAT	ATCTCG	ACGGCTAT	540
Qy	4885	TACTGG	SACCACA	AGAGGCC	CCCTTACT	CAGATATT	GAGGAC	CACTGGAG	GGCCTGGAT	4944
Dh	541	GACCGG	ACCAAC	AGGAGGCC	CCCTGACT	CGGATCT	GAGGCT	ACGTGG	AGGGCCTGGAT	600
Qy	4945	GACGAG	GAGGAGGT	GAGCAT	GAGGAG	GAGTATGAT	GAAGATGCT	CAGGTAGT	GGAAGAT	5004
Dh	601	GATCAG	GAGGAGCAT	GAGGAT	GAGGAG	GAGTATGAT	GAAGATGCT	CAGGTAGT	GGAAGAC	660
Qy	5005	GAGAGGG	CAGGAGGAG	GAGGAG	GAAGGTGA	AGAGGAGG	ACGTGACT	GTGAGGGG	CAGGACGAG	5064
Dh	661	GAGGAG	CAGGAT	GAGGAG	GAGGAAGT	GAAGAGGAG	ACGTGAGT	GGAGAGG	GGAGGAG	720
Qy	5065	GAGGAT	CAAGAAG	GTATAC	GATG	CAGAGGTAGAT	GCGAGG	AAAGATGA	GAAGAAGCTT	5124
Dh	721	GAGGAT	CAAGAAG	GTATAC	GATG	CAGAGGTAGAT	GAGGAG	GAAGATGA	GAAGAAGCTT	780
Qy	5125	GGTGA	AGAAAGGG	GT	CAGAAG	CGAAAATGAG	AACCTGAG	ATGAGGGAG	GAAGATGAT	5184
Dh	781	GGTGA	AGAAAGGG	GT	CAGAAG	CGAAAATGAG	AACCTGAG	ATGAGGGAG	GAAGATGAT	840
Qy	5185	GACTA	AGTAGAAT	AACTAT	TTTGA	AAAAATTCCT	ATTGTG	ATTGACTGT	TTTTTACC	5244
Dh	841	GACTA	AGTAGAAT	AACTAT	TTTGA	AAAAATTCCT	ATTGTG	ATTGACTGT	TTTTTACC	900
Qy	5245	ATCC	CCCT	-----	CCCC	CCCAAT	CTGCC	CCCTGAA	ACTTTTCTG	5298
Dh	901	ATCC	CCCT	CTCCCC	CCCCCT	CTCTAAT	CCTGCC	CCCTGAA	ACTTTTCTG	960
Qy	5299	CATT	TCGTGTGG	ATGAG	CGGAAAG	CTGTACT	GGGGTGT	GTGAGGGG	CAGGGG	5358
Dh	961	CGTT	TCGTGTGG	ACAC	GAGGGG	GAAGAGT	GTACT	GGGGTGT	CGGGGGA	1019
Qy	5359	GAGCG	GTGACT	AAAA	TACTAT	TTTTTACT	GGCC	5391		
Dh	1020	CTG	GGGTGGA	TAAAA	TACTAT	TTTTTACT	GGCC	1052		

RESULT 7
US-08-466-603-3
; Sequence 3, Application US/08466603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnajda, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466, 603
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314, 503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: mus sp
;
US-08-466-603-3

Query Match 11.2%; Score 649.6; DB 1; Length 980;
Best Local Similarity 83.0%; Pred. No. 1.2e-124;
Matches 807; Conservative 0; Mismatches 144; Indels 21; Gaps 5;

QY 4437 ACAGAGCGCGAGAGATGGAGATGGCAGACGCGATTCTTCAGAGCTGCGGAACAGGGC 4496
DB 10 AGAGAGCGCGAGAGATGGAGATGGACAAACGGATTATTAGAGCTGCGGAACAGGAC 69

QY 4497 GCCCTCTGATGTGAAGNACTGCCCTGGACACAGCTCGGTGCGAATGAAGCAAACTCGA 4556
DB 70 GCCCTCTGATGTGAAGAGCTGGCTCGGATAACTGTAAGTCAATTGAAGGCAAAATCGA 129

QY 4557 AGCCCTCACAGATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCCCTCAC 4616
DB 130 AGGCCTCACAGATGAGTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCCCTCAC 189

QY 4617 CTCATCTCAGACTTACCAAGTTA---AGTTGAGAAAGCTTGAACTA-----AG 4664
DB 190 CTCATTTTCCAACTTACCAAGTTTAAACAAACTCAAGAAAGCTTGAATTAAGCGGAAACAG 249

QY 4665 AGTCTCAGGGGCTGGAAGTATTGGCAGAAAGTGTCCAACTCAGCATCTATATATT 4724
DB 250 AATCTCAGGGGACCTGGAAGTATTGGCAGAAAGTGTCCGAACTTAAAGCATCTAAATTT 309

QY 4725 AAGTGGCAACAAAATTAAAGACCTCAGCAACAATAGAGCCACTGAACAGTTAGAAAACCT 4784
DB 310 AAGTGGCAACAAAATAAAGATCTCAGCAACAATAGAGCCGCTGAAGATGATAGAACTCT 369

QY 4795 CAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACCACTGAACGACTACGAGAAAACGT 4844
DB 370 CAAGAGCTTAGACCTTTTAACTGTAGGTGACCAACCTGAATGCCCTACCGAGAAAACGT 429

QY 4845 GTTCAAGCTTCTCTGCAACTCACAATATCTGACAGCTGTGTACTGGGACCAACAGGAGGC 4904
DB 430 GTTCAAGCTTCTCTGCCCCAGGTCATGTCCTCGATGGGTGTGACAGGCAACACAGGAGGC 489

QY 4905 CCCTTACTCAGATATTGAGGACCACTGGAGGGCCTGACGACGAGGAGGGGTGAGCA 4964
DB 490 CCCCAGCTCCCATGTTGAGGCTACGTGGA-----GGATGACGACGAGGAAGTGAAGA 543

QY 4965 TGAGAGGAGTATGATGAAGATGCTCAGTAGTGAAGATGAGAGGGCGGAGGAGGAGGA 5024
DB 544 TGAGAGGAGTATGATGAATGATCCAGCTAGTCCAGCTAGTGGAAAGATGAAGAGGAGGTTGAGGA 603

QY 5025 GGAGGAAGTCAAGAGGAGGAGCTGAGTGGGGGAGCAGGAGGATGAAGAGGTTTAA 5084
DB 604 GGAAGAGGGGAGGAGGAGGATGAGTGGGAGGAGGAGGAGGATGAGGAAGGTTACAA 663

QY 5085 CGATGGAGAGTAGATGGCAGGAGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCA 5144
DB 664 TGACGGGGAAGTGGATGACGAGGAGACGCAAGAGAGAGCTGGTGAAGAGAGAGGGAGTCA 723

QY 5145 GAAGCGAAAATGAGAACCTGAAGATGAGGAGGAAGATGATGACTAAGTAGAATAACCTAT 5204
DB 724 GAAGCGAAAACGAGAACCGGACGATGAGGCGGAAGAGGATGACTAAGGA-ATGAACCTGT 782

QY 5205 TTTGAAAAATTCCTATTGTGATTGACTGTTTTTACCCTATATCCCTCCCTCCCAATC 5264
DB 783 TTGGGGAATTCCTATTGTGATTGACTGTTTTTACCCTATATCCCTCCCTCCCTATTTC 842

QY 5265 CTGCCCCCTGAAACTTACTTTTTCTGATTGTAACATTTCTGTGGGAATGAGACGGGAAA 5324
DB 843 CTGCCCCCGCAACTTATTTTTCTGATTGTAGCATTTCTGTGGGAAGGAGGGGAAA 902

QY 5325 AGTGTACTGGGGTTG--TGGAGGAGGAGGAGGACAGGCGGTGGACTTAAATATCTATT 5382
DB 903 AGTGTACTGGGGTTGATGGGGGTGGGGGAGGGGTGGATATAAATACTATT 962

QY 5383 TTTTACTGCCAAA 5394
DB 963 TTTTACTGCCACA 974

RESULT 8
US-08-314-503A-3
; Sequence 3, Application US/08314503A
; Patent No. 5734022
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated with
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 980 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: mus sp
;
US-08-314-503A-3

Query Match 11.2%; Score 649.6; DB 1; Length 980;
Best Local Similarity 83.0%; Pred. No. 1.2e-124;
Matches 807; Conservative 0; Mismatches 144; Indels 21; Gaps 5;

Db 370 CAAGAGCCTAGACCTGTTTAACTGTGAGGTGACCAACCTGAACTGCCCTACCGAGAAACGT 429
QY 4845 GTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGTACTGGGACACACAGGAGGC 4904
Db 430 GTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGTACTGGGACACACAGGAGGC 489
QY 4905 CCCTTACTCAGATATTGAGGACCACTGGAGGCTGGATGACGAGGAGGAGGTGAGCA 4964
Db 490 CCCGACTCCGATGTTGAGGCTACGTGGA-----GGATGACGAGGAGGAGATGAGGA 543
QY 4965 TGAGGAGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGA 5024
Db 544 TGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGA 603
QY 5025 GGAGGAGGAGTGAAGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5084
Db 604 GGAAGAGGAGGAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 663
QY 5085 CGATGGAGAGTATGATGAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5144
Db 664 TGACGGGAGGAGTGAAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 723
QY 5145 GAACGGAAGTGAAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5204
Db 724 GAACGGAAGTGAAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
QY 5205 TTTCAAAATTCCTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5264
Db 783 TTGGGGAATTCCTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 842
QY 5265 CTGCCCCCTGAAACTTACTTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 5324
Db 843 CTGCCCCCTGAAACTTACTTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 902
QY 5325 AGTCTACTGGGGTTG--TGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5382
Db 903 AGTCTACTGGGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 962
QY 5383 TTTACTGCCAAA 5394
Db 963 TTTACTGCCACA 974

RESULT 10

US-08-466-717-3
Sequence 3, Application US/08466717
Patent No. 5874234
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
TITLE OF INVENTION: No. 5874234el Mammalian Protein Associated With
TITLE OF INVENTION: Uncontrolled Cell Division
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,717
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,503
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Posorske Esq., Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.47218
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 980 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: mus sp
US-08-466-717-3

Query Match 11.2%; Score 649.6; DB 2: Length 980;
Best Local Similarity 83.0%; Pred No. 1.2e-124;
Matches 807; Conservative 0; Mismatches 144; Indels 21; Gaps 5;
QY 4437 ACAGAGAGCGGAGAGATGGAGATGGGACGAGCGGATTCATTTCAGAGCTCGGGAACAGGCG 4496
Db 10 AGAGAGAGCGGAGAGATGGAGATGGGACAAACGGATTTATTTAGAGCTGCGGAACAGGAC 69
QY 4497 GCCTCTGATGTGAAGAAGCTTGCCTTGGACAAACAGTCGGTGAATGAAGGCAAACTCGA 4556
Db 70 GCCTCTGATGTGAAGAAGCTTGCCTTGGATAACTGTAAGTCAATTAAGGCAAAATCGA 129
QY 4557 AGCCCTCACAGATGAATTTGAAGAAGCTTGAAGTAACTTAAGTAACTCAAGGAGGCTCAC 4616
Db 130 AGCCCTCACAGATGAATTTGAAGAAGCTTGAAGTAACTTAAGTAACTCAAGGAGGCTCAC 189
QY 4617 CTCAATCTCAGACTTACCAAACTTA---AAGTTGAGAAAGCTTGAACCTA-----AG 4664
Db 190 CTCCATTTCCAACTTACCAAACTTAAACAACTCAAGAGCTTGAATTAAGGCAAAACAG 249
QY 4665 AGTCTCAGGGGCTTGGAGTATTTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTT 4724
Db 250 AATCTCAGGGGACCTGGAAAGTATTTGGCAGAAAAGTGTCCGAACTTAAAGCACTTAAATTT 309
QY 4725 AAGTGGCAACAAATTAAGAGCTTCAGCAACAATAGAGGCACTGAAACAGTTAGAAAACCT 4784
Db 310 AAGTGGCAACAAATTAAGAGATCTCAGCAACAATAGAGGCTGGAAGAGTTAGAGAATCT 369
QY 4785 CAAGAGCTTAGACCTTTTCAATTTGCGAGGTAACTCAACCTGAAACGACTACGGAGAAAACGT 4844
Db 370 CAAGAGCCTTAGACCTGTTTAACTGTGAGGTGACCAACCTGAATGCTTACCGAGAAAACGT 429
QY 4845 GTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGTACTGGGACACACAGGAGGC 4904
Db 430 GTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTGTACTGGGACACACAGGAGGC 489
QY 4905 CCCTTACTCAGATATTGAGGACCACTGGAGGCTGGATGACGAGGAGGAGGAGGAGGAGGAG 4964
Db 490 CCCGACTCCGATGTTGAGGCTACGTGGA-----GGATGACGAGGAGGAGATGAGGA 543
QY 4965 TGAGGAGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGA 5024
Db 544 TGAGGAGGAGTATGATGAATATGCCACGCTAGTGAAGATGAAGAGGAGGAGGAGGAGGAGGAG 603
QY 5025 GGAGGAAGTGAAGAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5084
Db 604 GGAAGAGGAGGAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 663
QY 5085 CGATGGAGAGTATGATGAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5144
Db 664 TGACGGGAGGAGTGAAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 723
QY 5145 GAACGGAAGTGAAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5204
Db 724 GAACGGAAGTGAAGGAGGAGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 782

CORRESPONDENCE ADDRESS:	
ADDRESSEE: Banner & Allegretti, Ltd.	
STREET: 1001 G Street, N.W.	
CITY: Washington, D.C.	
STATE: District of Columbia	
COUNTRY: U.S.A.	
ZIP: 20001	
COMPUTER READABLE FORM:	
MEDIUM TYPE: Floppy disk	
COMPUTER: IBM PC compatible	
OPERATING SYSTEM: PC-DOS/MS-DOS	
SOFTWARE: PatentIn Release #1.0, Version #1.25	
CURRENT APPLICATION DATA:	
APPLICATION NUMBER: PCT-US95/12414	
FILING DATE:	
CLASSIFICATION:	
PRIOR APPLICATION DATA:	
APPLICATION NUMBER: US 08/314,503	
FILING DATE: 22-SEP-1994	
ATTORNEY/AGENT INFORMATION:	
NAME: Hoscheit Esq., Dale H.	
REGISTRATION NUMBER: 19,090	
REFERENCE/DOCKET NUMBER: 1107.51507	
TELECOMMUNICATION INFORMATION:	
TELEPHONE: 202 508-9153	
TELEFAX: 202 508-9299	
INFORMATION FOR SEQ ID NO: 3:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 980 base pairs	
TYPE: nucleic acid	
STRANDEDNESS: double	
TOPOLOGY: linear	
MOLECULE TYPE: cDNA	
ORIGINAL SOURCE:	
ORGANISM: mus sp	
PCT-US95-12414-3	

Query Match	
Best Local Similarity 83.0%; Score 649.6; DB 5; Length 980;	
Matches 807; Conservative 0; Mismatches 144; Indels 21; Gaps 5;	

QY	4437	ACAGAGCGGAGATGGAGTGGGACGCGATTCATTACAGACTCGGAAACAGGC	4496
DB	10	AGAGAGCGGAGATGGAGTGGGACGCGATTCATTACAGACTCGGAAACAGGC	69
QY	4497	GCCCTCTGATGTGAAGAAGCTTCCCCTGGACACAGTCGTTCAATGAAGGCAAACTCGA	4556
DB	70	GCCCTCTGATGTGAAGAAGCTTCCCCTGGACACAGTCGTTCAATGAAGGCAAACTCGA	129
QY	4557	AGCCCTCACAGATGAATTTGAAGAATCGAATTTCTTAAGTAAATAACAAGGCGCTCAC	4616
DB	130	AGGCCCTCACGATGAGTTTGAAAGACTGGAATTCCTAAGTACAACTCAACGTTAGGCGCTCAC	189
QY	4617	CTCAATCTCAGACTTACCAGGTTA--RAGTTGAGAAAGCTTGACTA-----AG	4664
DB	190	CTCATTTCCAACTTACCAGGTTAAGCAAACTCAAGAACTGTAATTAAAGCGAAAACAG	249
QY	4665	AGTCTCAGGGGGCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCACGCATCTATATT	4724
DB	250	AATCTCAGGGGACCTGGAAGTATTGGCAGAAAGTGTCCGAACTTAAAGTAAATTT	309
QY	4725	AAGTGGCACAAATAAAGACCTCAGCAATAGAGCCACTGAAACAGTTTAGAAAACT	4784
DB	310	AAGTGGCACAAATAAAGTCTCAGCAATAGAGCCACTGAAACAGTTTAGAAAACT	369
QY	4785	CAGAGCTTAGACTTTTCAATTCGAGGTAAACCACTGAACGACTACGGAGAAAAGT	4844
DB	370	CAGAGCTTAGACTTTTCAATTCGAGGTAAACCACTGAACGACTACGGAGAAAAGT	429
QY	4845	GTTCAAGCTTCTCCTCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGC	4904
DB	430	GTTCAAGCTTCTCCTCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGC	489

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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Mus sp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..548
US-08-466-603-4

Query Match      8.8%; Score 508; DB 1; Length 759;
Best Local Similarity 83.3%; Pred. No. 1.4e-95;
Matches 615; Conservative 0; Mismatches 115; Indels 8; Gaps 3;

QY 4657 GAACCTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCAGCGAT 4716
Db 24 GAAACACAGATCTCAGGGGACCTGGAAGTATTGGCAGAGAAATGTCCGAACCTTAAGCAT 83
QY 4717 CTATATTTAAGTGGCAACAAATTAAGACCTCAGCACATAGAGCCACTGAACAGTTA 4776
Db 84 CTAATTTTAAAGTGGCAACAAATAAAGATCTCAGCACATAGAGCCGCTGAAGAAGTTA 143
QY 4777 GAAACACCTCAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGGA 4836
Db 144 GAGATCTCAAGAGCCTAGACCTGTTTAACTGTGAGGTGACCAACCTGAATGCTTACCGA 203
QY 4837 GAAACAGTGTTCAGCTTCTCTGCACTCACATATCTCGACAGCTGTTACTGGGACCAC 4896
Db 204 GAAACAGTGTTCAGCTTCTCTGCACTCACATATCTCGACAGCTGTTACTGGGACCAC 263
QY 4897 RAGGAGGCCCTTACTCAGATATTGAGGACCACTGAGAGGCGCTGGATGACGAGGAGGAG 4956
Db 264 RAGGAGGCCCTTACTCAGATATTGAGGACCACTGAGAGGCGCTGGATGACGAGGAGGAG 317
QY 4957 GGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGTAGTGAAGATGAGGAGGCGGAG 5016
Db 318 GATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGTAGTGAAGATGAGGAGGCGGAG 377
QY 5017 GAGGAGGAGGAGGAGTGAAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAA 5076
Db 378 GTTGAGGAGGAGGAGGAGGAGGAGGAGGATGTGAGTGGAGGAGGAGGAGGATGAGGAA 437
QY 5077 GCTTATACGATGAGAGGATGAGTGGCGGAGGAGGATGAAGAGAGCTTGTGTAAGAGAA 5136
Db 438 GCTTACAATGCGGGGAAAGTGGATGACGAGGAGGAGGAGGAGGATGAGGAA 497
QY 5137 AGGGGTCAGAGCGAAAAATGAGAACCTGAAGATGAGGAGGAGGAGGATGACTAAGTAGAA 5196
Db 498 GGGATCAGAGCGAAACGAGAACCGGACGATGAGGCGGAGGAGGATGACTAAGGA-AT 556
QY 5197 TAACCTATTTGAAAAATTCCTATTGTGATTTGACTGTTTACCATATCCCTCCCTCC 5256
Db 557 GAACCTGTTTGGGAAATTCCTATTGTGATTTGACTGTTTACCATATCCCTCCCTCC 616
QY 5257 CTTCAATCTGCCCCCTGAAACTTACTTTTCTGATTGTAACATTTGCTGTGGGAATGAG 5316
Db 617 TCCTATCTGCCCCCGGAAACTTATTTTCTGATTGTAGCATTTGCTGTGGGAAGGAG 676
QY 5317 ACGGGAAGAGTACTGGGGGTGTTGGAGGAGGAGGAGGAGGCGGTGGACTAAAT 5376
Db 677 AGGGGAAGAGTACTGGGGGTGATG-GGGGTGGGGGTGGGGGAGGGGAATAAAT 735
QY 5377 ACTATTTTACTGCCAAA 5394
Db 736 ACTATTTTACTGCCACA 753

RESULT 14
US-08-314-503A-4
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; Sequence 4, Application US/08314503A
; Patent No. 5734022
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Mus sp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..548
US-08-314-503A-4

Query Match      8.8%; Score 508; DB 1; Length 759;
Best Local Similarity 83.3%; Pred. No. 1.4e-95;
Matches 615; Conservative 0; Mismatches 115; Indels 8; Gaps 3;

QY 4657 GAACCTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCAGCGAT 4716
Db 24 GAAACACAGATCTCAGGGGACCTGGAAGTATTGGCAGAGAAATGTCCGAACCTTAAGCAT 83
QY 4717 CTATATTTAAGTGGCAACAAATTAAGACCTCAGCACATAGAGCCACTGAACACAGTTA 4776
Db 84 CTAATTTTAAAGTGGCAACAAATAAAGATCTCAGCACATAGAGCCGCTGAAGAAGTTA 143
QY 4777 GAAACACCTCAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGGA 4836
Db 144 GAGATCTCAAGAGCCTAGACCTGTTTAACTGTGAGGTGACCAACCTGAATGCTTACCGA 203
QY 4837 GAAACAGTGTTCAGCTTCTCTGCACTCACATATCTCGACAGCTGTTACTGGGACCAC 4896
Db 204 GAAACAGTGTTCAGCTTCTCTGCACTCACATATCTCGACAGCTGTTACTGGGACCAC 263
QY 4897 AAGGAGGCCCTTACTCAGATATTGAGGACCACTGAGAGGCGCTGGATGACGAGGAGGAG 4956
Db 264 AAGGAGGCCCTTACTCAGATATTGAGGACCACTGAGAGGCGCTGGATGACGAGGAGGAG 317
QY 4957 GGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGTAGTGAAGATGAGGAGGCGGAG 5016
Db 318 GATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGTAGTGAAGATGAGGAGGCGGAG 377
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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: Pailo
; CURRENT APPLICATION NUMBER: US/09/764,855
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 193
; LENGTH: 25423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-855-193

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Query Match 4.1%; Score 237.6; DB 10; Length 25423;
Best Local Similarity 85.7%; Pred. No. 7.4e-26;
Matches 276; Conservative 0; Mismatches 44; Indels 2; Gaps 1;

QY	655	TTCAATGTATAAAATCAGTCTTGGCGGGCAGCGTGGCTCACACTATAATCCAGCACT	714
Db	4770	TACAAATATATAAAATTAGTGGCGGGTACGGTGGCTCACACTGTAAATCCCAAGCACT	4711
QY	715	TTGGGAGTCCCAGCGGGCGGGTCCAGAGTCAAGAGATGAGAGCACCATCATGGCCAAACAT	774
Db	4710	TTGGGAGGCCAAGGTGCAGCGATCACGAGGTCAAGAGATCAAGACCATCTTGGCCACAT	4651
QY	775	GGTGAACCCCTGTCTCTACTATAAATACAAAAAATTATCTGGGTGGTGGGACACATGCC	834
Db	4650	GGTGAACCCCAACTCTCTATAAATATC--AAAAATTAACCTGGGCGTGATGGCATGTGCC	4593
QY	835	TGTAATCCCAACTACTTAGGGAGCGCTGAGCGAGGAAATCGGTTGAACCTGGGAGCGCGAG	894
Db	4592	TGTAGTCCCAAGCTACTTCGGGAGGCTGAGGCAGGAAATCGCTTGAACCTGGGAGGTGAG	4533
QY	895	GTTCGAGTCAGCGGAGATCGCAACATTGCATCCAGCCTGCACACAGACGAGACTCCAT	954
Db	4532	GTTCGAATGAGCGGAGATCGCAACACTGCATCCAGCCTGCCAACAGAACAAAGACTCCGT	4473
QY	955	CCCAAAACAAAAACAAACAAA	976
Db	4472	CTCAAAAAAAAAAAAAAGAAAA	4451

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RESULT 5
US-09-764-855-194/c
; Sequence 194, Application US/09764855
; Patent No. US20020119919A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P110
; CURRENT APPLICATION NUMBER: US/09/764,855
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 194
; LENGTH: 25424
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-855-194

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Query Match 4.1%; Score 237.6; DB 10; Length 25424;
Best Local Similarity 85.7%; Pred. No. 7.4e-26;
Matches 276; Conservative 0; Mismatches 44; Indels 2; Gaps 1;

Qy	655	TTCAATGTAATAAATCAGTCTCTGGCCGGCAGGTGGCTCACACTATATATCCAGCACT	714
Db	4772	TACAAATATATAAAATTAGTGGCCGGGTACGTGGCTCACACTGTAATCCAGCACT	4713
Qy	715	TTGGGAGTCCCCAGCGGGCGGTTCACAGAGTCAAGAGATGGAGACCACATCATGGCCAAACAT	774
Db	4712	TTTGGAGGCCAGGTGGACGATCAGAGTCAAGAGATCAAGACCACTCTGGCCAAACAT	4653

Qy	775	GGTGAACCCCTGTCTCTACTATATAAATACAAAAAATATCTGGGTGTGGTGGCATGCC	834
Db	4652	GGTGAACCCCACTCTACTATAAAATAC--AAAAATTAACCTGGCGTGTGGCATGTGCC	4595
Qy	835	TGTAATCCCAACTACTAGGGAGGCTCAGCGAGGAGAAATCGCTTGAACCTGGGAGCGGAG	894
Db	4594	TGTAATCCCAAGCTACACCTGCGGAGGCTCAGCGAGGAGAAATCGCTTGAACCTGGGAGGTGGAG	4535
Qy	895	GTTCCAGTGAACCGAGATCGCACATTCACACTCCAGCCTGGCAACAGACGAGACTCCAT	954
Db	4534	GTTCAATGACCGAGATCGCACACTGCACCTCCAGCCTGGCAACAGACGAGACTCCGT	4475
Qy	955	CCCAAAACAAACAAACAAAA	976
Db	4474	CTCAAAAAAAAAAAAAAAAAAAAA	4453

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RESULT 6
US-09-764-870-595/c
; Sequence 595, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 595
; LENGTH: 13046
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-870-595

```

Query Match 4.1%; Score 235.6; DB 10; Length 13046;
Best Local Similarity 83.2%; Pred. No. 1.3e-25;
Matches 268; Conservative 0; Mismatches 54; Indels 0; Gaps 0

Qy	655	TTCATTTGTA AAAAATCAGTCTTGCGCGGCGCAGGTGGCTCACACTATAATCCAGCACT	714
Db	2729	TTAGCTTTAAAAGAAAAAAGTTGGCGGCGCAGGTGGCTCACACTGTAATCCAGCACT	2670
Qy	715	TTGGAGTCCACGCGGCGGCTCAGAGGTCACAGATGAGACCATCATGGCCACAT	774
Db	2669	TTGGGAGCTGAGGCAGCAGATCAGAGGTCACAGATCGAGACCATCTTAGCCACAT	2610
Qy	775	GGTGAACCCCTGTCTCTACTATAATACAAAAAATATCTGGGTGGTGGGCACATGCC	834
Db	2609	GGTGAACCCCGTCTCTAGCTAAAAATACAAAAAATTAGCTGGCGGTGGTGGCGCAGGCC	2550
Qy	835	TGTAATCCCAACTACTTAGGAGGCTGAGCGAGGAATCGCTTGAACCTGGGAGCGGAG	894
Db	2549	TGTAGTCCCAAGTACTCTGGAGCTTGAGCGGGAGAAATCGCTTGAACCCAGGACGAGAA	2490
Qy	895	GTTGCAGTGAGCCGAGATCGCACCATTCGACTCCAGCCTGGCAACAGAGCGAGACTCCAT	954
Db	2489	GTTGCAGTGAGCCCAAGATTTGGCCACTGCATCTCCAGCCTGGCAGACAGAGCGAGCTCCGT	2430

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RESULT 7
US-09-362-436-281
; Sequence 281, Application US/09962436
; Patent No. US20020081301A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel
; TITLE OF INVENTION: Cancer
; TITLE OF INVENTION: Sets
; Gene Dete

```

```
; FILE REFERENCE: 689290-75
; CURRENT APPLICATION NUMBER: US/09/962.436
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,082
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/234,924
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 281
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-436-281

Query Match      4.1%; Score 234.8; DB 10; Length 167343;
Best Local Similarity 75.5%; Pred. No. 2.2e-25;
Matches 305; Conservative 0; Mismatches 97; Indels 2; Gaps 1;

QY 601 ACATGCTCTGACTACTGCTACAAATAGCCTCCCAACTCTTGTCTCTACTTAAATTCATT 660
DB 71422 ATAACTGTTGTTTTCACGGAAGCAGTGGTTTCCAAATGTTTTTAATCATGTAAATCCATCA 71481
QY 661 GTAAAAAATCAGTCTTGGCGGGCAGGTGGCTCACACCTTATAATCCAGCACTTTGGGA 720
DB 71482 GTAAAAAACAATTTAAGCTGGGTGGCTCACACCTGTAAATCCAGCACTTTGGGA 71541
QY 721 GTCCAGGCGGGCGGTACAGAGTCAAGAGATGAGAGACCATCATGCGCAACATGGTGA 780
DB 71542 GGCCAAAGGCGGCAGATCAGAGGTCAAGAGATCGAGAGCAGCCTGGCCAAACATGGTGA 71601
QY 781 ACCCTGCTCTACTATAATAATACAAAAAATATCTGGGTGTGGTGGCAGATGCTCTGAAT 840
DB 71602 ACCCTTCTCTACTATAAAAT--ATAAAATTTAGCGGGGTGGTGGCAGCCTATAGT 71659
QY 841 CCCAACTACTAGGAGGCTGAGGAGGAGAAATCGCTTGAACCTGGGAGGCGGAGGTTGCA 900
DB 71660 CCCAGCTACTCAGAAGACTGAGGAGGAGAAATCGCTTGAACCGGGAGGAGGTTGCA 71719
QY 901 GTGAGCGGAGTGCACCATTCACCTCCAGCTGCGAGTGGCAACAGAGCAGACTCCATCCCAA 960
DB 71720 GTGAGCGGAGTTGACCACTGCATCCAGCTCAGCTAGCAAAAGAGCAGACTCCATCTCAA 71779
QY 961 ACAAAACAAACAAACCAATGTAAACATGCTGTAAACATGT 1004
DB 71780 AAAAGAAACAAACCAATTTAAGACTGCATCCCAATATATTT 71823

RESULT 8
US-09-964-824A-273
; Sequence 273, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 273
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-273
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Query Match      4.1%; Score 234.8; DB 10; Length 167343;
Best Local Similarity 75.5%; Pred. No. 2.2e-25;
Matches 305; Conservative 0; Mismatches 97; Indels 2; Gaps 1;

QY 601 ACATGCTTTCACATATACTGCTACAAATAGCCTCCCAACTCTTGTCTCTACTTAAATTCATT 660
DB 71422 ATAACTGTTGTTTTCACGGAAGCAGTGGTTTCCAAATGTTTTTAATCATGTAAATCCATCA 71481
QY 661 GTAAAAAATCAGTCTTGGCGGGCAGGTGGCTCACACCTTATAATCCAGCACTTTGGGA 720
DB 71482 GTAAAAAACAATTTAAGCTGGGTGGCTCACACCTGTAAATCCAGCACTTTGGGA 71541
QY 721 GTCCAGGCGGGCGGTACAGAGTCAAGAGATGAGAGACCATCATGCGCAACATGGTGA 780
DB 71542 GGCCAAAGGCGGCAGATCAGAGGTCAAGAGATCGAGAGCAGCCTGGCCAAACATGGTGA 71601
QY 781 ACCCTGCTCTACTATAATAATACAAAAAATATCTGGGTGTGGTGGCAGATGCTCTGAAT 840
DB 71602 ACCCTTCTCTACTATAAAAT--ATAAAATTTAGCGGGGTGGTGGCAGCCTATAGT 71659
QY 841 CCCAACTACTAGGAGGCTGAGGAGGAGAAATCGCTTGAACCTGGGAGGCGGAGGTTGCA 900
DB 71660 CCCAGCTACTCAGAAGACTGAGGAGGAGAAATCGCTTGAACCGGGAGGAGGTTGCA 71719
QY 901 GTGAGCGGAGATCGCACCATTCACCTCCAGCTGCGAGTGGCAACAGAGCAGACTCCATCCCAA 960
DB 71720 GTGAGCGGAGTTGACCACTGCATCCAGCTCAGCTAGCAAAAGAGCAGACTCCATCTCAA 71779
QY 961 ACAAAACAAACAAACCAATGTAAACATGCTGTAAACATGT 1004
DB 71780 AAAAGAAACAAACCAATTTAAGACTGCATCCCAATATATTT 71823

RESULT 9
US-09-764-877-3989
; Sequence 3989, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; PRIOR application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3989
; LENGTH: 12452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3989

Query Match      4.0%; Score 234; DB 10; Length 12452;
Best Local Similarity 82.2%; Pred. No. 2.3e-25;
Matches 281; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

QY 635 AACCTCTTGTCTCTACTTAAATTCATTGTAAAAATCATAGTCTTGGCCGGCAGCGTGGCTC 694
DB 4966 AACCCCATCTCTACTAAAAATACCAAAAAAAGGCGCCAGCAGCTGGCTC 5025
QY 695 ACACCTATAATCCAGCACTTTGGAGTCCAGGCGGGGGTCCAGAGTCAAGAGATG 754
DB 5026 ACACCTGTAATCCAGCACTTTGGGAAGCGGCGGAGATCAGAGTCAAGATC 5085
QY 755 GAGACCATCATGCGCAACATGGTGAACCCCTGTCTCTACTATAAAATACAAAAAATATTC 814
DB 5086 GAGACCATCTGGCTAAATGGTGAACCCCGCTGTACTTAAATAACAAAAATAGC 5145
QY 815 TGGGTGGTGGCACATGCCTGTAAATCCCAACTACTAGGAGGCTGAGGAGGAGATCG 874
DB 5146 CAGGAGTGGTGGCAGGTGCCTGTAGTCCAGCTACTTGGGAGGCTGAGGAGGAGATGG 5205
QY 875 CTTGAACCTGGGAGCGGAGGTTGCAGTGAGCCGAGATCGACCATTTGCATCCAGCT - 933
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; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match      4.0%; Score 232.4; DB 10; Length 174493;
Best Local Similarity 87.5%; Pred. No. 4.9e-25;
Matches 266; Conservative 0; Mismatches 36; Indels 2; Gaps 1;

QY 673 TCTTGGCCGGGCGGCGCTGCTCACACCTATATATCCAGCAGCTTTGGGAGTCCGAGCGGG 732
Db 119476 TATGGGCTGGGCACAGTGGCTCACACCTGTATATCCAGCAGCTTTGGGAGCGGAGCGAGG 119417

QY 733 CGGGTCACGAGGTCAAGAGATGGAGACCATCATGGCCAAACATGGTGAAACCTGTCTCTA 792
Db 119416 CGGATCACAAGGTCAAGAGATCGAGACCACCTCGGCCAACATGGTGAAACCTGTCTCTA 119357

QY 793 CTATAAATCAAAAAATTTATCTGGGTGGTGGGCACATGCCTGTAATCCCAACTACTAG 852
Db 119356 CTAAAAATAC--AAAAATTTAGCTGGGCATGGTGGTGCATGGCTGTAGTCCAGCTACTCG 119299

QY 853 GGAGGCTGAGGCGAGGAGAACTGCTTGAACCTGGGAGGCGGAGGTTGCAGTGGAGCGAGAT 912
Db 119298 GGAGGCTGAGGCGAGGAGAACTGCTTGAACCTGGGAGGCGGAGGTTGCAGTGGAGCTGAGAT 119239

QY 913 CGCACCATTTGCACCTCCAGCTGGCAACAGAGAGAGACTCCATCCCAAAACAAACAAAC 972
Db 119238 CACACCACCTGCACCTCCAGCTGGCAACAGAGAGAGACTCCATCCCAAAACAAACAAAC 119179

QY 973 AAAA 976
Db 119178 AAAA 119175

RESULT 12
US-09-764-877-2311
; Sequence 2311, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2311
; LENGTH: 7927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2311

Query Match      4.0%; Score 231.6; DB 10; Length 7927;
Best Local Similarity 85.7%; Pred. No. 4.8e-25;
Matches 269; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 664 AAAATCACTCTTTGGCCGGCAGCGTGGCTCACACCTATATATCCAGCAGCTTTGGGAGTC 723
Db 3019 AAAATAAATGTTGGCCGGCGCGGTGGCTCACACCTGTATATCCAGCAGCTTTGGGAGGC 3078

QY 724 CCAGCGGCGGCGGTGCTCACAGAGTCAAGAGATGGAGACCATGTCATGGCCACATGTGTCAAACC 783
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
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; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(174493)
; OTHER INFORMATION: n = A,T,C or G
US-09-804-471A-3

Query Match      4.0%; Score 232.8; DB 10; Length 99014;
Best Local Similarity 83.8%; Pred. No. 4e-25;
Matches 275; Conservative 0; Mismatches 52; Indels 1; Gaps 1;

QY 664 AAAATCAGTCTTGGCCGGGCGGCGTGGCTCACACCTATATATCCAGCAGCTTTGGGAGTC 723
Db 94010 AAAATAAATAATTTGGCCGGGCGGAGTGGCTCACACCTGTATATCCAGCAGCTTTGGGAGGC 93951

QY 724 CCAGCGGCGGCGGTGCTCACAGAGTCAAGAGATGGAGACCATCATGGCCAAACATGGTGAAACC 783
Db 93950 TGAGCGGGTGGATCATGAGTCAAGAGATCCAGACCATCTCGCTAACACAGCTGTAACC 93891

QY 784 CTGTCTCTACTATAAATACAAAAATTTATCTGGGTGTGGGCACATGCCTGTAATCCC 843
Db 93890 TCGTCTCTACTAAAAATACAAAAAATTAGCCGGGTGTGGTGGCACACACCTTTAGTCCC 93831

QY 844 AACTACTAGGAGGCTGAGGCGAGAGATCGCTTGAACCTGGGAGGCGGAGTTGCAGTG 903
Db 93830 AGCTACTCGGGAGGCTGAGGCGAGAGATCGCTTGAACCTGGGAGGCGGAGTTGCAGTG 93771

QY 904 AGCCGAGATCGCACCTATGCACTCCAGCCT--GGCAACAGAGAGAGCTCCATCCCAAAAC 962
Db 93770 AGCCAAGATTGGCCACTGCACTCCAGCCTGGGCGAGAGTGAAGTCCATCTCAAAA 93711

QY 963 AAAACAAAAAACCATTGTAACATG 990
Db 93710 AAAAAAAGAGGAAATAAAAAAATG 93683

RESULT 11
US-09-804-471A-3/c
; Sequence 3, Application US/09804471A
; Patent No. US20020132322A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
```

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Db 3079 CAAGCAGGTGGATCAGCAGGTGACGAGAGTGAGACCATCTGGCTAACACAGTGAACCC 3138
QY 784 CNGTCTCTACTATAATACAAAAAATTATCTGGGTGTGGTGGCACATGCCCTGTAAATCCC 843
Db 3139 CGGTCTCTACTAAAAATACAAAAAATTAGCTGGCGTGGTGCGAGGTGCCCTGTAGTCCC 3198
QY 844 AACTACTAGGAGGCTGAGGCAGGAGATCGCTTGAACCTGGGAGCGGAGGTTGCGAGTG 903
Db 3199 AGCTACTGGGAGGCTGAGGCAGGAGATGGCTCAACCCGCGAGGTGGAGCTTGCAGTG 3258
QY 904 AGCCGAGATCGCACCATTTGCTACTCCAGCCTGG-CAACAGAGCGAGATCCATCCCAAAAC 962
Db 3259 AGCCAAAGATCGCGCCACTGCATCTCCAGCCTGGACAACAGAGCGAGACTCCATCTCAAAA 3318
QY 963 AAAACAAAACAAA 976
Db 3319 GAAAAAIAAAAAA 3332

RESULT 13
US-09-764-877-3785
; Sequence 3785, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3785
; LENGTH: 337
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3785

Query Match 4.0%; Score 231.4; DB 10; Length 337;
Best Local Similarity 85.2%; Pred. No. 3.8e-25;
Matches 270; Conservative 0; Mismatches 46; Indels 1; Gaps 1;

QY 673 TCTTGGCCGGGCGCGTGGCTCACACCTATAATCCACGACATTTGGGAGTCCCGAGCGGG 732
Db 9 TATAGCCGGCGGTGTGGCTCACCGCTGTAATCCAGCACTTCGGGAGCGCGAGCGGG 68
QY 733 CGGGTCACAGGTCAAGAGATGGAGACCATCATGCCACATGGTGAACCCCTGTCTCTA 792
Db 69 CGGATCACAGGTCAAGGATCGAGACCATCTGGCTAACACGGGTGAACCCCGCTCTTA 128
QY 793 CTATAAATCAAAAAAATTATCTGGGTGTGGTGGCACATGCTGTAAATCCCAACTACTAG 852
Db 129 CTGAATAATCAAAAAAATTAGCCGGCGTGTGGTGGCGGCGCTGTAGTCCACGCTACTTG 188
QY 853 GGAGGCTGAGGCAGGAGATCGCTTGAACCTGGGAGCGGAGGTTGCGAGTGAGCCGAGAT 912
Db 189 GGAGGCTGAGGCAGGAGATGCGGTGAACCCGGGAGCGAGCTTGCAGTGAGCCGAGAT 248
QY 913 CGCACCATTTGCATCCAGCCT-GGCACAGAGCGAGACTCCATCCCAAAACAAAACAAA 971
Db 249 CGCGCCACTGCATCTCAGCTCGAGCTGGGCCACAGCGAGACTCCGCTCTCAAAAAAIA 308
QY 972 CAAAACCATGTAAAACA 988
Db 309 AAAAAAIAAAAAA 325

RESULT 14
US-09-764-847-1173/c
; Sequence 1173, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
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; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1173
; LENGTH: 7683
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1173

Query Match 4.0%; Score 230.8; DB 10; Length 7683;
Best Local Similarity 83.5%; Pred. No. 6.2e-25;
Matches 274; Conservative 0; Mismatches 52; Indels 2; Gaps 1;

QY 649 TTAAAAATTCATTATAAAATCAGTCTTGGCCGGGCGACGCTGCTCACACCTATATAATCCC 708
Db 7479 TTCATATCTTTTATAAAATTTTATTTCTTGGCTGGCGAGGTGCTCATGCTGTAATCCC 7420
QY 709 AGCACTTTGGGAGTCCCGAGCGGCGGTCCAGAGTCAAGAGATGAGACCATCATGCG 768
Db 7419 AGCACTTTGGGAGGCTGAGCGCGGCGGATCACGAGGTCAAGAGATCGAGACCATCTGCG 7360
QY 769 CAACATGGTGAACCCCTGTCTCTACTATAAATACAAAAAATTTATCTGGGTGTGGTGGCA 828
Db 7359 CAACATGGTCAAGACCCCTGTCTCTACTATAAAATAC--AAAAATTTGCTGGGCGTGGTG 7302
QY 829 CATGCCCTGTAAATCCCAACTACTAGGAGGCTGAGGAGGAGATCGCTTGAACCTGGGAG 888
Db 7301 CGTGCTGTAGTCCCGACTACTTTGGGAGGCTGAGGAGGAGATCGCTTGAACCGAGGAG 7242
QY 889 GCGGAGGTTCAGTGGAGCGGAGATCGCACCATTTGCACCTCCAGCTCGCAACAGACGAGA 948
Db 7241 TCAGAGGTTCAGTGAGCGCGAGATTCACCATTTACTTAGCTGCGGCAAGAGAGAGA 7182
QY 949 CTCATATCCCAACAAAACAAAACAAA 976
Db 7181 CTCATCTCAAAAAAIAAAAAAIAAAAA 7154

RESULT 15
US-09-764-877-3325/c
; Sequence 3325, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3325
; LENGTH: 3813
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3325

Query Match 4.0%; Score 230.6; DB 10; Length 3813;
Best Local Similarity 83.3%; Pred. No. 6.2e-25;
Matches 274; Conservative 0; Mismatches 54; Indels 1; Gaps 1;

QY 674 CTGGCCGGGCGCGTGGCTCACACCTATAATCCACGACATTTGGGAGTCCCGAGCGGG 733
Db 3813 CTTGGCTGGGCGTGGTGGCTCACGCTGTATCTCCAGCACTTTGGGAGCGCGAGGTGGG 3754
QY 734 GGGTCACGAGGTCAAGAGATGGAGACCATCATGGCCAAACATGTTGAACCCCTGTCTCTAC 793
Db 3753 GGATCAGGAGTCAAGAGATCGAGACCATCTCTGCTAATATGTTGAACCCCTGTCTCTAC 3694
```

[illegible]

Search completed: December 8, 2002, 21:58:35
Job time : 1768 secs

/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end was primed, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email: liangf@life.com

BASE COUNT	317 a	190 c	300 g	223 t	4 others
ORIGIN					
Query Match		14.0%	Score 808.2;	DB 9;	Length 1034;
Best Local Similarity		90.1%	Pred. No. 3e-91;		
Matches 911; Conservative 4;		Mismatches 77;	Indels 19;	Gaps 4;	
Qy	4431	CTGCAGACAGAGCGCGAGAGATGGAGATGGCGAGACGAGATTCATTTCAGAGTCGGGAA	4490		
Db	1	CTGCAGAGAGAGCGCGAGAGACGGAGATGGCGAGACGGATTCATTTCAGCTCGCGAA	60		
Qy	4491	CAGGCGCCCTCTGATGTCGAAGACATTCGCCGACACAGTCGGTCGAATCAAGGCA	4550		
Db	61	CAGGAGCCCTCTGATGTCGAAGACATTCCTGGACACAGTCGGTCGAATCAAGGCA	120		
Qy	4551	ACTCGAAGCCCTCAGAGATGAATTTGAAGAACTGGAATCTTAAGTAAATCAACGGAG	4610		
Db	121	ACTCGAAGCCCTCAGAGATGAATTTGAAGAACTGGAATCTTAAGTAAATCAACGTAGG	180		
Qy	4611	CTTCACCTCAATCTCAGACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACATA	4662		
Db	181	CCTCACCYCAATCGCAAACTTACCAGATGTAACCAAACTTAAGAAGCTTGAATCAAGCA	240		
Qy	4663	----AGAGTCTCAGGGGGCTGGAAGTATTGGCAGAAAGATGTCCAAACCTCACGCATCT	4718		
Db	241	TACAGAGTCTCAGGGGGCTGGAAGTATTGGCAGAAAGTGTCCGACCTCACGCATCT	300		
Qy	4719	ATATTTAAGTGGCAACAAATTTAAGACCTCAGCACAAATAGGCCACTGAACAGTAGA	4778		
Db	301	AAATTTAAGTGGCAACAAATTTAAGACCTCAGCACAAATAGGCCACTGAAGAAGTTAGA	360		
Qy	4779	AAACCTCAGAGCTTAGACCTTTTCAATTTGGAGGTAAACAACTGAACGACTACGGAGA	4838		
Db	361	AAACCTCAGAGCTTAGACCTTTTCAATTTGGAGGTAAACAACTGAACGACTACCGAGA	420		
Qy	4839	AAACGTGTTCAAGCTTCTCCTCAACTCACATATCTCGACAGCTGTTCATGGGACCAAA	4898		
Db	421	AAATGTGTTCAAGCTCCTCCGCACTCACATATCTCGACGGCTATGACGGGACGACAA	480		
Qy	4899	GGAGGCCCTTACTCAGATATTGAGGACCACTGGAGGGCTTGATGACGAGGAGGAGG	4958		
Db	481	GGAGGCCCTTACTCAGATATTGAGGACCACTGGAGGGCTTGATGATGAGGAGGAGGA	540		
Qy	4959	TGAGCATGAGGAGGACTATGATGAAGATGCTCAGTATGAGAGATGAGAGGGCGCAGGA	5018		
Db	541	TGAGGATGAGGAGGAGTATGATGAAGATGCTCAGTATGAGAGATGAGAGGGCGCAGGA	600		
Qy	5019	GGAGGAGGAGGAGGTGAAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAAG	5078		
Db	601	TGAGGAGGAGGAGGTGAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGATCAAGAAG	660		
Qy	5079	TTATACGATGAGAGGTAGATGGCAGAGAGATGAAGAGAGCTTGGTGAAAGCAAGAG	5138		
Db	661	TTATACGATGAGAGGTAGATGACGAGGAAGATGAAGAAGCTTGGTGAAAGCAAGAG	720		
Qy	5139	GGGTCAAGCGAAAATGAGACCTGAAGATGAGGAGAGATGATGACTTAAGTAGAATA	5198		
Db	721	GGGTCAAGCGAAAACGAGACCTGAAGATGAGGAGAGATGATGACTTAAGTAGAATA	780		
Qy	5199	ACCTATTTGAAAATTCCTATTGTGATTTGACTGTTTTTTACCACATATCCCT---	5252		
Db	781	ACCTATTTGAAAATTCCTATTGTGATTTGACTGTTTTTTACCACATATCCCTCTCCGCC	840		

Qy	5253	CCCCCTCCAACTCGCCCCCTGAACACTTTCTTTCTGATTGTAACATTGCTGTGGAA	5312
Db	841	CACCCCTCCAACTCGCCCCCTGAACACTTTCTTTCTGATTGTAACATTGCTGTGGAA	900
Qy	5313	TGAGACGGGAAAAAGTGACTGGGGGTTGTGGAGGAGGAGGAGCGAGCGGTGGACTA	5372
Db	901	CGAGAGGGGAAGAGTGACTGGGGGTTGCGGGGAGGAGATGCGGGGTGGGGTGGAAAT	959
Qy	5373	AAATACTATTTTTTACTGCCAAATAAAAATAATATTTGTAATAATTAACATGGG	5423
Db	960	AAATACTATTTTTTACTGCCACTCTTTATTTTTTTCCTCTACTTTCTTTCTTKTG	1010
RESULT 2			
AL560249			
LOCUS	AL560249 LTI_FL011_BCl	923 bp	mRNA linear EST 16-FEB-2001
DEFINITION	AL560249 LTI_FL011_BCl Homo sapiens cDNA clone CS0DG002YI23 5 prime mRNA sequence.		
ACCESSION	AL560249		
VERSION	AL560249.1	GI:12906528	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
TITLE	Full-length cDNA libraries and normalization		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.		
FEATURES	Location/Qualifiers		
source	1..923		
organism	"Homo sapiens"		
db_xref	"taxon.9606"		
clone	"CS0DG002YI23"		
clone_lib	"LTI_FL011_BCl"		
sex	"male"		
tissue_type	"B cells from Burkitt lymphoma"		
lab_host	"DH10B"		
note	"Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dR) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"		
BASE COUNT	299 a	163 c	279 g 175 t
ORIGIN	7 others		
Query Match	13.3%	Score 770:	DB 9: Length 923;
Best Local Similarity	92.1%	Pred. No. 1.7e-86;	
Matches	851: Conservative	7: Mismatches	52: Indels 14: Gaps 4:
Qy	4327	TGGGGGCTCGAGAACCGAGCGAGCTGGTTGAGTCTTCAAAGTCTCTAAACGTGCGGCCG	4386
Db	2	TGGGGGCTCGAGAACCGAGCGGA-STGGTTGAGCCTTCAAAGTCTCTAAACGCGCGGCCG	60
Qy	4387	TGGGTTTCAGAGTTATTTCGATTGAAATTCGGCTGGCAGACAGACCTCTCGACACAGAGCG	4446
Db	61	TGGGTTTCGGGGTTTATTGATTGAAATTCGCCGCGGGGAGCCCTCTGCGAGAGAGAGCG	120
Qy	4447	CGAGATGGAGATGGGGCAGACGGATTTCATTTCAGAGCTGCGGAAACAGCGCCCTCTGAT	4506
Db	121	CGAGATGGAGATGGGGCAGACGGATTTCATTTCAGAGCTGCGGAAACAGCGCCCTCTGAT	180
Qy	4507	GTGAAGAACTTGCCTCGGCAACACAGTCGGTTCGATGAATGAAGGCAAACTCGAAGCCCTCACA	4566

Db	181	GTAAAGAACTTGCTCTGGACACAGTCGGTCGAATGAAGCAAACTCGAAGGCCTCACA	240
Qy	4567	GATGAATTTGAAGAACTTGAATCTTAAGTAATAATCAACGAGGCTCAGCTCAATCTCA	4626
Db	241	GATGAATTTGAAGAACTTGAATCTTAAGTAATAATCAACGAGGCTCAGCTCAATCTCA	300
Qy	4627	GACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG	4674
Db	301	AACTTACCAAGTTAACAACAACTTAAGAAAGCTTGAACCTAAGCGGATACAGAGTCTCAGGG	360
Qy	4675	GGCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTAAAGTGGCAAC	4734
Db	361	GGCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTAAAGTGGCAAC	420
Qy	4735	AAAATTAAAGACCTCAGCACAAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTA	4794
Db	421	AAAATTAAAGACCTCAGCACAAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTA	480
Qy	4795	GACCTTTTCAATTCGAGGTAAACCACTGAACGACTACGAGAAAACGTTGTTCAAGCTT	4854
Db	481	GACCTTTTCAATTCGAGGTAAACCACTGAACGACTACGAGAAAATGTGTTCAAGCTC	540
Qy	4855	CTCCTGCAACTCAGATATCTCGACAGCTGTACTGGACACACAGGAGGCCCTTACTCA	4914
Db	541	CTCCTGCAACTCAGATATCTCGACAGCTGTACTGGACACACAGGAGGCCCTGACTCG	600
Qy	4915	GATATTGAGGACACGTTGAGGGCTCGATGACGAGGAGGAGGCTGAGCATGAGGAGG	4974
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Qy	5035	GAACGAGGACGTCAGTGTGAGGGGAGGAGGAGGATGAAGAAGTTATAACGATGAGAG	5094
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LOCUS			
DEFINITION			
AL533191 LTI_FL015_Brn1 Homo sapiens cdna clone CS0DN003YK10 5			
prime, mRNA sequence.			
ACCESSION			
AL533191			
VERSION			
AL533191.1 GI:12796684			
KEYWORDS			
EST.			
SOURCE			
human.			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 894)			
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.			
Full-length cDNA libraries and normalization			
Unpublished (2001)			
Contact: Genoscope			
Genoscope - Centre National de Sequenage			
BP 191 91006 EVRY cedex - France			
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.			
Location/Qualifiers			
1..894			
FEATURES			
source			

/organism="Homo sapiens"			
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/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"			
BASE COUNT	293 a	159 c	270 g
ORIGIN	2 others		
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Best Local Similarity 13.1%; Score 756.6; DB 9; Length 894;			
Matches 829; Conservative 1; Mismatches 50; Indels 13; Gaps 3;			
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Db	61	GGCGGGGAGCTCTGCAGAGAGAGCGCGAGATGGAGATGGCAGACGATTTCATT	120
QY	4478	CAGAGCTGGGACACAGGGCGCCCTCTGATGTCAAAAGACTTCCTCGTGGACACAGTCGGT	4537
Db	121	TGAGCTGGGACACAGGAGCGCCCTCTGATGTGAAGAACTTCTCTGTCGACACAGTCGGT	180
QY	4538	CGAATGAAGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTTGAATTTTAAGTA	4597
Db	181	CGAATGAAGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTTGAATTTTAAGTA	240
QY	4598	AAATCAACGAGGCTCTCACTCAATCTCAGCTTACCAAGTTA---AAGTTGAGAAAGC	4654
Db	241	CAATCAACGCTAGGCTCTCACTCAATCTCAGCTTACCAAGTTA---AAGTTGAGAAAGC	300
QY	4655	TTGAACCTA-----AGAGTCTCAGGGGCTCGAAGTATTGGCAAAAAGTCTCCAA	4705
Db	301	TTGAACCTA-----AGAGTCTCAGGGGCTCGAAGTATTGGCAAAAAGTCTCCGA	360
QY	4706	ACCTCAGCATCTATATTAAAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCAC	4765
Db	361	ACCTCAGCATCTATATTAAAGTGGCAACAAATTAAGACCTCAGCACAATAGAGCCAC	420
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RESULT 4
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LOCUS AL535686 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF016YA23 5
DEFINITION prime, mRNA sequence.
ACCESSION AL535686
VERSION AL535686.1 GI:12799179
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 875)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. 875
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF016YA23"
/cv="LTI_FL013_FBrn1"
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week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 291 a 156 c 267 g 160 t 1 others
ORIGIN

Query Match 13.0%; Score 751; DB 9; Length 875;
Best Local Similarity 92.9%; Pred. No. 4e-84;
Matches 813; Conservative 0; Mismatches 50; Indels 12; Gaps 2;

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QY 4478 CAGAGCTGGGAACAGGGCCCTCTGTGATGTAAGAAGTTCCTCTGGACACATCGGT 4537
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QY 4598 AATATCAACGAGGCGCTCACCTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAGAAAGC 4654
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QY 4766 TGAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTCAATTGCGAGGTAACCAACTGA 4825
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QY 5006 AGAGGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5065
Db 661 AGGAGGACGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 5066 AGGATGAAGAAGGTTATAACGATGGAGAGGTAGATGCCGAGGAAGATGAAGAAGAGCTTG 5125
Db 721 AGGATGAAGAAGGTTATAACGATGGAGAGGTAGATGCCGAGGAAGATGAAGAAGAGCTTG 780
QY 5126 GTGAAGAAGAAAGGGTCAGAAGCGAAAATGGAACCTGAAAGATGAGGGGAGAAGATGATG 5185
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Db 841 ACTAAGTGGAAATACCTATTGTAATAATTCCTAT 875

RESULT 5
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LOCUS AL540827 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE004YL15 5 prime
DEFINITION , mRNA sequence.
ACCESSION AL540827
VERSION AL540827.1 GI:12871345
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 903)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
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DEFINITION	AL537874	LTI_Fl013_FBrnl	Homo sapiens cDNA clone CS0DF028YN19 5	
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prime, mRNA sequence.

ACCESSION	AL537874
VERSION	AL537874.1
	GI:12801367

KEYWORDS	ORGANISM
SOURCE	Homo sapiens
EST.	human.
KEYWORDS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
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JOURNAL Unpublished (2001)

Genoscope - Centre National de Sequencage

Email: segreg@genoscope.cns.fr, Web : www.genoscope.cns.fr.

source

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week, 24 week and 26 week)"

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/note="Organ: Fetal brain; V
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pCMVSPORT 6 vector. Library

division of Invitrogen 9800

fliang@lifetech.com URL :

BASE COUNT	290 a	156 c	265 g	155 t
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290 a				

Best Local Similarity 91.9%; Pred. No. 3.8e-

[illegible]

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Db 901 TTGACGGGTTTAAACCATATTCCTTTTCCCGCCCTTCAATTCCTGGCGCCTG 960
QY 5276 AACCTACTTTTCTGATTGTAA 5298
Db 961 AAAACTTATTTTTTCCCGGAA 983

RESULT 8
AL547157 875 bp mRNA linear EST 27-FEB-2001
LOCUS AL547157 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1010YL13 5
DEFINITION prime, mRNA sequence.
ACCESSION AL547157
VERSION AL547157.1 GI:12880969
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 875
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/clone="CS0D1010YL13"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 288 a 157 c 267 g 161 t 2 others
ORIGIN

Query Match 12.6%; Score 731.6; DB 9; Length 875;
Best Local Similarity 92.4%; Pred. No. 1e-81;
Matches 804; Conservative 2; Mismatches 51; Indels 13; Gaps 3;

QY 4359 GTCTTCAAAGTCCTAAACGTGGCGCGTGGTTCGAGGTTTATGATTCGAATTCGGCTG 4418
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QY 4419 GCACGAGGCTCTGCACAGACGAGCGCGAGAGATGCAGATGGCAGCGGATTCATTC 4478
Db 61 GCGCGGAGCCTCTGCAGAGAGAGAGCGCGAGASATGAGATGGCAGACGGATTCATT 120
QY 4479 AGAGCTCGGNAACAGGCGCGCCTGTGATGTGAAGAACTTCGCCCTGGACAACAGTCGGTC 4538
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QY 4539 GAATGAGGCAAACTCAAGCCCTCAGATGAATTTGAGACACTGGAATTCCTAAGTAA 4598
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QY 4599 AATCAACGGAGCGCTCACCTCAATCTCAGACTTACCAAGCTTA---AAGTTGAGAAGCT 4655
Db 241 AATCAACGTAGGCTCACCTCAATCGCAAACTTACCAAGCTTAACCAAACTTAAGAGCT 300
QY 4656 TGAACTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTGTCCAAA 4706
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Db 361 CCTCAGCATCTAAATTTAAGTGGCAACAAAATTAAGACCTCAGCACAAATAGAGCCACT 420
QY 4767 GAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTTGGGAGGTAAACCAACTGNA 4826
Db 421 GAAAAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTTGGGAGGTAAACCAACTGAA 480
QY 4827 CGACTACGGGAAAACGCTGTTCAAGCTTCTCTGCAAACTCACATATCTCGACAGCTGTTA 4886
Db 481 CGACTACCGGAAAATGTCTTCAAGCTCTCCCGCAACTCACATATCTCGACGGGTATGA 540
QY 4887 CTGGGACCACAAGAGGCGCCCTTACTCAGATATTGAGGACCACGCTGGAGGGCCTGGATGA 4946
Db 541 CCGGGACGACAAGAGGCGCCCTGACTCGGATGCTGAGGCTACGTTGGAGGCGCTGGATGA 600
QY 4947 CGAGGAGGAGGGTGAACATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGA 5006
Db 601 TGAGGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGA 660
QY 5007 GGAGGCGGAGGAGGAGGAGGAGGAGTGAAGGAGGAGCTGAGTGGAGGGGACGAGGA 5066
Db 661 GGAGGACGAGGATGAGGAGGAGGAGGAGTGAAGGAGGAGCTGAGTGGAGGAGGAGGA 720
QY 5067 GGATGAAGAAGGTTATACGATGGAGAGTAGATGCGGAGGAAGATGAAGAAGAGCTTTGG 5126
Db 721 GGATGAAGAAGGTTATACGATGGAGAGGTAGATGACGAGGAAGATGAAGAAGAGCTTTGG 780
QY 5127 TGAAGAAGAAGGGGTCAGAACGCGAAAATGAGAACTGAAGATGAGGAGGAAGATGATGA 5186
Db 781 TGAAGAAGAAGGGGTCAGAACGCGAAAACGAGAACTGAAGATGAGGAGGAAGATGATGA 840
QY 5187 CTAAGTAGAATAACCTATTATTTGAAAAAATTC 5216
Db 841 CTAAGT-GGATACCTATTATTTGAAAAAATTC 869

RESULT 9
AL571434/c
LOCUS AL571434 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1023YE09 3
DEFINITION prime, mRNA sequence.
ACCESSION AL571434
VERSION AL571434.1 GI:12928726
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 894
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1023YE09"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
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Db 421 TAGCMACCTGAAAAAGTTAGAAAAACCTCAAGAGCTTAGACCTTTTCAATTGCGAGGTAA 480
QY 4817 CCAACCTGAACGACTACGAGAGAAACGTTTCAAGCTTCTCCTGCAACTCACATATCTCG 4876
Db 481 CCAACCTGAACGACTACGAGAGAAATGTGTTCAAGCTCCTCCCGCAACTCACATATCTCG 540
QY 4877 ACAGCTGTACTGGGACACAAAGAGGCGCCCTTACTCAGATATTGAGGACCACCTGGAGG 4936
Db 541 ACGCTATACCGGACGACAAAGAGGCGCCCTGACTCGGATGCTGAGGGCTACGTGGAGG 600
QY 4937 GCCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAG 4996
Db 601 GCCTGGATGATGAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAG 660
QY 4997 TGGAGATGAGGAGGCGGACGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGCTGAGTGGAG 5056
Db 661 TGGAGAGGAGGAGGAGGAGGATGAGGAGGAGGAGGAGTGAAGAGGAGGAGCTGAGTSSAG 720
QY 5057 GGGACGAGGAGGATGAAGAAGGTTTAAACGATGAGAGGTAGATGGCGAGGAAGATGAAG 5116
Db 721 AGGAGGAGGAGTGAAGAAGGTTTAAACGATGAGAGGTAGATGGAGAGGTAGATGACGAGGAAGATGAAG 780
QY 5117 AAGAGCTTGGTGAAGAGAAAGGGGTGAGAAAGCGGAAATGAGAACCTGGAAGATGAGGAG 5176
Db 781 AAGAGCTTGGTGAAGAGAAAGGGGTGAGAAAGCGGAAATGAGAACCTGGAAGATGAGGAG 840
QY 5177 AAGATGATGACTAAGT 5192
Db 841 -AGATGATGACTAAGT 855

RESULT 11
LOCUS
DEFINITION AL517375 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA003YC02 5
prime, mRNA sequence.
ACCESSION AL517375
VERSION AL517375.1 GI:12780868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 992)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/organism="Homo sapiens"
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/clone="CS0DA003YC02"
/clone_lib="LTI_NFL011_NBC1"
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
301 a 174 c 289 g 217 t 11 others

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BASE COUNT
ORIGIN

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Query Match 12.3%; Score 710.4; DB 9; Length 992;
Best Local Similarity 88.4%; Pred. No. 4e-79;
Matches 813; Conservative 8; Mismatches 81; Indels 18; Gaps 4;

QY 4455 GGAGATGGGCAGACGATTCAATTCAGAGCTGCGGAACAGGGCGCCCTCTGATGTGAAGA 4514
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QY 4515 ACTTGTCCCTGGACCAACAGTCGGTCGGAATGAAGCAAACTCGAAGCCCTCACAGATGAATT 4574
Db 61 ACTTGTCCCTGGACCAACAGTCGGTCGGAATGAAGCAAACTCGAAGCCCTCACAGATGAATT 120
QY 4575 TGAAGAACTGGAAATCTTAAAGTAAATAACAACGAGGCGCTCACCTCAATCTCAGACTTACC 4634
Db 121 TGAAGAACTGGAAATCTTAAAGTAAATAACAACGAGGCGCTCACCTCAATCGCAAACTTACC 180
QY 4635 AAGTTTA--AAAGTTGAGAAAGCTTGAACATA-----AGAGTCTCAGGGGGCCTGGA 4682
Db 181 AAGTTTAAACAAACTTAAAGAAGCTTGAACATAACGCGGATCTCAGGGGGCCTGGA 240
QY 4683 AGTATTGGCAGAAAAAGTGTCCTCAAACTCACGCATCTATATTTAAAGTGGCAACAAAATTA 4742
Db 241 AGTATTGGCAGAAAAAGTGTCCTCAAACTCACGCATCTAATTTAAAGTGGCAACAAAATTA 300
QY 4743 AGACCTCAGACACAAATAGAGCCACTGAAACAGTTAGAAAACTCAAGAGCTTAGACCTTTT 4802
Db 301 AAACCTCAGACACAAATAGAGCCACTGAAAAAGTTAGAAAACTCAAGAGCTTAGACCTTTT 360
QY 4803 CAATTGCGAGGTAAACCAACTGAACGACTACGGAGAAACGTTTCAAGCTTCTCCTGCA 4862
Db 361 CAATTGCGAGGTAAACCAACTGAACGACTACGGAGAAATGTGTTCAAGCTTCTCCTGCA 420
QY 4863 ACTCACATATCTCGACAGCTGTTACTGGACCAACAGGAGGCGCCCTTACTCAGATATTGA 4922
Db 421 ACTCACATATCTCGACAGCTGTTACTGGACCAACAGGAGGCGCCCTGACTCGGATCTGA 480
QY 4923 GGACACAGTGGAGGGCGCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGA 4982
Db 481 GGGCTACGTGGAGGGCGCTGGATGATGAGGAGGAGGTGAGGAGGAGTATGATGA 540
QY 4983 AGATGCTCAGGTAGTGGAAAGTGAAGGCGGAGGAGGAGGAGGAGGTGAAGAGA 5042
Db 541 AGATGCTCAGGTAGTGGAAAGTGAAGGCGGAGGAGGAGGAGGAGGAGGTGAAGAGA 600
QY 5043 GGACGTGACTGGAGGGCGGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGATGG 5102
Db 601 GGACGTGACTGGAGGGCGGAGGAGGATGAAGAAGGTTATAACGATGGAGAGGTAGATGA 660
QY 5103 CGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAANAATGAGAAC 5162
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QY 5163 TGAAGATGAGGGAGAGATGATGACTAAGTAGAATAAACCCTATTTTGAANAATTCCTATTG 5222
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QY 5223 TGATTTGACTGTTTTTACCCTATATCCCTCCCTCCCTC---CAATCCTGCCCTGAAACT 5279
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QY 5280 TACTTTTCTCATGTTACATATGCTGTGGGAATCAGACGGGAAAGGTGACTGGGGGT 5339
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RESULT 12
AK020753
LOCUS

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AK020753 1141 bp mRNA linear HTC 19-JAN-2002

DEFINITION	Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430101K10:acidic nuclear phosphoprotein 32, full insert sequence.
ACCESSION	AK020753
VERSION	AK020753.1 GI:12861438
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) 0 day neonate thymus cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library
ORGANISM	clone:A430101K10.
REFERENCE	Mus musculus
AUTHORS	1 Carninci,P. and Hayashizaki,Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Todawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076851
REFERENCE	4
AUTHORS	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaide,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Rongwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5 (bases 1 to 1141)
AUTHORS	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
TITLE	Direct Submission
JOURNAL	Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
FEATURES	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Gemomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 229.4. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGCTTAATTAATTAATCCGCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
misc_feature	Location/Qualifiers 1. .1141 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="FANTOM_DB:A430101K10" /db_xref="MGD:MG1:1911820" /db_xref="taxon:10090" /clone="A430101K10" /tissue_type="thymus" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="0 day neonate"
gene	1. .1141 /gene="Anp32"
misc_feature	1. .1141 /gene="Anp32" /note="acidic nuclear phosphoprotein 32 data source:MGD, source key:MG1:108447, evidence:ISS" /db_xref="MGD:MG1:108447"
BASE COUNT	348 a 210 c 338 g 245 t
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Query Match	12.3%; Score 710; DB 11; Length 1141;
Best Local Similarity	83.4%; Pred. No. 4.2e-79;
Matches	897; Conservative 0; Mismatches 155; Indels 24; Gaps 7;
Qy	4336 GAGAACCGAGCGGAGCTGGTTGAGCTCTTCAAGTCTTAAACGTCTTAAACGTGGCGCGCTGGTTCGA 4395
Db	2 GAGAACCGAGCGGAGCTGGTTGAGCTCTTCAAGTCTTAAACGTCTTAAACGTGGCGCGCTGGTTCGG 61
Qy	4396 GGTTTATTGATTGAATTCGGCTGGCAGCAGCTCTGCGAG--ACAGAGAGCGCGAGAGA 4453
Db	62 GGTTTATTGATTGAATTCGGCTGGCAGCAGCTCTTGCAGAAAGAGAGAGCGCGAGAGA 121
Qy	4454 TGGAGATGGCGAGACCGATTTCATTACAGCTGGGGAACAGGGCGCCCTCTGTATGTCTGAAG 4513
Db	122 TGGAGATGGAGCAACCGATTATTAGAGCTGGGACAGACGCCCTCTGTATGTCTGAAG 181
Qy	4514 AACTTGGCCCTGGAGCAACAGCTGGTTCGTAATGAAGCAAACTCGAAGCCCTCACAGATGAAT 4573
Db	182 AGCTGGTCTTGGATTAAGTGAAGTCAATTAAGAGCAAAATCGAAGGCTCTCACGGATGAGT 241
Qy	4574 TTGAAGACTCGGAATCTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAGACTTAC 4633

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QY 4682 AAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTA 4741
Db 362 AAGTATTGGCAGAGAAATGTCGAACTTAAAGCATCTAATTTAAGTGGCAACAAATTA 421
QY 4742 AAGACCTCAGACAATAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAGACCTTT 4801
Db 422 AAGATCTCAGACAATAGAGCCGCTGAAGAAGTTAGAAATCTCAAGAGCTTAGACCTGT 481
QY 4802 TCAATTCGAGGTAAACCACTCAAGCACTACGAGAAACGTTCAAGCTT-CTCCTG 4860
Db 482 TTAAGTGGAGGTGACCACTGAATGCTTACCGAGAAACGTTCAAGGTTCTCGGCC 541
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Db 542 CAAGTCATGTACCTCGATGCTATGACAGGACCAACAAGAGGCCCGGACTCCGATGTT 601
QY 4921 GAGGACCACTGAGGGCCCTGGATGACGAGGAGGAGGGGTGAGCATGAGGAGGATGAT 4980
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QY 4981 GAAGATGCTCAGGTAGTGAAGATGAGGAGGCGAGGAGGAGGAGGAGGAGGAGGAG 5040
Db 656 GAATATGCCAGTTAGTGGGAAGATGAAGAGGAAGAGGATGAGGAGGAAGAGGGAGGAA 715
QY 5041 GAGGACGTGAGTGGAGGGACGAGGAGGATGAAGAAGTTATACGATGGAGAGGTAGAT 5100
Db 716 GAGGATGAGTGGAAAGGAGGAGGAGGATGAGGAGGATGAGGAGGAGGAGGAGGAGGAA 775
QY 5101 GCGGAGAAAGATGAAGAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGCGAAATGAGAA 5160
Db 776 GAGGAGAAAGACGAAGAAGAGCTTGGTGAAGAAGAAGGAGTGAAGAAGGAGGAGGAG 835
QY 5161 CCTGAAGATGAGGAGGAGGAGGATGATGACTAGTAGAATAACCTATTTTGAATAATTCCTAT 5220
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RESULT 13
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LOCUS
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AGENCOURT_7567365 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5060491
5', mRNA sequence.
ACCESSION BQ232856
VERSION BQ232856.1 GI:20414256
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 895)
AUTHORS NIH-MGC http://imgc.nhl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999).
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
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Tissue Procurement: DCTD/DTP/Cazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13328 row: n column: 12
High quality sequence stop: 676.
Location/Qualifiers
1. 895
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Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

BASE COUNT 294 a 163 c 276 g 161 t 1 others
ORIGIN
Query Match 12.1%; Score 702.8; DB 14; Length 895;
Best Local Similarity 92.2%; Pred. No. 3.7e-78;
Matches 799; Conservative 0; Mismatches 53; Indels 15; Gaps 5;

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QY 4403 TGATTGAATTCGGTGGCAGAGAGCCCTCTGCAGACAGAGAGCGCGAGATGGATGG 4462
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QY 4463 GCAGACGATTTCATTGAGCTGCGGAACAGGGCGCCCTCTGATGTGAAGAACTTGCCC 4522
Db 121 GCAGACGATTTCATTGAGCTGCGGAACAGGGCGCCCTCTGATGTGAAGAACTTGCCC 180

QY 4523 TGGCAACAGTCGGTGAATGAAGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAAC 4582
Db 181 TGGCAACAGTCGGTGAATGAAGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAAC 240

QY 4583 TGGAAATCTTAAATTAATCAACGAGGCGCTCACTCAATCTCAGACTTACCAAGTTA- 4641
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QY 4751 GCACAAATAGCCCTGAACAGTTAGAAACCTCAAGAGCTTAGACCTTTTCAATTCG 4810
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QY 4871 ATCTCGACAGCTGTTTACCTGGGACCAACAAGAGGCGCCCTTACTCAGATATTGAGGACCA 4930
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QY 4931 TGGAGGCGCTGATCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4990
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QY 4991 AGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5050

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||||| 661 AGGTAGTGAAGACGAGGACGAGATGANGAGGAGGAGTGAACAGGAGGACGTGA 720
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||||| 721 GTGAGAGGAGGAGGATGAACAGCTTATAACGATGAGAGGAGTAGATGACGAGGAAG 780
||||| 5111 ATGAAGAAGAGCTTGGTGAAGAA-GAAAGGGGTGAGAAGCGAAATGAGAA-CCTGAAGA 5168
||||| 781 ATGAAGAAGAGCTTGGTGAAGAACGAAGGGTCAAGAAGCGAAACGAGAAGACCTGAAGA 840
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ACCESSION AL545880
VERSION AL545880.1 GI:12878473
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 834)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 272 a 153 c 257 g 148 t 4 others
ORIGIN

Query Match 12.1%; Score 699.4; DB 9; Length 834;
Best Local Similarity 92.2%; Pred. No. 1e-77;
Matches 759; Conservative 3; Mismatches 49; Indels 12; Gaps 2;

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QY 4411 TTCGGCTGCAGAGAGCTCTGAGACAGAGAGCGAGATGGAGATGGGACAGCG 4470
DB 68 TTCGCCGCGGCGGAGGCTCTGAGARAGAGAGCGCGARATGGAGATGGGACAGCG 127
QY 4471 ATTCATTTCAGAGCTCGGGAACAGGCGCCCTCTGATGTGAAGAAGTTCGCCCGACAAC 4530
DB 128 ATTCATTTCAGAGCTCGGGAACAGGCGCCCTCTGATGTGAAGAAGTTCGCCCGACAAC 187
QY 4531 AGTCGGTGAATGAAGGCAAACTCGAAGCCCTCAGATGAATTTGAAGAACTGGAATTC 4590
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||||| 4648 AGAAGCTTTGAATA-----AGAGTCTCAGGGGCGCTGGAAGTATTTGGCAGAAAAG 4698
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||||| 4699 TGTCCAAACCTCAGCATCTATATTTAAGTGCACAACAAATTAAGAGCTCAGCACAATA 4758
||||| 368 TGTCCAAACCTCAGCATCTAATTTAAGTGGCAACAAATTAAGAGCTCAGCACAATA 427
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||||| 548 GGTATGACCGGGGACAAAGAGGCCCTGACTCGGATGCTGAGGGGTACGTTGAGGCG 607
||||| 4939 CTGGATGACGAGGAGGAGGTGAGATGAGGAGGAGTAGTATGATGAAGATGCTCAGGTAGTG 4998
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||||| 5059 GACGAGGAGGATGAAGAAGCTTATACGATGAGAGGAGTAGATGGCGAGGAAGATGAAGAA 5118
||||| 728 GAGGAGGAGGATGAAGAAGCTTATACGATGAGAGGAGTAGATGAGGAGGAGATGAAGAA 787
||||| 5119 GAGCTTGGTGAAGAGAAAGGGTCAAGAGCGGAAATGAGAAC 5161
||||| 788 GAGCTTGGTGAAGAGAAAGGGTCAAGAGCGGAAACGARAAC 830

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DEFINITION prime, mRNA sequence.
ACCESSION AL518247
VERSION AL518247.1 GI:12781740
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 802)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 258 a 148 c 248 g 143 t 5 others
ORIGIN

Query Match 11.6%; Score 673.2; DB 9; Length 802;
Best Local Similarity 91.8%; Pred.No. 1.8e-74;
Matches 735; Conservative 2; Mismatches 52; Indels 12; Gaps 2;

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QY 4413 CGGCTGCCAGAGAGCCTCTGCAGACAGAGCGGAGAGATGGAGTGGCGACACGAT 4472
Db 62 CCGCGCGCGCGGAGCGCTCTGCAGAGAGAGCGGAGAVMGAGAGCGGCGACACGAT 121

QY 4473 TCATTACAGAGCTCGGGAACACGCGCCCTCTGATGTGAAGAACTTCCCTGCACACAG 4532
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QY 4533 TCGGTGCAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAATTCCT 4592
Db 182 TCGGTGCAATGAAGGCAAACTCGAAGCCCTCACAGATGAATTTGAAGAACTGGAATTCCT 241

QY 4593 AAGTAAATCAACGAGGCTTCACTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAG 4649
Db 242 AAGTAAATCAACGAGGCTTCACTCAATCTCAGACTTACCAAAAGTTA---AAGTTGAG 301

QY 4650 AAAGCTTGAACTA-----AGAGTCTCAGGGGCGCTGGAAGTATTCGCAAAAAGTG 4700
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QY 4701 TCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAATTAAGACCTCAGCACAATAGA 4760
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QY 4821 CPTGAACGACTACGGAGAAAACGTTCAAGCTTCTCTGCAACTCACATATCTCGACAG 4880
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QY 4941 GGATGACGAGGAGGAGGTGAGCATGAGGAGGATGATGATGAGATGCTCAGGTAGTGA 5000
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Search completed: December 8, 2002, 19:14:33
Job time : 4922 secs

22 917.6 15.9 2449 30 US-09-760-469-601 Sequence 601, App
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24 889 15.4 889 22 US-09-591-500-3 Sequence 3, Appli
25 883 15.3 1155 1 PCT-US01-08631-12193 Sequence 12193, A
26 869.2 15.0 2398 16 US-09-205-070-14975 Sequence 14975, A
27 869.2 15.0 2398 17 US-09-340-623-14975 Sequence 14975, A
28 869.2 15.0 2398 33 US-09-898-888-14975 Sequence 14975, A
29 869.2 15.0 2398 33 US-09-898-888A-14975 Sequence 14975, A
30 867.8 15.0 1052 1 PCT-US02-25766-3866 Sequence 3866, Ap
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32 865 15.0 895 22 US-09-591-500-21 Sequence 21, Appl
33 839.4 14.5 895 22 US-09-591-500-23 Sequence 23, Appl
34 831.4 14.4 907 22 US-09-591-500-6 Sequence 6, Appli
35 791 13.7 916 14 US-09-038-847A-2 Sequence 2, Appli
36 791 13.7 916 17 US-09-393-302-25 Sequence 25, Appl
37 791 13.7 925 31 US-09-825-886-25 Sequence 25, Appl
38 764.4 13.2 925 37 US-09-997-722-245 Sequence 245, App
39 764.4 13.2 925 38 US-10-035-832-1497 Sequence 1497, Ap
40 762.6 13.2 907 22 US-09-591-500-13 Sequence 13, Appl
41 761 13.2 907 22 US-09-591-500-25 Sequence 25, Appl
42 760.2 13.1 906 22 US-09-591-500-33 Sequence 33, Appl
43 757.8 13.1 907 22 US-09-591-500-28 Sequence 28, Appl
44 753 13.0 907 22 US-09-591-500-9 Sequence 9, Appli
45 751.6 13.0 908 22 US-09-591-500-32 Sequence 32, Appli

ALIGNMENTS

RESULT 1
US-09-591-500-1
; Sequence 1, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4453)..(5154)
; OTHER INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 5785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 GAGCCTGACATAGTTTCTGGCTGTGAATGCTCAATAAATATTTGTTTAAATGAGTAGAAA 240
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QY 3841 GTTTTAGGTATTAATCTGACAGAACAGATACAAACCAGATCATTTGTGAGTCAGAAGTGG 3900
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QY 4021 TTGCTGTTATTAATTTCTGATGATATTCCTCAGTTTACTTTTAAACCTAGTCTATAGAT 4080
Db 4021 TTGCTGTTATTAATTTCTGATGATATTCCTCAGTTTACTTTTAAACCTAGTCTATAGAT 4080
QY 4081 TCAAGATATCCCTGTGAGGTCCTAAAGTAAAGAAAGAAATGGGTACTTTGGAAGC 4140
Db 4081 TCAAGATATCCCTGTGAGGTCCTAAAGTAAAGAAAGAAATGGGTACTTTGGAAGC 4140
QY 4141 TGATTCACAGTAAGTAGTGTAGAGGGAGTGCCITGTGTAATTCACAAATTAACAAGTGA 4200
Db 4141 TGATTCACAGTAAGTAGTGTAGAGGGAGTGCCITGTGTAATTCACAAATTAACAAGTGA 4200
QY 4201 GCATCAGATAAGATTTCTTTAGTCACACACACCTTACCTTCTTAGGAAGATCCATAT 4260
Db 4201 GCATCAGATAAGATTTCTTTAGTCACACACACCTTACCTTCTTAGGAAGATCCATAT 4260
QY 4261 ACTTGAATTAATTTGCTGCTTGACCCAGGTACTTATCAGTCCCTTTTATTAATATTTG 4320
Db 4261 ACTTGAATTAATTTGCTGCTTGACCCAGGTACTTATCAGTCCCTTTTATTAATATTTG 4320
QY 4321 TAAATATTTGGGCTCGAGAACCGGAGCGAGCTGGTGTAGTCTTCAAAAGTCTCAAAAGCTG 4380
Db 4321 TAAATATTTGGGCTCGAGAACCGGAGCGAGCTGGTGTAGTCTTCAAAAGTCTCAAAAGCTG 4380
QY 4381 CGGCCGTGGGTTTCGAGGTTTATTTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAG 4440
Db 4381 CGGCCGTGGGTTTCGAGGTTTATTTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAG 4440
QY 4441 AGAGCGCAGAGATGGAGTGGCAGACGATTCATTCAGAGCTGCCGAAACAGGCGCCC 4500
Db 4441 AGAGCGCAGAGATGGAGTGGCAGACGATTCATTCAGAGCTGCCGAAACAGGCGCCC 4500
QY 4501 TCTGATGTGAAGAATTTGCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCC 4560
Db 4501 TCTGATGTGAAGAATTTGCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCC 4560

QY 4561 CTCACAGATGAATTTGAAGAACTGGAAATTTCTTAAGTAAATCAACGAGGCCTCACCTCA 4620
Db 4561 CTCACAGATGAATTTGAAGAACTGGAAATTTCTTAAGTAAATCAACGAGGCCTCACCTCA 4620
QY 4621 ATCTCAGACATTACCAAGTTAAAGTTAGAAAGCTTGAACTAAGAGTCTCAGGGGCCCTG 4680
Db 4621 ATCTCAGACATTACCAAGTTAAAGTTAGAAAGCTTGAACTAAGAGTCTCAGGGGCCCTG 4680
QY 4681 GAAGTATTTGCGAGAAAGTGTCCAAACCTCACGCATCTATATTTAAAGTGCAACAAAAT 4740
Db 4681 GAAGTATTTGCGAGAAAGTGTCCAAACCTCACGCATCTATATTTAAAGTGCAACAAAAT 4740
QY 4741 AAAGACCTCAGCACATAGAGCCACTGAAACAGTGTAGAAAACCTCAAGAGCTTAGACCTT 4800
Db 4741 AAAGACCTCAGCACATAGAGCCACTGAAACAGTGTAGAAAACCTCAAGAGCTTAGACCTT 4800
QY 4801 TTCAATTTGCCAGGTAAACCACTACGAGTACGAGAAACAGTGTCAAGCTTCTCCCTG 4860
Db 4801 TTCAATTTGCCAGGTAAACCACTACGAGTACGAGAAACAGTGTCAAGCTTCTCCCTG 4860
QY 4861 CAACTCACATATCTCGACAGCTGTACTGGGACCAAGAGGCCCTTACTCAGATATTT 4920
Db 4861 CAACTCACATATCTCGACAGCTGTACTGGGACCAAGAGGCCCTTACTCAGATATTT 4920
QY 4921 GAGGACCACTGAGGGCCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGTAGAT 4980
Db 4921 GAGGACCACTGAGGGCCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGTAGAT 4980
QY 4981 GAAGATGCTCAGGTAGTGGAAAGTGAAGGGCGAGGAGGAGGAGGAGGAGGAGGAG 5040
Db 4981 GAAGATGCTCAGGTAGTGGAAAGTGAAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAG 5040
QY 5041 GAGGACGTGAGTGGAGGGACGAGGAGGTGAAGAGGTTTAAACGATGGAGAGGTAGAT 5100
Db 5041 GAGGACGTGAGTGGAGGGACGAGGAGGTGAAGAGGTTTAAACGATGGAGAGGTAGAT 5100
QY 5101 GGGGAGGAAGTGAAGAGAGCTTGTGTGAAGAAAGGGGTGAGAGGCGAAATGAGAA 5160
Db 5101 GGGGAGGAAGTGAAGAGAGCTTGTGTGAAGAAAGGGGTGAGAGGCGAAATGAGAA 5160
QY 5161 CCTCAGATCAGGAGAGATGATGACTAGTAGAATAACCTATTTTGAAGAAATTCCTAT 5220
Db 5161 CCTCAGATCAGGAGAGATGATGACTAGTAGAATAACCTATTTTGAAGAAATTCCTAT 5220
QY 5221 TGTGATTTGACTGTTTTTACCCATATCCCTCCCTCCCTCCCAATCCTGCCCTGAAACTT 5280
Db 5221 TGTGATTTGACTGTTTTTACCCATATCCCTCCCTCCCTCCCAATCCTGCCCTGAAACTT 5280
QY 5281 ACTTTTCTCGATTTGAACATTTCTGTTGGGAATGACACGGGAAAAGTGTACTGGGGTTG 5340
Db 5281 ACTTTTCTCGATTTGAACATTTCTGTTGGGAATGACACGGGAAAAGTGTACTGGGGTTG 5340
QY 5341 TGGAGGAGGAGGCGAGGAGGCGGTGGACTAAAATACTATTTTACTGCCAAATAAAAT 5400
Db 5341 TGGAGGAGGAGGCGAGGAGGCGGTGGACTAAAATACTATTTTACTGCCAAATAAAAT 5400
QY 5401 AATATTTGTAATTAATTAACCTGGGATAGTCTTTGTAGATGATTAATTAATTTCT 5460
Db 5401 AATATTTGTAATTAATTAACCTGGGATAGTCTTTGTAGATGATTAATTAATTTCT 5460
QY 5461 CTCTCTCTTTTTATTTTTTACACATTTCTTTTAAAGTATAGTCCCTTTAGTCCAAG 5520
Db 5461 CTCTCTCTTTTTATTTTTTACACATTTCTTTTAAAGTATAGTCCCTTTAGTCCAAG 5520
QY 5521 GAAAAGGCACTCAATCCACTTATTAATGCTTCTACTGTGTTCAAGTAAAATAAGCTCC 5580
Db 5521 GAAAAGGCACTCAATCCACTTATTAATGCTTCTACTGTGTTCAAGTAAAATAAGCTCC 5580
QY 5581 AGGATTTAAACAAAAGAGGAAAGAAAATTTTACAATGAAAATGTTGCTAAAAATTTAAA 5640
Db 5581 AGGATTTAAACAAAAGAGGAAAGAAAATTTTACAATGAAAATGTTGCTAAAAATTTAAA 5640
QY 5641 ACAAAATACAGTAAATGTATTGTTAAAGCAAAATTTCTATTTTAAAAATTTTAAATGAAG 5700

Db	5641	ACAAATTACAGTAAATGTATTTGTAAGCAAAATCTATTTTAAATTTATTAATAAGGA	5700
Qy	5701	AATAATTTGCTAAAGCAAAATTTTGGAAAAATAAATATGCACCTTTATACTTTGATTTTATT	5760
Db	5701	AATAATTTGCTAAAGCAAAATTTTGGAAAAATAAATATGCACCTTTATACTTTGATTTTATT	5760
Qy	5761	TATTAACAATGATTTATAAGCTT	5785
Db	5761	TATTAACAATGATTTATAAGCTT	5785

```

RESULT 2
US-60-172-373-13384
; Sequence 13384, Application US/60172373
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymor
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 13384
; LENGTH: 6753
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 419322.6
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 677-976, 1431-1454, 2474-2802, 5035, 5037, 5071
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-13384

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Query Match 78.9%; Score 4563.6; DB 61; Length 6753;
Best Local Similarity 86.0%; Pred. No. 0;
Matches 4688; Conservative 0; Mismatches 745; Indels 21; Gaps 5;

QY	1	AAGCTTTCTGATCTCTAAATCAAGCTCAGCTCCCTAAAGCTCTTGCTCCCGTACTGAAA	60
Db	1		
		AAGCTTTCTGATCTCTAAATCAAGCTCAGCTCCCTAAAGCTCTTGCTCCCGTACTGAAA	60
QY	61	CTTTTCTTATGTAACTCTCATAAACACATAGCATAAATGTTTGCAGTGTCTTCTTCCT	120
Db	61		
		CTTTTCTTATGTAACTCTCATAAACACATAGCATAAATGTTTGCAGTGTCTTCTTCCT	120
QY	121	ATCAGTTGCAAGTTCAGCAGAGCTCATATATTTTCATTTTCATTCGCTACTATAGCCCTA	180
Db	121		
		ATCAGTTGCAAGTTCAGCAGAGCTCATATATTTTCATTTTCATTCGCTACTATAGCCCTA	180
QY	181	GAGCCTGACATAGTTTCTGGCTGTGAATGCTCAATAAATATTTGTTAAATCAGTAGAAA	240
Db	181		
		GAGCCTGACATAGTTTCTGGCTGTGAATGCTCAATAAATATTTGTTAAATCAGTAGAAA	240
QY	241	CATAAAGTATCTATTTCAITGAAGGAAGAATAATTAGCTACATTTTCTTTTCTTGCC	300
Db	241		
		CATAAAGTATCTATTTCAITGAAGGAAGAATAATTAGCTACATTTTCTTTTCTTGCC	300
QY	301	TTAAATATTTGAGGAATTTGCTTATATGTCATATAATAAAAAGTTAAAGCCTTATACATAT	360
Db	301		
		TTAAATATTTGAGGAATTTGCTTATATGTCATATAATAAAAAGTTAAAGCCTTATACATAT	360
QY	361	ACTAAGGAATTTGGACATTTAAATTCAGCTAGCCTTTCTTATAACAAAATACTGAATTC	420
Db	361		
		ACTAAGGAATTTGGACATTTAAATTCAGCTAGCCTTTCTTATAACAAAATACTGAATTC	420
QY	421	TGTCCTTAATTTGTTTCCCTATTCTTTCCCATTTGAGATGACACCAAAATCCCTCTAG	480

Db	421	TGTCCTAAATTTGTTCTTCCCTATTCTTCCCATTTGAGATGACACCAAAATCCCTCTAG	480
Qy	481	CTGCTCAAAACCAAGTACCCGTATGTTATTCTTAAATATCTCTTAACTTGCTTCTCATAT	540
Db	481	CTGCTCAAAACCAAGTACCCGTATGTTATTCTTAAATATCTCTTAACTTGCTTCTCATAT	540
Qy	541	GCAATTTGTTAAACAAGTCATCTTCAGTCTGTATCCATATTCTCCCTTCCAGACCAACA	600
Db	541	GCAATTTGTTAAACAAGTCATCTTCAGTCTGTATCCATATTCTCCCTTCCAGACCAACA	600
Qy	601	ACATGTCCTTGACTATAGTCAATAGCCTCCCAACTCTTGTCCTACTTAAATATCATT	660
Db	601	ACATGTCCTTGACTATAGTCAATAGCCTCCCAACTCTTGTCCTACTTAAATATCATT	660
Qy	661	GTA AAAAATCAGTCTTGGCGGCGGCTGAGTGGCTCACACCTATAATCCAGCACATTGGGA	720
Db	661	GTA AAAAATCAGTCTTNN	720
Qy	721	GTCCAGCGGGGGGTCAACGAGTCAAGAGATGGAGACCATCATGGCCAACATGGTGAA	780
Db	721	NN	780
Qy	781	ACCCTGTCTACTATAAATACAAAAAATATCTGGGTGGTGGGCACATGCCTGTATAAT	840
Db	781	NN	840
Qy	841	CCCAACTACTAGGAGGCTGAGCAGGAGAAATCGCTTGAACCTGGGAGCGGAGGTTGCA	900
Db	841	NN	900
Qy	901	GTGAGCGGAGATCGCACCAATTGCACCTCCAGCCTGGCAACAGACGAGACTCCATCCCAA	960
Db	901	NN	960
Qy	961	ACAAAACAAAACCAACCATGTAAACATGCTGTAAACATGTGAGATGTCGTTGTCAG	1020
Db	961	NN	1020
Qy	1021	AAGTCTTACATGCTTTTTCATATGCTAAGATAAAACCAATGATTTCTTGTTCTTCT	1080
Db	1021	AAGTCTTACATGCTTTTTCATATGCTAAGATAAAACCAATGATTTCTTGTTCTTCT	1080
Qy	1081	AAAGCCAAAGAAAATAAGATGTTGTTTCAGCAACCTTGTTCTTCGCCCATGCTTTTCCCT	1140
Db	1081	AAAGCCAAAGAAAATAAGATGTTGTTTCAGCAACCTTGTTCTTCGCCCATGCTTTTCCCT	1140
Qy	1141	AGCTCACTCTTTTAGCAAGTCGACCTGATTTCTTCTGTTAGTCGTGTTCTGCGCTCG	1200
Db	1141	AGCTCACTCTTTTAGCAAGTCGACCTGATTTCTTCTGTTAGTCGTGTTCTGCGCTCG	1200
Qy	1201	TGGTCTGGCTTCTTCTGTTAGTCGTGTTCCACCTGCTGGCTGTTGGCTGCTTCA	1260
Db	1201	TGGTCTGGCTTCTTCTGTTAGTCGTGTTCCACCTGCTGGCTGTTGGCTGCTTCA	1260
Qy	1261	TTCTGCTGGAATGCTCTCCACTCCAGATCCCTTACTAGATCTTAGCTCAGTCATCACCT	1320
Db	1261	TTCTGCTGGAATGCTCTCCACTCCAGATCCCTTACTAGATCTTAGCTCAGTCATCACCT	1320
Qy	1321	CGCAGGAGATCTTCAACCATTCACCTGCATACACCTATAGCTGCTGCTCCCTAGAGACAT	1380
Db	1321	CGCAGGAGATCTTCAACCATTCACCTGCATACACCTATAGCTGCTGCTCCCTAGAGACAT	1380
Qy	1381	CATTCTGTTTCTTCTTCACTTCTCCTAGCACCTTACTGCTTCTGAAATATATCTACTTTGATGT	1440
Db	1381	CATTCTGTTTCTTCTTCACTTCTCCTAGCACCTTACTGCTTCTGAAATATATCTACTTTGATGT	1440
Qy	1441	TTATTCTTCTTCTTACTTCTTACTAGGATACCTGGGTCAATTAAGAGGAGGATATTCTCTC	1500
Db	1441	NN	1500
Qy	1501	TTATTCTTCTTCTTAAACCTTAATGCTTAGGCTGTAGAAGTTATACAATATTGAAGAATA	1560
Db	1501	TTATTCTTCTTCTTAAACCTTAATGCTTAGGCTGTAGAAGTTATACAATATTGAAGAATA	1560

Db 3721 CTCATTAATAAATGCTCAGAAAGTAAAAAATATTCCTCTCTAAATAACATAC 3780
QY 3781 ATGCCACTCAAAATTTTATCTCTACACATTCGCGTATCTAAACCTAGTTAGATACCTTG 3840
Db 3781 ATGCCACTCAAAATTTTATCTCTACACATTCGCGTATCTAAACCTAGTTAGATACCTTG 3840
QY 3841 GTTTTAGTATAATCTGACAGAACAGATACAAACCAAGATCACATTTGTGAGTCAGAAGTGG 3900
Db 3841 GTTTTAGTATAATCTGACAGAACAGATACAAACCAAGATCACATTTGTGAGTCAGAAGTGG 3900
QY 3901 AAAATTCATAATCATGATGATACCAATAAAAGATAGATTAGCTTTTACAGGATGTTT 3960
Db 3901 AAAATTCATAATCATGATGATACCAATAAAAGATAGATTAGCTTTTACAGGATGTTT 3960
QY 3961 TTGGCATTTTATCTTTCATTTGAGGGGAGATCTCACCAAAATATGCTTTTCATGGTTCA 4020
Db 3961 TTGGCATTTTATCTTTCATTTGAGGGGAGATCTCACCAAAATATGCTTTTCATGGTTCA 4020
QY 4021 TTGTGTTTATTTAAATTTCTGTGATGCATATCTCAGGTTTACTTTAAACCTAGTCTATAGAT 4080
Db 4021 TTGTGTTTATTTAAATTTCTGTGATGCATATCTCAGGTTTACTTTAAACCTAGTCTATAGAT 4080
QY 4081 TCAAGATATCCCGTGTCAGGTCTCTAAAAGTAAAAAGAAATGGGTACTTGTGAAGGC 4140
Db 4081 TCAAGATATCCCGTGTCAGGTCTCTAAAAGTAAAAAGAAATGGGTACTTGTGAAGGC 4140
QY 4141 TGATTCACAGTAAGTAGTGTAGAGGGAGTGCCTTGTGTATTCACAAATATCAACGTGA 4200
Db 4141 TGATTCACAGTAAGTAGTGTAGAGGGAGTGCCTTGTGTATTCACAAATATCAACGTGA 4200
QY 4201 GCATCAGATAAGATTTCTTTAGTCACACACACCTACTCTTCTACTAGGAGATCCATAT 4260
Db 4201 GCATCAGATAAGATTTCTTTAGTCACACACACCTACTCTTCTACTAGGAGATCCATAT 4260
QY 4261 ACTTGAATAATTTGTTCTGCTTGACCCAGGTTACTTATCAGTCCCTTTATTAATAATTTG 4320
Db 4261 ACTTGAATAATTTGTTCTGCTTGACCCAGGTTACTTATCAGTCCCTTTATTAATAATTTG 4320
QY 4321 TAAATATTTGGGCTCGAGACCGGAGCGAGCTGGTTGAGTCTTCAAAAGTCTTAAACGTG 4380
Db 4321 TAAATATTTGGGCTCGAGACCGGAGCGAGCTGGTTGAGTCTTCAAAAGTCTTAAACGTG 4380
QY 4381 CGGCGCTGGGTTCCGAGTTTATTCATTTGAATTCGGCTGGC - ACGAGAGCTCTGCGAGC 4438
Db 4381 CGGCGCTGGGTTCCGAGTTTATTCATTTGAATTCGGCTGGC - ACGAGAGCTCTGCGAGC 4438
QY 4439 AGAGAGCGCGAGATGGAGATGGCGAGCGGATTCATTCAGAGCTCGCGAACAGGCGCG 4498
Db 4441 AGAGAGCGCGAGATGGAGATGGCGAGCGGATTCATTCAGAGCTCGCGAACAGGAGCG 4500
QY 4499 CCTCTGATGTAAGAAGACTTCCCTCGACAAACAGTCCGGTGAATGAAGGCAAACTCGAAG 4558
Db 4501 CCTCTGATGTAAGAAGACTTTCCTCGACAAACAGTCCGGTGAATGAAGGCAAACTCGAAG 4560
QY 4559 CCCTCAGAGTGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACCGAGGCTCACCT 4618
Db 4561 CCCTCAGAGTGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACCGAGGCTCACCT 4620
QY 4619 CAATCTCAGACTTACCAAGTTA - - - AAGTTGAGAAAGCTTGAAC - - - - - AGAG 4666
Db 4621 CAATCGCAAACTTACCAAGTTAATAACAACTTAAGAAAGCTTGAAC - - - - - AGAG 4680
QY 4667 TCTCAGGGGGCTCGAGATGATTCGCAAGAAAGTCTCAAAACCTCAGCGATCTATATTTAA 4726
Db 4681 TCTCAGGGGGCTCGAGATGATTCGCAAGAAAGTCTCGCAAACTCAGCGATCTATATTTAA 4740
QY 4727 GTGCAACAAATTTAAAGACTCAGCAATAGAGCCACCTGAACAGTGTAGAAACCTCA 4786
Db 4741 GTGCAACAAATTTAAAGACTCAGCAATAGAGCCACCTGAACAGTGTAGAAACCTCA 4800
QY 4787 AGAGCTTAGACCTTTCAATTTGCGAGGTAAACCAACCTGAACAGTGTAGAGAAACCTGT 4846

Db 4801 AGAGCTTAGACCTTTTCAATTTGCGAGGTAAACCAACCTGAACGACTACCCAGAAATGTCT 4860
QY 4847 TCAAGCTTCTCTCGAACTCACAATATCTCGACAGCTGTTACTGGGGACCAACAAGAGGCC 4906
Db 4861 TCAAGCTTCTCTCGAACTCACAATATCTCGACAGCTTATGACCGGACGACAAGAGGCC 4920
QY 4907 CTTTACTCAGATATTGAGGACCACTGAGGCTGAGTACGAGGAGGAGGCTGAGCAGTG 4966
Db 4921 CTGACTCGGATGCTGAGGGCTAGCTGAGGGCTGATGATGAGGAGGA - GATGAGGATG 4979
QY 4967 AGGAGGAGTATGATGAAGATGCTCAGTAGTGAAGATGAGGAGGCGGAGGAGGAGG 5026
Db 4980 AGGAGGAGTATGATGAAGATGCTCAGTAGTGAAGACGAGGAGGACGAGGATGANGG 5039
QY 5027 AGGAGGCTGAAGAGGAGGAGCTGAGTGGAGGGACGAGGAGGATGAAGAAGGTTATAAG 5086
Db 5040 AGGAGGCTGAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGATGAAGAAGGTTATAAG 5099
QY 5087 ATGGAGAGGTAGATGCGGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTCA 5146
Db 5100 ATGGAGAGGTAGATGACGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTCA 5159
QY 5147 AGCGAAATTCAGAACCTGAAGATGAGGAGGAAGATGATGACTAACTAGATAACCTATT 5206
Db 5160 AGCGAAACGAGAACCTGAAGATGAGGAGGAAGATGATGACTAACTAGATAACCTATT 5219
QY 5207 TGAATAATTCCTATTGCTGATTTGACTGTTTACCCTATATCCCT - - - - - CCCCCCTCC 5260
Db 5220 TGAATAATTCCTATTGCTGATTTGACTGTTTACCCTATATCCCTCTCCCCCCCCCTCC 5279
QY 5261 AATCCTGCCCTTGAACCTACTTTTTCTGATGTTAACTTCTCTGCTGGGAATGAGACGG 5320
Db 5280 AATCCTGCCCTTGAACCTACTTTTTCTGATGTTAACTTCTCTGCTGGGAATGAGACGG 5339
QY 5321 GAAAGTGTACTGGGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5380
Db 5340 GAAAGTGTACTGGGGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5399
QY 5381 TTTTCTACTGCCAAATTAATAATTTTGAATAATTTTAACTGGGATACTAGCTTT 5434
Db 5400 TTTTCTACTGCCACTCTTATTTTTTTTCCCTACTTTTTTCTGTGTCGGGTTTT 5453

RESULT 3

US-09-976-594-207
; Sequence 207, Application US/09976594
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROI
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 207
; LENGTH: 3955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1041138.7
; NAME/KEY: unsure
; LOCATION: 2235, 2268
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-207

Query Match 42.2%; Score 2441.2; DB 36; Length 3955;
Best Local Similarity 95.9%; Pred. No. 6e-207;
Matches 2542; Conservative 0; Mismatches 90; Indels 18; Gaps 3;

QY	2803	TTGTAGAGTTTGATTTTGTGATGTCAGTGTGGTAGATGAATTTGTGGGAAGCAAAAACAAGAT	2862
Db	1	TTGTAGAGTTTGATTTTGTGATGTCAGTGTGGTAGATGAATTTGTGGGAAGCAAAAACAAGAT	60
QY	2863	AGAGTTCAATGACAGTGAAGTTTATTTGTATAGCTATATAAAGAAATGTTGAAGGT	2922
Db	61	AGAGTTCAATGACAGTGAAGTTTATTTGTATAGCTATATAAAGAAATGTTGAAGGT	120
QY	2923	TTGAAATCCATTTAGTGGCAGTAAAGGTTTACAGAACGAAACTATTTGAGAAAGTACACAAG	2982
Db	121	TTGAAATCCATTTAGTGGCAGTAAAGGTTTACAGAACGAAACTATTTGAGAAAGTACACAAG	180
QY	2983	GCAAGTCTTACTTTCAAGGCAGTTTATGTAAGCTCAATTCATTTGTCOAGTGTCTTGCT	3042
Db	181	GCAAGTCTTACTTTCAAGGCAGTTTATGTAAGCTCAATTCATTTGTCOAGTGTCTTGCT	240
QY	3043	ATGCTGGGTTATAGGATTTGGAACATATGATCAATCTGACACACATCAGTAAACTGAA	3102
Db	241	ATGCTGGGTTATAGGATTTGGAACATATGATCAATCTGACACACATCAGTAAACTGAA	300
QY	3103	TAGGATTTATAAATCCACAAGCATTTTACTAGTGAATCTGTGATATTTTCTAGCTACT	3162
Db	301	TAGGATTTATAAATCCACAAGCATTTTACTAGTGAATCTGTGATATTTTCTAGCTACT	360
QY	3163	CTTGCTGTGTTTATTTGAATCTTTTGCTCATATCCTATAGTAAAGATTTACAGGAAATATA	3222
Db	361	CTTGCTGTGTTTATTTGAATCTTTTGCTCATATCCTATAGTAAAGATTTACAGGAAATATA	420
QY	3223	TTTTTATTTGCTAGAAATTTAGCCCTTTTAGTCTTTTGAATCTATGCTCATATCTTAT	3282
Db	421	TTTTTATTTGCTAGAAATTTAGCCCTTTTAGTCTTTTGAATCTATGCTCATATCTTAT	480
QY	3283	AGTAAGAGTTTCAGGGAATGTATTTCTATTTGCTGGAATTTTAGCCCTTTTCAAGTCTTTTG	3342
Db	481	AGTAAGAGTTTCAGGGAATGTATTTCTATTTGCTGGAATTTTAGCCCTTTTCAAGTCTTTTG	540
QY	3343	AGCCCTCTTTTGTGTTATGGGACATAGTATGAGACAAAGATGAATGATCTATTCC	3402
Db	541	AGCCCTCTTTTGTGTTATGGGACATAGTATGAGACAAAGATGAATGATCTATTCC	600
QY	3403	AATTCACATGATGGGAAATGAAGCAAAAATGTTATTCACTCAAGGCTTCTGCCATGTT	3462
Db	601	AATTCACATGATGGGAAATGAAGCAAAAATGTTATTCACTCAAGGCTTCTGCCATGTT	660
QY	3463	TCCTGTGGAATTTAGGCTCAGACACAAATTTCCCTAAATGCTGTGCTCAACTTCTCAA	3522
Db	661	TCCTGTGGAATTTAGGCTCAGACACAAATTTCCCTAAATGCTGTGCTCAACTTCTCAA	720
QY	3523	TAGAACATATATTAATTTATCTTCTGAGTGTTTTCACAAATCCCATAGCCCTGT	3582
Db	721	TAGAACATATATTAATTTATCTTCTGAGTGTTTTCACAAATCCCATAGCCCTGT	780
QY	3583	GAAAAGATTTTATAGGAAATATTTATTTAATATAGCATATTTTGTCAATGTGGGACA	3642
Db	781	GAAAAGATTTTATAGGAAATATTTATTTAATATAGCATATTTTGTCAATGTGGGACA	840
QY	3643	TAGGACTAGTACTGCTGAAAACCATCTCATGATCCTTGTGTGAAGAACTAATTCACACTA	3702
Db	841	TAGGACTAGTACTGCTGAAAACCATCTCATGATCCTTGTGTGAAGAACTAATTCACACTA	900
QY	3703	GAAATACTATTTTCTTGCTCAATTAACATATAATGTCAGAAAGTAAATAATTC	3762
Db	901	GAAATACTATTTTCTTGCTCAATTAACATATAATGTCAGAAAGTAAATAATTC	960
QY	3763	CTCTCTAAATAACATACATGCTCAATTTTATTTTATCTTACCCTGCGGTATCTAA	3822
Db	961	CTCTCTAAATAACATACATGCTCAATTTTATTTTATCTTACCCTGCGGTATCTAA	1020
QY	3823	ACCTAGTTAGATACTTTTGTGTTTATGTTATTAATCTGACAGAACATACAAACGATCAC	3882
Db	1021	ACCTAGTTAGATACTTTTGTGTTTATGTTATTAATCTGACAGAACATACAAACGATCAC	1080
QY	3883	ATTGTGAGTCAGAAGTGGAAATTCATTAATTCATGATACCAATAAAGATAGATTTA	3942
Db	1081	ATTGTGAGTCAGAAGTGGAAATTCATTAATTCATGATACCAATAAAGATAGATTTA	1140
QY	3943	GCATTTTACAGGATGTTTGTGGCATTTTATCTTCTTTCATTTGAGGGAGATCTCACCAAAA	4002
Db	1141	GCATTTTACAGGATGTTTGTGGCATTTTATCTTCTTTCATTTGAGGGAGATCTCACCAAAA	1200
QY	4003	TATGTCCTTTCATGTTTCATTTGTTTAAATTTCTGTGATGATATCTCAGGTTTACT	4062
Db	1201	TATGTCCTTTCATGTTTCATTTGTTTAAATTTCTGTGATGATATCTCAGGTTTACT	1260
QY	4063	TAAACCTAGTCTATAGATTCAAAGATATCCCGTGTGAGTCTCTAAAAGTAAAGAAAAA	4122
Db	1261	TAAACCTAGTCTATAGATTCAAAGATATCCCGTGTGAGTCTCTAAAAGTAAAGAAAAA	1320
QY	4123	ATGGGTACTTTGTCAGGCTGATTCACAGTAAGTGTGTAGAGGGAGTGCCTTGTGTATT	4182
Db	1321	ATGGGTACTTTGTCAGGCTGATTCACAGTAAGTGTGTAGAGGGAGTGCCTTGTGTATT	1380
QY	4183	CACAAATTTATCAACGTGAGCATCAGATAAGATTTTCTTTAGTCACACACACCTTCTCT	4242
Db	1381	CACAAATTTATCAACGTGAGCATCAGATAAGATTTTCTTTAGTCACACACACCTTCTCT	1440
QY	4243	TACTAGAGATCCATATACTTGAATTTGTTCTGCTTGACCCAGGTTTACTTATCAGTC	4302
Db	1441	TACTAGAGATCCATATACTTGAATTTGTTCTGCTTGACCCAGGTTTACTTATCAGTC	1500
QY	4303	CCATTTATTAATTTGTAATATTGGGCTCGAAGCCGAGCGGAGCTGGTGTGAGTCT	4362
Db	1501	CCATTTATTAATTTGTAATATTGGGCTCGAAGCCGAGCGGAGCTGGTGTGAGTCT	1560
QY	4363	TCAAAGTCTTAAACGTGCGGCTGAGGTTTCGAGGTTTATTTGAATGAATTCGGCTGGCAC	4422
Db	1561	TCAAAGTCTTAAACGTGCGGCTGAGGTTTCGAGGTTTATTTGAATGAATTCGGCTGGCAC	1620
QY	4423	GAGAGCTCTGACAGACAGAGCGGAGATGGAGATGGGACAGCGGATTCATTCAGAG	4482
Db	1621	GAGAGCTCTGACAGAGAGCGGAGATGGAGATGGGACAGCGGATTCATTTAGAG	1680
QY	4483	CTCGGAACAGGGCGGCTCTGATGTGAAAGAACTTGCCTTGACACACAGTCCGTCGAAT	4542
Db	1681	CTCGGAACAGAGCGGCTCTGATGTGAAAGAACTTGCCTTGACACACAGTCCGTCGAAT	1740
QY	4543	GAAGGCAAACTCGAAGCCCTCAGATGATTTGAGAACTGGAATCTTTAAGTAAATC	4602
Db	1741	GAAGGCAAACTCGAAGCCCTCAGATGATTTGAGAACTGGAATCTTTAAGTAAATC	1800
QY	4603	AACGAGGCTCACCTCAATCTCAGACTTACCAAGTTA---AAGTTGAGAAAGCTTGAA	4659
Db	1801	AACGAGGCTCACCTCAATCTCAGACTTACCAAGTTA---AAGTTGAGAAAGCTTGAA	1860
QY	4660	CTA-----AGAGTCTCAGGGGCTGGAAGTATTTGGCAGAAAAGTGTCCAAACCTC	4710
Db	1861	CTAAGCCATAACAGAGTCTCAGGGGCTGGAAGTATTTGGCAGAAAAGTGTCCGAACTC	1920
QY	4711	ACGATCTATTTAAGTGGCAACAAAATTTAAGACCTCAGCACAATAGAGCCACTGAAA	4770
Db	1921	ACGATCTATAATTTAAGTGGCAACAAAATTTAAGACCTCAGCACAATAGAGCCACTGAAA	1980
QY	4771	CAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTTGGAGGTAACCAACCTGAAAGC	4830
Db	1981	AGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTTGGAGGTAACCAACCTGAAAGC	2040
QY	4831	TACGGAGAAAACCTGTTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTTACTTGG	4890
Db	2041	TACGGAGAAAATGTTTCAAGCTTCTCTGCAACTCACATATCTCGACAGCTTACTTGG	2100
QY	4891	GACCAAGAGGCCCCCTTACTCAGATATTTAGAGACACCGTGGAGGCCCTTGGATGACGAG	4950
Db	2101	GACCAAGAGGCCCCCTTACTCAGATATTTAGAGACACCGTGGAGGCCCTTGGATGACGAG	2160
QY	4951	GAGGAGGCTGAGCATGAGGAGGATGATGAAGATGCTCAGCTAGTGGAGATGAGGAG	5010
Db	5011	GAGGAGGCTGAGCATGAGGAGGATGATGAAGATGCTCAGCTAGTGGAGATGAGGAG	5070

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Db 2161 GAGGAGGATGAGGAGGAGTATGATCAAGATGCTCAGGTAGTGGAGACGAGGAG 2220
QY 5011 GCCGAGGAGGAGGAGGAGGTGAAGAGGAGGACGTGAGTGGAGGGACGAGGAGGAT 5070
Db 2221 GACGAGGATGAGGANGAGGAGGTGAAGAGGAGGACGTGAGTGGAGANGAGGAGGAT 2280
QY 5071 GAAGAAGGTTTAAACGATGGAGGAGGTAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAA 5130
Db 2281 GAAGAAGGTTTAAACGATGGAGGAGGTAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAA 2340
QY 5131 GAAGAAGGGGTGAGAACGGAATGAGAACCTGAAGATGAGGAGGAGGAGATGACTAA 5190
Db 2341 GAAGAAGGGGTGAGAACGGAATGAGAACCTGAAGATGAGGAGGAGGAGATGACTAA 2400
QY 5191 GTAGATAACCTATTGTAAGAAATTCCTATTGTGATTGATGCTGTTTACCCTATATCCCC 5250
Db 2401 GTGGAATPAACCTATTGTAAGAAATTCCTATTGTGATTGATGCTGTTTACCCTATATCCCC 2460
QY 5251 T-----CCCCCCTCCAATCCTGCCCCCTGAAACCTTACTTTTTCTGATTGTAACATTCG 5304
Db 2461 TCTCCCCCCCCCTCCAATCCTGCCCCCTGAAACCTTACTTTTTCTGATTGTAACATTCG 2520
QY 5305 TGTGGGAATGAGACGGGAAAAGTGTACTGGGGGTTGTGGAGGGAGGAGGCGAGGCGG 5364
Db 2521 TGTGGGAACGAGAGGGGAAAGTGTACTGGGGGTTGTGGAGGGAGGAGGCGAGGCGG 2580
QY 5365 GTGACTAAAAATACTATTTTTACTGCCAAATAAAAAATAATTTGTAATATTAACTGGGA 5424
Db 2581 GTGGAATAAAATACTATTTTTACTGCCACTTTATTTTTTCCCTACTCTTTCTTTCTTGT 2640
QY 5425 TACTAGCTTT 5434
Db 2641 GTCCGGTTTT 2650
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RESULT 4

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US-60-240-409-207
; Sequence 207, Application US/60240409
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny L.
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 P
; CURRENT FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 207
; LENGTH: 3955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 1041138.7
; NAME/KEY: unsure
; LOCATION: 2235, 2268
; OTHER INFORMATION: a, t, c, g, or other
US-60-240-409-207
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Query Match 42.2%; Score 2441.2; DB 68; Length 3955;
Best Local Similarity 95.9%; Pred. No. 6e-207;
Matches 2542; Conservative 0; Mismatches 90; Indels 18; Gaps 3;

QY 2803 TGTAGAAGTTTGATTTTGATGTCAGTGTGGTAGATCAATTTGTGGGAAGCAAAACAAGAT 2862
Db 1 TGTAGAAGTTTGATTTTGATGTCAGTGTGGTAGATCAATTTGTGGGAAGCAAAACAAGAT 60
QY 2863 AGAGTTCAATGACAGTGAAAAGTTTATTGCTATAAGCTATATAAAGAAAATGTTGAAGGT 2922
Db 61 AGAGTTCAATGACAGTGAAAAGTTTATTGCTATAAGCTATATAAAGAAAATGTTGAAGGT 120
QY 2923 TTGAATCCATTAAGTGGCAGTAAAGGTGTACAGCAAGCAACATTTTGAGAAGTACACAAG 2982
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Db 121 TTGAATCCATTAGTGGCAGTAAAGGTGTACAGACGAACACTATTTTGAGAAGTACACAAG 180
QY 2983 GCAAGTCTTACTTTCAAGGCAGTTTATGTAAAGCTCATTTCAATTTGCTCAGTGTCTTCTTGT 3042
Db 181 GCAAGTCTTACTTTCAAGGCAGTTTATGTAAAGCTCATTTCAATTTGCTCAGTGTCTTCTTGT 240
QY 3043 ATGTGTGGGTTATAGGATTTGGAACATATGATCAATCTGAGCACACATCAGTAAACTGAA 3102
Db 241 ATGTGTGGGTTATAGGATTTGGAACATATGATCAATCTGAGCACACATCAGTAAACTGAA 300
QY 3103 TAGGATTTATTAATCCACAAGCATTTTACTAGTGAATCTGTGATATTTTCTAGCTACT 3162
Db 301 TAGGATTTATTAATCCACAAGCATTTTACTAGTGAATCTGTGATATTTTCTAGCTACT 360
QY 3163 CTTGCTTGTGTTTATTGGAATCTTTTGCCTCATATCCTATAGTAAAGATTTTCAGAAATATA 3222
Db 361 CTTGCTTGTGTTTATTGGAATCTTTTGCCTCATATCCTATAGTAAAGATTTTCAGAAATATA 420
QY 3223 TTTTATTTTGCCTAGAAATTTTACGCTTTTGTAGTGTGTTTGTGAACTATTTGCTCATATTTCT 3282
Db 421 TTTTATTTTGCCTAGAAATTTTACGCTTTTGTAGTGTGTTTGTGAACTATTTGCTCATATTTCT 480
QY 3283 AGTAAGAGTTTCAGGGAATGTATTTCTATTTCTGTGGAATTTTACGCTTTTCAGGTTTGTG 3342
Db 481 ACTAAGAGTTTCAGGGAATGTATTTCTATTTCTGTGGAATTTTACGCTTTTCAGGTTTGTG 540
QY 3343 AGCCCTCTTTTGTCTTATGGGACATAGTATGAGACAAGATGAAATGATCTTCTATTTCCC 3402
Db 541 AGCCCTCTTTTGTCTTATGGGACATAGTATGAGACAAGATGAAATGATCTTCTATTTCCC 600
QY 3403 AATTCACATGATGGGAAAATGAAGCAAAAATGTTTATTCACCAAGGCTTCTGCCATGTT 3462
Db 601 AATTCACATGATGGGAAAATGAAGCAAAAATGTTTATTCACCAAGGCTTCTGCCATGTT 660
QY 3463 TCCTGTGGAATTCAGGCTCAGACACAAAATTTCTTAATAGCCTGTCTCTAACTTCTCAA 3522
Db 661 TCCTGTGGAATTCAGGCTCAGACACAAAATTTCTTAATAGCCTGTCTCTAACTTCTCAA 720
QY 3523 TAGACACATATATTAATTTATCTTCTCCTGAGTGTGTTTCCACAAATCCCATAGCCGT 3582
Db 721 TAGACACATATATTAATTTATCTTCTCCTGAGTGTGTTTCCACAAATCCCATAGCCGT 780
QY 3583 GAAAAGATTGTTTATAGGAAAATATATTTTAAATATAGCATATTTTGTCAATGTGGGACA 3642
Db 781 GAAAAGATTGTTTATAGGAAAATATATTTTAAATATAGCATATTTTGTCAATGTGGGACA 840
QY 3643 TAGGACTAGTACCTGCTGAAACCATCTCATGATCCTTGTGTAAGAACTAATTCACACTA 3702
Db 841 TAGGACTAGTACCTGCTGAAACCATCTCATGATCCTTGTGTAAGAACTAATTCACACTA 900
QY 3703 GAAATACTATTTTCCCTGCTCATTAATAAACATAAATGTCTCAGAAAGTAAATAATTATTC 3762
Db 901 GAAATACTATTTTCCCTGCTCATTAATAAACATAAATGTCTCAGAAAGTAAATAATTATTC 960
QY 3763 CTCCTAAATAAACATACATGCCACTCAAATTTTATTTCTCTACCACTTGGCGTATCTAA 3822
Db 961 CTCCTAAATAAACATACATGCCACTCAAATTTTATTTCTCTACCACTTGGCGTATCTAA 1020
QY 3823 ACCTAGTTAGATACHTTGGTTTTTAGGTATAATCTGACAGAACAGATACAAACAGATCAC 3882
Db 1021 ACCTAGTTAGATACHTTGGTTTTTAGGTATAATCTGACAGAACAGATACAAACAGATCAC 1080
QY 3883 ATGTGAGTCAAGAGTGGAAAATTCATAATTCATGATGATACCAATAAAGATAGATTTA 3942
Db 1081 ATGTGAGTCAAGAGTGGAAAATTCATAATTCATGATGATACCAATAAAGATAGATTTA 1140
QY 3943 GCTTTTACAGGATGTTTTTGGCAATTTTATTTCTTTTCATTTTGGGGGAGATCTCACCAAAA 4002
Db 1141 GCTTTTACAGGATGTTTTTGGCAATTTTATTTCTTTTCAATTTGAGGGGAGATCTCACCAAAA 1200
QY 4003 TATGCTTTTCAATGTTTCAATGTTTATTTAAATTTCTGTGATGATATTTCTCAGGTTACTT 4062
Db 1201 TATGCTTTTCAATGTTTCAATGTTTATTTAAATTTCTGTGATGATATTTCTCAGGTTACTT 1260
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Qy 4063 TAAACCTAGTCTATAGATTCAAAGATATCCCGTGTCCAGTCTCTAAAGAGTAAAAAGAAAA 4122
Db 1261 TAAACCTAGTCTATAGATTCAAAGATATCCCGTGTCCAGTCTCTAAAGAGTAAAAAGAAAA 1320
Qy 4123 ATGGGTACTTGTGAAGGCTGATTACAGTAAGTAGTGTAGAGGGAGTGCCTTGTGTATT 4182
Db 1321 ATGGGTACTTGTGAAGGCTGATTACAGTAAGTAGTGTAGAGGGAGTGCCTTGTGTATT 1380
Qy 4183 CACAAATTATCAACGTGAGCATCAGATAAGATTTCCTTTAGTCACACACACTACCTTCT 4242
Db 1381 CACAAATTATCAACGTGAGCATCAGATAAGATTTCCTTTAGTCACACACACTACCTTCT 1440
Qy 4243 TACTAGGAAGATCCATATACATTGAATAATGTCTCTGTGACCCAGAGTACTTATCAGTC 4302
Db 1441 TACTAGGAAGATCCATATACATTGAATAATGTCTCTGTGACCCAGAGTACTTATCAGTC 1500
Qy 4303 CCTTTATTATAATTTGTAAATATTGGGGCTCGAGAACCCAGCGGAGCTGGTTGAGTCT 4362
Db 1501 CCTTTATTATAATTTGTAAATATTGGGGCTCGAGAACCCAGCGGAGCTGGTTGAGCCT 1560
Qy 4363 TCAAAGTCTTAAACGTGCGGCCGTGGTTCGAGGTTTATTGATGAATTCGGCTGGCAC 4422
Db 1561 TCAAAGTCTTAAACGTGCGGCCGTGGTTCGAGGTTTATTGATGAATTCGGCGGGCGC 1620
Qy 4423 GAGAGCCTCTGACAGACAGAGCGCGAGAGATGGAGATGGCGACAGCGGATTCATTCAGAG 4482
Db 1621 GCGAGCCTCTGACAGAGAGAGCGCGAGAGATGGAGATGGCGACAGCGGATTCATTCAGAG 1680
Qy 4483 CTGCGGAACAGGGCGCCTCTCTGATGTGAAGAACCTTGGCCCTGGGACACAGTCGGTCGAAT 4542
Db 1681 CTGCGGAACAGGGCGCCTCTCTGATGTGAAGAACCTTGGCCCTGGGACACAGTCGGTCGAAT 1740
Qy 4543 GAAGGCARACTCGAAGCCTCAGACGATGAATTTGAAGAACTGGAATCTTAAAGTAAATC 4602
Db 1741 GAAGGCARACTCGAAGCCTCAGACGATGAATTTGAAGAACTGGAATCTTAAAGTAAATC 1800
Qy 4603 AACGGAGGCTCACCTCAATCTCAGACTTTACCAAAAGTTA ---AAGTTGAGAAAGCTTGAA 4659
Db 1801 AAGCTAGGCTCACCTCAATCTCAGACTTTACCAAAAGTTAAGAAAGCTTGAA 1860
Qy 4660 CTA-----AGAGTCTCAGGGGCGCTGGAAGTATTGGCGAGAAAGTGTCCAAACCTC 4710
Db 1861 CTAAGCGATAACAGAGTCTCAGGGGCGCTGGAAGTATTGGCGAGAAAGTGTCCGAACCTC 1920
Qy 4711 ACGCATCTATATTAAAGTGTGCAACAAATTAAGACCTCAGCACAAATAGAGCCTGAAA 4770
Db 1921 ACGCATCTATATTAAAGTGTGCAACAAATTAAGACCTCAGCACAAATAGAGCCTGAAA 1980
Qy 4771 CAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACCAACCTGAACGAC 4830
Db 1981 AAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACCAACCTGAACGAC 2040
Qy 4831 TAGCGAGAAAACGTTTCAAGCTTCTCCTGCAACTCACAATATCTCGACAGCTGTTACTTGG 4890
Db 2041 TACCGAGAAAATGTGTCAAGCTTCTCCTGCAACTCACAATATCTCGACAGCTGTTACTTGG 2100
Qy 4891 GACCACAAGGAGGCCCTTACTCAGATATTGAGGACCACTGGAGGGCCTGGATGACGAG 4950
Db 2101 GACGACAAGGAGGCCCTGACTCGGATGCTGAGGCTAGCTGGAGGGCTGGATGATGAG 2160
Qy 4951 GAGGAGGGTGAAGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAG 5010
Db 2161 GAGGAGGATGAGGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGAG 2220
Qy 5011 GCGGAGGAGGAGGAGGAGGAGTGAAGAGGAGGAGTGAAGGGGACGAGGAGGAT 5070
Db 2221 GAGGAGGATGAGGAGGAGGAGGAGTGAAGAGGAGGAGGAGTGAAGGGGACGAGGAGGAT 2280
Qy 5071 GAAGAAGGTTTAAACGATGAGAGGTTAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAA 5130
Db 2281 GAAGAAGGTTTAAACGATGAGAGGTTAGATGAGGAGGAAGATGAAGAAGAGCTTGGTGAA 2340
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Qy 5131 GAAGAAGGGGTCAGAACGCGAANAATGAGAACCTGAAAGATGAGGGAGAGATGATGACTAA 5190
Db 2341 GAAGAAAGGGGTCAGAACGCGAANAATGAGAACCTGAAAGATGAGGGAGAGATGATGACTAA 2400
Qy 5191 GTAGAATAACCTATTGTAANAATTCCTATTGTTGACTGTTTACCCATATCCCC 5250
Db 2401 GTGAATAAACCTATTGTAANAATTCCTATTGTTGACTGTTTACCCATATCCCC 2460
Qy 5251 T-----CCCCCTCCAATCCTGCCCTGAAACTTTACTTTTTCTGATTGTAACATTCG 5304
Db 2461 TCTCCCCCCCCCTCCATCTCCTCCCTGAACTTATTTTTCTGATTGTAACATTCG 2520
Qy 5305 TGTGGGAATGAGACGCGGAAAAGTGTACTGCGGGGTTGTGAGGAGGAGGAGGAGGAGG 5364
Db 2521 TGTGGGAACGAGAGGGAAGAGTGTACTGCGGGGTTGCGGGGAGGAGGAGGAGGAGG 2580
Qy 5365 GTGACTAAATACTATTCTACTGCAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5424
Db 2581 GTGGAATAAATACTATTCTACTGCCACTCTTATTTTTTCCCTACTTTTTTCTTTGT 2640
Qy 5425 TACTAGCTTT 5434
Db 2641 GTCGGGTTTT 2650

RESULT 5
US-09-760-469-94
; Sequence 94, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ54
; CURRENT APPLICATION NUMBER: US/09/760,469
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 94
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-760-469-94

Query Match 16.08; Score 925.6; DB 30; Length 1197;
Best Local Similarity 91.7%; Pred. No. 3.5e-73;
Matches 1018; Conservative 0; Mismatches 74; Indels 18; Gaps 3;
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Db 393 GGCCTGGAAGTATTGGCAGAAAAAGTCCGAAACCTCAGCATCTAAATTTAAAGTGGCAAC 452
QY 4735 AAAATTAAGACCTTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAAACCTCAAGAGCTTA 4794
Db 453 AAAATTAAGACCTTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAAACCTCAAGAGCTTA 512
QY 4795 GACCTTTTCAATTCGAGGTAAACAACTGAACGACTACGAGAAAAACGTTTCAAGCTT 4854
Db 513 GACCTTTTCAATTCGAGGTAAACAACTGAACGACTACGAGAAAAACGTTTCAAGCTC 572
QY 4855 CTCCTGCAACTACATATCTCGACAGCTGTACTTGGACCAACAAGGAGGCCCTTACTCA 4914
Db 573 CTCCTGCAACTACATATCTCGACAGCTGTACTTGGACCAACAAGGAGGCCCTTACTCG 632
QY 4915 GATATTGAGGACCGTGGAGGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAG 4974
Db 633 GATCTGAGGCTACGTGGAGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 692
QY 4975 TATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 5034
Db 693 TATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 752
QY 5035 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5094
Db 753 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 812
QY 5095 GTAGATGCGAGGAAGATCAAGAACAGCTTGGTGAAGAAAGAGGGGTCAAGAGCGAAAA 5154
Db 813 GTAGATGCGAGGAAGATCAAGAACAGCTTGGTGAAGAAAGAGGGGTCAAGAGCGAAAA 872
QY 5155 TGAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5214
Db 873 CGAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 932
QY 5215 TCCTATTGATGATGCTGTTTACCCATATCCCTTACCCCTTACCCCTTACCCCTTACCCCT 5268
Db 933 TCCTATTGATGATGCTGTTTACCCATATCCCTTACCCCTTACCCCTTACCCCTTACCCCT 992
QY 5269 CCCCTGAACTTACTTTTCTGATTAACATTCGTTGCGGATGAGAGCGGAGGAGGAGGAG 5328
Db 993 CCCCTGAACTTACTTTTCTGATTAACATTCGTTGCGGATGAGAGCGGAGGAGGAGGAG 1052
QY 5329 TACTGGGGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5388
Db 1053 TACTGGGGTGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1112
QY 5389 GCCAAATAAATAATTTCTTAATATA 5418
Db 1113 GCCAAATAAATAATTTCTTAATATA 1142

RESULT 6

US-10-216-583-94

; Sequence 94, Application US/10216583
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT254CIN
; CURRENT APPLICATION NUMBER: US/10/216,583
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/760,469
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963

; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1983
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 1197
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-583-94

Query Match 16.0%; Score 925.6; DB 42; Length 1197;
Best Local Similarity 91.7%; Pred. No. 3.5e-73;

Matches 1018; Conservative 0; Mismatches 74; Indels 18; Gaps 3;

QY 4327 TTGGGGCTCGAGAACGCGAGCGAGCTGTGAGTCTTCAAAGTCTCTAAACGCTGGCGCG 4386
Db 33 TGGGGCTCGAGAACGCGAGCGAGCTGTGAGCTTCAAAGTCTCTAAACGCGCGCG 92
QY 4387 TGGGTTCGAGGTTTATTGATTGAATTCGGCTCGCAGGAGGCTCTGCAGACAGAGCG 4446
Db 93 TGGGTTCGAGGTTTATTGATTGAATTCGGCTCGCAGGAGGCTCTGCAGACAGAGCG 152
QY 4447 CGAGAGATCGAGATGGCAGACGGATTTCAGAGCTCGCGAACAGGCGCCCTCTGAT 4506
Db 153 CGAGAGATCGAGATGGCAGACGGATTTCATTTAGAGCTCGCGAACAGGAGCCCTCTGAT 212
QY 4507 GTGAAAGAACTTCCCTGGCAACAGCTCGGTGCGAATGAAGGCAAACTCGAAGCCCTCACA 4566
Db 213 GTGAAAGAACTTCCCTGGCAACAGCTCGGTGCGAATGAAGGCAAACTCGAAGCCCTCACA 272
QY 4567 GATGAATTTGAAGAACTCGAATTTCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCA 4626
Db 273 GATGAATTTGAAGAACTCGAATTTCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCA 332
QY 4627 GACTTACCAAAAGTTAAAGT---TGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 4674
Db 333 AACTTACCAAAAGTTAAACAACTTAAGAAGCTTGAACCTAAGCGATAACAGAGTCTCAGGG 392
QY 4675 GGCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAAC 4734
Db 393 GGCCTGGAAGTATTGGCAGAAAGTGTCCGAACCTCAGCATCTAAATTTAAGTGGCAAC 452
QY 4735 AAAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTA 4794
Db 453 AAAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTA 512
QY 4795 GACCTTTTCAATTCGAGGTAACCAACCTGAACGACTACGGAGAAAAAGCTGTTCAGCTT 4854
Db 513 GACCTTTTCAATTCGAGGTAACCAACCTGAACGACTACGGAGAAAAAGCTGTTCAGCTC 572
QY 4855 CTCCTGCAACTACATATCTCGACAGCTGTACTTGGACCAACAAGGAGGCCCTTACTCA 4914
Db 573 CTCCTGCAACTACATATCTCGACAGCTGTACTTGGACCAACAAGGAGGCCCTTACTCG 632
QY 4915 GATATTGAGGACCGTGGAGGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAG 4974
Db 633 GATCTGAGGCTACGTGGAGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 692
QY 4975 TATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 5034
Db 693 TATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 752
QY 5035 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5094
Db 753 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 812
QY 5095 GTAGATGCGAGGAAGATCAAGAACAGCTTGGTGAAGAAAGAGGGGTCAAGAGCGAAAA 5154

Db	813	GTAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAAGAAGCCGAAAA	872
QY	5155	TGAGAACCTTGAAGATGAGGAGGAAGCATGATGACTAAGTGTAGAAATAACCTATATTTTGAAGAAAT	5214
Db	873	CGAAGAACCTTGAAGATGAGGAGGAAGATGATGACTAAGTGTGAATPACCTATATTTTGAAGAAAT	932
QY	5215	TCCTATGTGTGATTTGACTGTGTTTTTACCATATTCOCCT-----CCCCCTCCCAATCCTGC	5268
Db	933	TCCTATGTGTGATTTGACTGTGTTTTTACCATATTCOCCTCTCCCCCCCCCTCCAATCCTGC	992
QY	5269	CCCTCGAAACTTACTTTTTTCTGTATGTAAACATTCCTGTGGATGAGACGGGAAAGATG	5328
Db	993	CCCTCGAAACTTATTTTTTCTGTATGTAAAGTTGCTGTGGAAACGAGAGGGGAAGATG	1052
QY	5329	TACTGGGGGTGTGGAGGGAGGAGGAGGAGGCGGTGGACTAAATACTATTTTTTACT	5388
Db	1053	TACTGGGGGTTCGGGGGGAGGGATGCGGGTGGGGTGGGAATAATACTATTTTTTACT	1112
QY	5389	GCCAAATAAAATAATATTTGTAATATTTAA 5418	
Db	1113	GCCAAAAAATAAAAAAAAAAAAAAAAAAAAA 1142	
RESULT 7			
US-09-644-871-8887			
; Sequence 8887, Application US/09644871			
; GENERAL INFORMATION:			
; APPLICANT: Holtzman, Douglas A.			
; APPLICANT: Pan, Yang			
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES			
; TITLE OF INVENTION: THEREFOR			
; FILE REFERENCE: 1600.1167-001			
; CURRENT APPLICATION NUMBER: US/09/644,871			
; CURRENT FILING DATE: 2000-08-28			
; PRIOR APPLICATION NUMBER: 60/151,059			
; PRIOR FILING DATE: 1999-08-27			
; NUMBER OF SEQ ID NOS: 9739			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 8887			
; LENGTH: 1595			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc_feature			
; LOCATION: (1)...(1595)			
; OTHER INFORMATION: n = A,T,C or G			
US-09-644-871-8887			
Query Match 15.9%; Score 917.6; DB 25; Length 1595;			
Best Local Similarity 90.5%; Pred. No. 1.7e-72;			
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps			
QY	4327	TTGGGGCTCGAAGAACCGAGCGGAGCTGTGTGAGTCTTCAAAGTCTCTAAACGTCCTAAACGTCGGCGC	4386
Db	196	TGGGGGCTCGAAGAACCGAGCGGAGCTGTGTGAGCTTCAAAGTCTCTAAACGTCGGCGC	255
QY	4387	TGGGTTTCGAGGTTTTATTGATTTCGGCTGGCACGAGAGCCTCTGCAGACAGAGAGCG	4446
Db	256	TGGGTTTCGAGGTTTTATTGATTTCGGCTGGCACGAGAGCCTCTGCAGACAGAGAGCG	315
QY	4447	CGAGAGATGAGATGGGCAGACGGATTCAATTCAGAGCTGCGGAACAGGCGCCCTCTGTAT	4506
Db	316	CGAGAGATGAGATGGGCAGACGGATTCAATTTAGAGCTGCGGAACAGGCGCCCTCTGTAT	375
QY	4507	GTGAAGAACTTCCTCGCTGGACAACTGCTCGTTCGAATGAAGGCAAACTCGAAGCCCTACA	4566
Db	376	GTGAAGAACTTCTCTCGGCACACAGTCGTCGAATGAAGGCAAACTCGAAGCCCTACA	435
QY	4567	GATGAATTTCAAGAACTGGGAATTTCTTAAGTAAATAACCGAGGCGCTCACCTCAATCTCA	4626
Db	436	GATGAATTTCAAGAACTGGGAATTTCTTAAGTAAATAACCGTAGGCTCACCTCAATCGCA	495

Qy	4627	GACTTACCAAGTTA---AAGTTGAGAAAGCTTGAAC	T-----AGAGTCTCAGGG	4674
Db	496	AACTTACCAAGTTAAACAACCTTAAGAAAGCTTGAAC	TGACGATAACAGAGTCTCAGGG	555
Qy	4675	GGCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTC	ACGCATCTATATTAAAGTGGCAAC	4734
Db	556	GGCCTGGAAGTATTGGCAGAAAAGTGTCCGAACCTC	ACGCATCTAAATTAAAGTGGCAAC	615
Qy	4735	AAATTTAAAGACCTCAGCAATAGAGGCACCTGAAC	ACAGTGTAGAAAACCTCAAGAGCTTA	4794
Db	616	AAATTTAAAGACCTCAGCAATAGAGGCACCTGAAC	ACAGTGTAGAAAACCTCAAGAGCTTA	675
Qy	4795	GACCTTTTCAATTCGAGGTAAACCAACCTGAAAC	AGCTACGGAGAAAACCTGTTCACAGCTT	4854
Db	676	GACCTTTTCAATTCGAGGTAAACCAACCTGAAAC	AGCTACCGAGAAAATGTGTCAAGCTC	735
Qy	4855	CTCCTGCAACTCACATATCTCGACAGCTCTTACT	CGGACCAACAGGAGGCCCTTACTCA	4914
Db	736	CTCCCGCAACTCACATATCTCGACGCTATGAC	CGGACACAGGAGGCCCTGTACTCG	795
Qy	4915	GATATTCAGGACCACTGGAGGCGCTTGGATGAC	GAGGAGGCGTGAAGAGGAG	4974
Db	796	GATGCTCAGGGCTACCTGGAGGCGCTTGGATGAT	GAGGAGGAGGATGAGGATGAGGAGGAG	855
Qy	4975	TATGATCAAGATCCTCAGGTAGTGGNAGATGAG	GAGGCGGAGGAGGAGGAGGAGG	5034
Db	856	TATGATCAAGATCCTCAGGTAGTGGNAGACGAG	GAGGAGGAGGAGGAGGAGGAGG	915
Qy	5035	GAAGAGGAGCACGTGAGTGAGGGGACGAGGAG	GATGAAGAAGGTTATTAACGATGAGAG	5094
Db	916	GAAGAGGAGCACGTGAGTGAGGAGGAGGAGGAT	GAGAAGGTTATTAACGATGAGAG	975
Qy	5095	GTAGATGGCAGGAAGATGAAGAAGAGCTTGTG	TGAAGAAGAGGGGTTCAGAACCGAAAA	5154
Db	976	GTAGATCAGCAGGAAGATGAAGAAGAGCTTGTG	TGAAGAAGAGGGGTTCAGAACCGAAAA	1035
Qy	5155	TGAGAACCTCAAGATGAGGAGAGAGATGATGACT	AAGTAGATAACCTATTTTGGAAAAAT	5214
Db	1036	CGAGAACCTCAAGATGAGGAGAGAGATGATGACT	AAGTAGATAACCTATTTTGGAAAAAT	1095
Qy	5215	TCCCTATTGTGATTGACTGTGTATACCCCATAT	CCCCCTCCCAATCCCTGC	5268
Db	1096	TCCCTATTGTGATTGACTGTGTATACCCCATAT	CCCCCTCCCAATCCCTGC	1155
Qy	5269	CCCTTGAAACTTACTTTTTTCTGATTGTAACAT	TGCTGTGGGAATGACACGGGAAGAGTG	5328
Db	1156	CCCTTGAAACTTACTTTTTTCTGATTGTAACCT	GTGCTGTGGGAATGACAGGGGGAAGAGTG	1215
Qy	5329	TACTTGGGGTGTGTGAGGGGAGGCGGACAGG	CGGCGGTGGACTAAATACTATTTTTACT	5388
Db	1216	TACTTGGGGTGTGTGAGGGGAGGAGTGGCG	GGTGGATAAATACTATTTTTACT	1275
Qy	5389	GCCAAATAAATAATATTTGTAATAATTTAACT	TGGGGAATACTAGCTTT	5434
Db	1276	GCCACTCTTATTTTTTCCCTTACTTTTTTCT	TGTGTCCGGGTT	1321

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RESULT 8
US-09-649-164-9117
; Sequence 9117, Application US/09649164
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; DATE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1165.001
; CURRENT APPLICATION NUMBER: US/09/649,164
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 60/150,606
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 9995
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9117

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Query Match	15.9%;	Score 917.6;	DB 25;	Length 1595;
Best Local Similarity	90.5%;	Prod. No. 1.7e-72;		
Matches 1019;	Conservative	0;	Mismatches 89;	Indels 18; Gaps 3;
4327	TTGGGGCTCGAAGACGAGCGAGCTGGTTGAGTCTTCAAAGTCTTAAACGCTGGCGGCG	4386		
b	196	TGGGGGCTCGAAGACGAGCGAGCTGGTTGAGCCTTCAAAGTCTTAAACGCGCGGCG	255	
y	4387	TGGGTTTCGAGGTTTATTGATTGAAATTCGCTGGCAGCAGAGGCTCTGCAGACAGAGAGCG	4446	
b	256	TGGGTTTCGGGGTTTATTGATTGAAATTCGCGCGCGGGAGGCTCTGCAGAGAGAGAGCG	315	
y	4447	CGAGAGATGGAGATGGGCAGAGGATTTCATTGAGAGCTCGCGAAACAGGGCGCCCTCTGAT	4506	
b	316	CGAGAGATGGAGATGGGCAGAGGATTTCATTAGAGCTCGCGAAACAGGACGCCCTCTGAT	375	
y	4507	GTCAAGAGACTTCCCTGGACACACAGTCGGTGGATGAAGGCAAACTCGAAGCCCTCACA	4566	
b	376	GTCAAGAGACTTGTCTGGACACACAGTCGGTGGATGAAGGCAAACTCGAAGCCCTCACA	435	
y	4567	GATGAATTTGAAGAACTGGAAATCTTTAAGTAAATCAACGGAGGCTTCACCTCAATCTCA	4626	
b	436	GATGAATTTGAAGAACTGGAAATCTTTAAGTAAATCAACGATAGGCTTCACCTCAATCGCA	495	

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; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-649-164-9117

Query Match          15.9%; Score 917.6; DB 25; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;

QY 4327 TTGGGGCTCGAAGACCGAGCGAGCTGGTTGAGTCTTCAAAGTCTCTAAAGTCTCGAGAGAGCG 4386
Db 196 TGGGGCTCGAAGACCGAGCGAGCTGGTTGAGTCTTCAAAGTCTCTAAAGTCTCGAGAGAGCG 255

QY 4387 TGGGTTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCGCTCTGAGAGAGAGCG 4446
Db 256 TGGGTTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCGCTCTGAGAGAGAGCG 315

QY 4447 CGAGAGATGGAGATGGCAGCGGATTCATTTCAGAGCTGCGGAACAGCGGCCCTCTGAT 4506
Db 316 CGAGAGATGGAGATGGCAGCGGATTCATTTCAGAGCTGCGGAACAGCGGCCCTCTGAT 375

QY 4507 GTGAAGAAGCTTGGCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACA 4566
Db 376 GTGAAGAAGCTTGGCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACA 435

QY 4567 GATGAATTTGAGAAGCTGGAATTCCTTAAGTAAATCAACAGGAGCGCTCACCTCAATCTCA 4626
Db 436 GATGAATTTGAGAAGCTGGAATTCCTTAAGTAAATCAACAGGAGCGCTCACCTCAATCTCA 495

QY 4627 GACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 4674
Db 496 AACTTACCAAGTTAACAACAACTTAAAGAGCTTGAAGTAAAGGATAACAGAGTCTCAGGG 555

QY 4675 GGCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGCGCATCTATATTTAAGTGGCAAC 4734
Db 556 GGCCTGGAAGTATTGGCAGAAAGTGTCCGAACCTCAGCGCATCTAATTTAAGTGGCAAC 615

QY 4735 AAAATTAAGACCTCAGCACAAATAGACCACTGAACAGGTTAGAAAACCTCAAGAGCTTA 4794
Db 616 AAAATTAAGACCTCAGCACAAATAGACCACTGAAAAAGTTAGAAAACCTCAAGAGCTTA 675

QY 4795 GACCTTTTCAATTCGAGAGTTAACCAACTGACGAGTACGAGAAACGTTGTTCAAGCTT 4854
Db 676 GACCTTTTCAATTCGAGAGTTAACCAACTGACGAGTACGAGAAATGTTTCAAGCTC 735

QY 4855 CTCTGCAACTCATAATCTCGACAGCTGTTACTGGGACCAAGAGGCGCCCTTACTCA 4914
Db 736 CTCCGCAACTCATAATCTCGACGCTATGACCGGACGACAAAGAGGCGCCCTGACTCG 795

QY 4915 GATATTGAGACCACTGGAGGCGCTGGATGACGAGAGAGAGGCTGAGCATGAGGAGAG 4974
Db 796 GATGCTGAGGCGCTACCTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGAG 855

QY 4975 TATGATCAAGATGCTCAGGTAGTGGAAAGTGAAGGCGGAGGAGGAGGAGGAGGAGCT 5034
Db 856 TATGATCAAGATGCTCAGGTAGTGGAAAGTGAAGGCGGAGGAGGAGGAGGAGGAGGAGT 915

QY 5035 GAAGAGGAGGACGTGATGGAGGAGGACGAGGAGGATGAAGAAGCTTATACGATGAGAG 5094
Db 916 GAAGAGGAGGACGTGATGGAGGAGGAGGAGGAGGATGAAGAAGCTTATACGATGAGAG 975

QY 5095 GTAGATGGCCAGAAATGAGAAGAGCTTGGTGAAGAGAAAGGGGTGAGAGCGGAGGAG 5154
Db 976 GTAGATGGCCAGAAATGAGAAGAGCTTGGTGAAGAGAAAGGGGTGAGAGCGGAGGAGG 1035

QY 5155 TGAGAACCTCAAGATGAGGAGAGAGATGATGACTAAGTGAATTAACCTATTTTGAAGAT 5214
Db 1036 CGAGAACCTCAAGATGAGGAGAGAGATGATGACTAAGTGAATTAACCTATTTTGAAGAT 1095
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QY 5215 TCCTATTGTGATTGACTGTGTTTTTACCATATCCCT-----CCCCCTCCAAATCTCTGC 5268
Db 1096 TCCTATTGTGATTGACTGTGTTTTTACCATATCCCTTCCCTCCCTCCCTCCAAATCTCTGC 1155

QY 5269 CCCTGAAAACCTACTTTTTTCTGATTGAATGTAACATGCTGTGGGAATGAGACGGGAAAGTG 5328
Db 1156 CCCTGAAAACCTACTTTTTTCTGATTGTACGCTGTGTGGGAACGAGAGGGGAAAGTG 1215

QY 5329 TACTGGGGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5388
Db 1216 TACTGGGGTGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1275

QY 5389 GCCAAATAAAATTAATTTGTAATTAATTAACCTGGGATAGCTTT 5434
Db 1276 GCACCTCTTATTTTTTCCCTACTTTTCTTTGTCCTCCGGTTTT 1321
```

```
RESULT 9
US-09-652-913-10130
; Sequence 10130, Application US/096552913
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean R.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1174-001
; CURRENT APPLICATION NUMBER: US/09/652,913
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,107
; NUMBER OF SEQ ID NOS: 10833
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10130
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-913-10130
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Query Match 15.9%; Score 917.6; DB 25; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;

QY 5329 TACTGGGGGTTGTGGAGGAGGAGGCGAGGAGCGGTGGACTAAATACTATTTTACT 5388
Db 1216 TACTGGGGGTTGCGGGGAGGGATGCGGGTGGGGTGGAAATACTATTTTACT 1275
QY 5389 GCCAAATAAATAATATTTGTAATATTAATACTGGGATACAGCTTT 5434
Db 1276 GCCACTCTTTATTTTCCCTACTTTTCTTTCTTTGTGTCGGGTTTT 1321

RESULT 11

US-09-699-999-6021
; Sequence 6021, Application US/09699999
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Vasicek, Thomas
; APPLICANT: Wang, Youzhan
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2032-001
; CURRENT APPLICATION NUMBER: US/09/699,999
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,361
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 7488
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6021
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-699-999-6021

Query Match 15.9%; Score 917.6; DB 27; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;

QY 4327 TTGGGGCTCGAAGCCGAGCGAGCTGGTTGAGTCTTCAAAGTCCCTAAACGTCGGGCGG 4386
Db 196 TGGGGGCTCGAAGACCAGCGGAGCTGGTTGAGCTTCAAAGTCCCTAAACGTCGGGCGG 255
QY 4387 TGGGTTTCGAGGTTTATTTGATTGAACTCGGCTGGCACCAGAGCGCTCTGCACACAGAGCG 4446
Db 256 TGGGTTTCGAGGTTTATTTGATTGAACTCCGGCGCGGGAGCGCTCTGCAGAGAGAGCG 315
QY 4447 CGAGAGATGGAGATGGGCAGACGATTTCATTCAGAGCTGCGGAACAGCGGCCCTCTGAT 4506
Db 316 CGAGAGATGGAGATGGGCAGACGATTTCATTTAGAGCTGCGGAACAGAGCGGCCCTCTGAT 375
QY 4507 GTGAAGAACTTGCCTGGACACAGTCGGTCGATGAATGAAGCGAACTCGAAGCCCTCACA 4566
Db 376 GTGAAGAACTTGTCTGGACACAGTCGGTCGAAATGAAGCGAACTCGAAGCGCCTCACA 435
QY 4567 GATGAATTTGAAGAACTGGAATCTTAAAGTAAATCAACGAGCGCTTCACCTCAATCTCA 4626
Db 436 GATGAATTTGNAGAACTGGAAATCTTAAAGTAAATCAACGAGCTAGCCCTCAATTCGCA 495
QY 4627 GACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACTA-----AGAGTCTCAGGG 4674
Db 496 AACTTACCAAGTTAACAACAACTTAAGAAGCTTGAACGATACAGCTACAGAGTCTCAGGG 555
QY 4675 GGCCTGGAAGTATTTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAAC 4734
Db 556 GGCCTGGAAGTATTTGGCAGAAAAGTGTCCGAACCTCAGCATCTAAATTTAAAGTGGCAAC 615
QY 4735 AAAATTAAGACCTTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTA 4794
Db 616 AAAATTAAGACCTTCAGCACAAATAGAGCCACTGAAAAAAGTTAGAAAACCTCAAGAGCTTA 675
QY 4795 GACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTTACGGAGAAAACGTTGTTCAAGCTT 4854

Db 676 GACCTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACCGAGAAAATGTGTTCAAGCTC 735
QY 4855 CTCCTGCAACTCACATATCTCGACAGCTTTACTTGGGACCAAGAGAGGCCCTTACTCA 4914
Db 736 CTCCTGCAACTCACATATCTCGACAGCTTTACTTGGGACCAAGAGAGGCCCTTACTCG 795
QY 4915 GATATTGAGGACCACGTCGAGGCGCTTGGATGACGAGGAGGAGGCTGAGCATCAGGAGGAG 4974
Db 796 GATGCTGAGGCTTACGTCGAGGCGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 855
QY 4975 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAAGT 5034
Db 856 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAAGT 915
QY 5035 GAAGAGGAGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATACGATGGAGAG 5094
Db 916 GAAGAGGAGACGTGAGTGGAGGGGAGGAGGAGGATGAAGAAGGTTATACGATGGAGAG 975
QY 5095 GTAGATGGCGAGGAAGATCAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAA 5154
Db 976 GTAGATGACGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAA 1035
QY 5155 TGGAACACCTGAAGATGAGGAGGAAGATGACTAAGTAGAATAACCTATTTTGAATAAT 5214
Db 1036 CGAGAACCTGAAGATGAGGAGGAAGATGACTAAGTAGAATAACCTATTTTGAATAAT 1095
QY 5215 TCCTATTGTGATTTGACTGTTTTTACCATATCCCT-----CCCCCTCCAAATCCTGC 5268
Db 1096 TCCTATTGTGATTTGACTGTTTTTACCATATCCCTCCTCCCTCCCTCCAAATCCTGC 1155
QY 5269 CCCCAGAACTTACTTTTTCTGATGTAACTTCTGCTGGGAATGACAGCGGAAAAGTG 5328
Db 1156 CCCCAGAACTTATTTTTCTGATGTAACTTCTGCTGGGAATGACAGCGGAAAAGTG 1215
QY 5329 TACTGGGGGTTGTGGAGGAGGAGGAGGAGGCGGTGGACTAAATACTATTTTACT 5388
Db 1216 TACTGGGGGTTGCGGGGAGGGATGCGGGTGGGGTGGAAATACTATTTTACT 1275
QY 5389 GCCAAATAAATAATATTTGTAATATTAATACTGGGATACAGCTTT 5434
Db 1276 GCCACTCTTTATTTTCCCTACTTTTCTTTCTTTGTGTCGGGTTTT 1321

RESULT 12

US-09-710-281-4371
; Sequence 4371, Application US/09710281
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Stbdal, Hilde
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.2036-001
; CURRENT APPLICATION NUMBER: US/09/710,281
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164,254
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 5803
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4371
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-710-281-4371

Query Match 15.9%; Score 917.6; DB 28; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;

Db 736 CTCCTCGCAACTACATATCTTCACGGCTATGACCGGACGACAAGGAGGCCCTCTGACTCG 795
QY 4915 GATATTGAGGACCACTGCGAGGCTGGATGACGAGGAGGAGGCTGACCATGAGGAGAG 4974
Db 796 GATCTGAGGCTACCTGCGAGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 855
QY 4975 TATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGCAGGAGGAGGAGGAAGGT 5034
Db 856 TATGATGAAGATGCTCAGTGTAGTGAAGACGAGGAGGACGAGGATGAGGAGGAGAGGT 915
QY 5035 GAAGAGGAGGACCTGAGTGGAGGCGACGAGGAGATGAAGAAGTTTATAACGATGGAGAG 5094
Db 916 GAAGAGGAGGACCTGAGTGGAGGCGAGGAGGAGGATGAAGAAGTTTATAACGATGGAGAG 975
QY 5095 GTAGATGCGGAGGAAGCTTGGTGAAGAAGAGCTTGGTGAAGAAGAGGCTCAGAACGCGAAA 5154
Db 976 GTAGATGACGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAGGCTCAGAACGCGAAA 1035
QY 5155 TGAGAACTGAAGATGAGGAGGAGAGATGATGACTAAGTAGAATAAACCTATTTTGAAGAAAT 5214
Db 1036 CGAGAACTGAAGATGAGGAGGAGAGATGATGACTAAGTAGAATAAACCTATTTTGAAGAAAT 1095
QY 5215 TCCTATTGTGATTGACTGTTTTTACCCATATCCCTT-----CCCCCTCCCAATCCTGC 5268
Db 1096 TCCTATTGTGATTGACTGTTTTTACCCATATCCCTTCCCCCCCCCTCCCAATCCTGC 1155
QY 5269 CCCCTGAAACTTACTTTTTCTGATTGTAACATTTGCTGGGAATGAGACGGGAAAGTG 5328
Db 1156 CCCCTGAAACTTATTTTTCTGATTGTAAGCTTGCTGGGAACGAGAGGGAAGTG 1215
QY 5329 TACTGGGGTTTGGAGGAGGAGGAGGAGGCGGTGGACTAAATACTATTTTACT 5388
Db 1216 TACTGGGGTTTGGCGGGAGGATGCGGTTGGGGTGGGAATAAAATACTATTTTACT 1275
QY 5389 GCCAAATAAATAATATTTTGAATATTAATCTGGGATAGCTTT 5434
Db 1276 GCCACTCTTATTTTTTCCCTACTTTTTCTTTGTTGTCGGTTTT 1321

RESULT 14

US-09-716-973-2254
; Sequence 2254, Application US/09716973
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2042-001
; CURRENT APPLICATION NUMBER: US/09/716,973
; CURRENT FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/167,325
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 2758
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2254
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-716-973-2254

Query Match 15.9%; Score 917.6; DB 28; Length 1595;
Best Local Similarity 90.5%; Pred. No. 1.7e-72;
Matches 1019; Conservative 0; Mismatches 89; Indels 18; Gaps 3;
QY 4327 TTGGGGCTCGAAGCCGAGCGAGCTGGTTGAGTCTTCAAAGTCTTAAACGTCGGCGCG 4386
Db 196 TGGGGGCTCGAAGCCGAGCGAGCGAGCTGGTTGAGCTTCAAAGTCTTAAACGTCGGCGCG 255
QY 4387 TGGGTTTCGAGGTTTATGATTGAATTCGGCTGCGACGAGAGGCTCTGCGACAGAGCGC 4446

Db 256 TGGGTTTCGGGGTTTATGATTGAATTTCCGCGCGCGGGAGCCTCTGCGAGAGAGAGCG 315
QY 4447 CGAGAGATGAGATGGCGACACGATTTCATTTCAGAGCTCGGGAACAGGCGCCTCTGAT 4506
Db 316 CGAGAGATGAGATGGCGACACGATTTCATTTCAGAGCTCGGGAACAGAGCGCCTCTGAT 375
QY 4507 GTGAAAGAACTTCCCTCGACACACGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACA 4566
Db 376 GTGAAAGAACTTCTCTCGACACACGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACA 435
QY 4567 GATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCTCACCCTCAATCTCA 4626
Db 436 GATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCTCACCCTCAATCTCA 495
QY 4627 GACTTACCAGGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 4674
Db 496 AACTTACCAGGTTAACAACAACTTAAGAAAGCTTGAACCTAAGCGATAACAGAGCTCAGGG 555
QY 4675 GGCCTGGAAGTATGGCAGAAAGTGTCCAAAACCTCACGCATCTATATTTAAGTGGCAAC 4734
Db 556 GGCCTGGAAGTATGGCAGAAAGTGTCCGAAACCTCACGCATCTAAATTTAAGTGGCAAC 615
QY 4735 AAAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAGAGCTTA 4794
Db 616 AAAATTAAGACCTCAGCACAAATAGAGCCACTGAAAGAGTTAGAAAACCTCAGAGCTTA 675
QY 4795 GACCTTTTCAATTGGAGGTAAACCAACCTGAACGACTACGAGAAAACGTTTCAAGCTT 4854
Db 676 GACCTTTTCAATTGGAGGTAAACCAACCTGAACGACTACCGAGAAAATGTTTCAAGCTC 735
QY 4855 CTCCTGCAACTCACATATCTCAGAGCTGTTACTGGGACCACAGAGGCGCCTTACTCA 4914
Db 736 CTCCTGCAACTCACATATCTCAGAGCTGTTACTGGGACCACAGAGGCGCCTCAGCTCG 795
QY 4915 GATATTGAGGACCACTGGAGGCTTGGATGACGAGGAGGAGGTTGAGCATGAGGAGGAG 4974
Db 796 GATGCTGAGGGCTACGTGGAGGCTTGGATGATGAGGAGGAGATGAGGATGAGGAGGAG 855
QY 4975 TATGATGAAGATGCTCAGTGTGGAAGATGAGGAGGCGAGGAGGAGGAGGAGGAGGT 5034
Db 856 TATGATGAAGATGCTCAGTGTGGAAGATGAGGAGGCGAGGAGGAGGAGGAGGAGGT 915
QY 5035 GAAGAGGAGGACGTGAGTGGAGGCGACGAGGAGGATGAAGAAGTTTAAACGATGGAGAG 5094
Db 916 GAAGAGGAGGACGTGAGTGGAGGCGAGGAGGAGGATGAAGAAGTTTAAACGATGGAGAG 975
QY 5095 GTAGATGCGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAA 5154
Db 976 GTAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAA 1035
QY 5155 TGAGAACTGAAGATGAGGAGGAGAGATGATGACTAAGTAGAATAAACCTATTTTGAAGAAAT 5214
Db 1036 CGAGAACTGAAGATGAGGAGGAGAGATGATGACTAAGTAGAATAAACCTATTTTGAAGAAAT 1095
QY 5215 TCCTATTGTGATTGACTGTTTTTACCCATATCCCTT-----CCCCCTCCCAATCCTGC 5268
Db 1096 TCCTATTGTGATTGACTGTTTTTACCCATATCCCTTCCCCCCCCCTCCCAATCCTGC 1155
QY 5269 CCCCTGAAACTTACTTTTTTCTGATTGTAACATTTGCTGGGAATGAGACGGGAAAGTG 5328
Db 1156 CCCCTGAAACTTATTTTTTCTGATTGTAACGTTGCTGGGAACGAGAGGGAAGTG 1215
QY 5329 TACTGGGGTTTGGAGGAGGAGGAGGCGGCTGGACTAAATACTATTTTACT 5388
Db 1216 TACTGGGGTTTGGCGGGGAGGAGTGGCGGTGGGGTGGGAATAAAATACTATTTTACT 1275
QY 5389 GCCAAATAAATAATATTTTGAATATTAATCTGGGATAGCTTT 5434
Db 1276 GCCACTCTTATTTTTTCCCTACTTTTTCTTTGTTGTCGGTTTT 1321

RESULT 15

GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 15:13:27 ; Search time 235 Seconds

(without alignments)
17048.694 Million cell updates/sec

Title: US-09-591-500-1

Perfect score: 5785

Sequence: 1 agcttctctgactctctaa.....aaacaatgattataagctt 5785

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 361435 seqs, 346278564 residues

Total number of hits satisfying chosen parameters: 722870

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_NA_New:*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq:*
- 7: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5785	100.0	5785	6	US-10-273-334-1
2	889	15.4	889	6	Sequence 1, Appli
3	866.6	15.0	895	6	Sequence 3, Appli
4	865	15.0	895	6	Sequence 15, Appl
5	839.4	14.5	895	6	Sequence 21, Appl
6	831.4	14.4	907	6	Sequence 23, Appl
7	762.6	13.2	907	6	Sequence 6, Appli
8	761	13.1	906	6	Sequence 13, Appl
9	760.2	13.1	906	6	Sequence 25, Appl
10	757.8	13.1	907	6	Sequence 33, Appl
11	753	13.0	907	6	Sequence 28, Appl
12	751.6	13.0	908	6	Sequence 9, Appli
13	727.4	12.6	907	6	Sequence 32, Appl
14	716	12.4	907	6	Sequence 30, Appl
15	711.8	12.3	905	6	Sequence 4, Appli
16	702	12.1	905	6	Sequence 11, Appl
17	681.2	11.8	905	6	Sequence 17, Appl
18	679.6	11.7	905	6	Sequence 7, Appli
19	679.6	11.7	905	6	Sequence 19, Appl
20	374.6	6.5	1937	5	Sequence 26, Appl
21	374.6	6.5	1937	5	Sequence 18913, A
22	245.8	4.2	63824	1	Sequence 18913, A
23	245.8	4.2	63824	1	Sequence 347, App
24	245.8	4.2	63824	6	Sequence 348, App
25	245.8	4.2	63824	6	Sequence 348, App
26	245.8	4.2	202100	1	Sequence 484, App

c 27	245.8	4.2	202100	6	US-10-282-174-484	Sequence 484, App
c 28	236.8	4.1	48763	6	US-10-282-048-3	Sequence 3, Appli
c 29	230.2	4.0	135259	6	US-10-240-425-1585	Sequence 1585, Ap
30	230	4.0	237326	6	US-10-301-844-2	Sequence 2, Appli
31	229.8	4.0	285	1	PCT-US02-10525-5	Sequence 5, Appli
c 32	229.8	4.0	220860	7	US-60-417-209-3	Sequence 3, Appli
c 33	229.6	4.0	16814	6	US-10-264-237-2871	Sequence 2871, Ap
c 34	228.4	3.9	302603	1	PCT-US02-32700-8	Sequence 8, Appli
35	228.4	3.9	302603	6	US-10-271-416-8	Sequence 8, Appli
c 36	227.8	3.9	20099	6	US-10-177-744A-12	Sequence 12, Appl
c 37	227.2	3.9	36296	6	US-10-240-425-1584	Sequence 1584, Ap
c 38	226.2	3.9	304905	1	PCT-US02-32700-1	Sequence 1, Appli
c 39	226.2	3.9	304905	6	US-10-271-416-1	Sequence 1, Appli
c 40	225.8	3.9	3794	6	US-10-275-505-20	Sequence 20, Appl
c 41	225	3.9	134292	6	US-10-240-425-1102	Sequence 1102, Ap
42	223.6	3.9	100267	6	US-10-240-425-1470	Sequence 1470, Ap
c 43	223.6	3.9	276820	1	PCT-US02-32700-9	Sequence 9, Appli
c 44	223.6	3.9	276820	6	US-10-271-416-9	Sequence 9, Appli
c 45	222.8	3.9	1202	5	US-09-724-676-35700	Sequence 35700, A

ALIGNMENTS

RESULT 1

US-10-273-334-1

; Sequence 1, Application US/10273334

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kocheavar, Gerald J.

; APPLICANT: Brody, Jonathan R.

; APPLICANT: Kodkol, Shrihari S.

; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

; FILE REFERENCE: 031787.0076

; CURRENT APPLICATION NUMBER: US/10/273,334

; PRIOR FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: US/09/591,500

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: PCT/US98/26433

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 5785

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (4453)..(5154)

; OTHER INFORMATION:

US-10-273-334-1

Query Match 100.0%; Score 5785; DB 6; Length 5785;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5785; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGCTTCTCGATCTCTAAATCAAGTCAGCTCCCTTAAGCTCTTGCTCCCGTACTGAAA 60

|||||

Db 1 AAGCTTCTCGATCTCTAAATCAAGTCAGCTCCCTTAAGCTCTTGCTCCCGTACTGAAA 60

|||||

QY 61 CTTTTCCTTATGTAAGTCTCTCAATAACACATAGCATATGTTTGGATGTTTCTTCCTCT 120

|||||

Db 61 CTTTTCCTTATGTAAGTCTCTCAATAACACATAGCATATGTTTGGATGTTTCTTCCTCT 120

|||||

QY 121 ATCAGTTGCAAGTTCACAGAGAGCTGATATATTTTCATTTCGCTACTATAGCCCTA 180

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Db 121 ATCAGTTGCAAGTTCACAGAGAGCTGATATATTTTCATTTCGCTACTATAGCCCTA 180

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QY 181 GAGCCTGACATAGTTTCTTGCTGTGAATGCTCAATAAATATTTGTTAAATGAGTAGAAA 240

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Db 181 GAGCCTGACATAGTTTCTTGCTGTGAATGCTCAATAAATATTTGTTAAATGAGTAGAAA 240

|||||

QY 241 CATAAAGTATCTATTTCATGGAAGAAAGATAAATAGCTACATTTTCTTTCTTTCTGTC 300
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241 CATAAAGTATCTATTTCATGGAAGAAAGATAAATAGCTACATTTTCTTTCTTTCTGTC 300
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
361 ACTAAGGAATTTGGACATTAATTTCAAGCTAGCCCTTCTATAACAANAATACGAATTTTC 420
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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901 GTAGCCGAGATCGACATTGCACTCCAGCTCGGCAACAGAGGAGACTCCATCCCAAA 960
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QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1261 TTTCTGCTTGGAAATGCTCTCCACTCCAGATGCTTACTAGATCTTTAGCTCAGTCACCC 1320
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QY 1321 CGCAGGAAGATCTTCCAACCATTCACCTGCATACACCTATGCTGCTCCCTAGAGAACAT 1380
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1321 CGCAGGAAGATCTTCCAACCATTCACCTGCATACACCTATGCTGCTCCCTAGAGAACAT 1380
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1501 TTATTTCTGTTTATAAACTTAATGCTTAGGCTGTAAGCTTATAACAATATTTGAGAATA 1560
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1561 AATCGTTAAATGTATACATTTTGAAGAAAGATAAATGTTGGATCCATTTAGTTGCA 1620
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1621 ACATTTGATCTGTGCTTAGACAGAGGCGCATGGTAAAGGACAAAGACATATTTTATAGG 1680
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1681 ACTGTACCTGAAAAATAAATAACTTGAACAGTTTATACAAGACTTATGTCAGGAAAC 1740
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1861 CATCTTGTATTTTCTTCTGGGAAACAGCTCAAAATGACTATTTAATGTTTACAATGATA 1920
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1861 CATCTTGTATTTTCTTCTGGGAAACAGCTCAAAATGACTATTTAATGTTTACAATGATA 1920
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1921 TCTTGCATCTGCCAGTAAATATATATAGACACTAGCAATCCAAATGTAAGATGAAC 1980
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1921 TCTTGCATCTGCCAGTAAATATATATAGACACTAGCAATCCAAATGTAAGATGAAC 1980
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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1981 AAGTCTTTTATAGAGGAGAGCCAAATACAAATAACAAAGGTGTTAATGCAGTA 2040
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2041 ATACAAACATACATACCATGTCATAGGAGTGCAGAGAGGTGCTTCTCCGAATGCAGTC 2100
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2041 ATACAAACATACATACCATGTCATAGGAGTGCAGAGAGGTGCTTCTCCGAATGCAGTC 2100
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2101 ACCCAGAAAGTCTTCTGTAGAAAGGATATCTTAAATGGTCTTTAAGGAAAGTAAACC 2160
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QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2161 AAAGGCAACTAAAGATTGCAAGGAGTCCCGAGGAAAGCAAAAGCAACCAAGGTACATA 2220
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2161 AAAGGCAACTAAAGATTGCAAGGAGTCCCGAGGAAAGCAAAAGCAACCAAGGTACATA 2220
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2221 GGCACAAAAGTAGCTGCTTCTTGGGAACTTCCAATAGTTTCTGTTGGAGCACACAGTTAG 2280
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2221 GGCACAAAAGTAGCTGCTTCTTGGGAACTTCCAATAGTTTCTGTTGGAGCACACAGTTAG 2280
QY ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2281 AAGTACTGTGCCATGGGACCAAGACTGAAGACATATGAGGTTCAAGGGCACAGAGCCC 2340
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2281 AAGTACTGTGCCATGGGACCAAGACTGAAGACATATGAGGTTCAAGGGCACAGAGCCC 2340
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2341 CATATATGTCATGATAAGATATTGGGAAGCCACTGGGGAGCTACTGAAACTTTTAAGCAG 2400
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2401 GAAATAAAATGTCATATATACACCTTAGAAATTTGATTTTTTCTCTCTTTTATCTTTC 2460

[illegible]

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Db	3541	TATCTTCTTCCTGAGTGTGTTTTCCACAAATCCCATAGCTGTGAAAGATTCGTTTTAGGG	3600
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Db	3601	AAATATTATTTTAAATATAGCATATTTTGTCAATGTGGGACATPAGGACTPAGTCTGCTG	3660
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Db	3781	ATGCCACTCAAAATTTATTCCTCTPACCACATGCGGTATCTAAACCTAGTATAGACTTTTG	3840
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Db	3901	AAAATTCATAATTCATGATGATACCAATAAAGATAGATTTAGCTTTTACAGGATGTTT	3960
QY	3961	TTGGCATTTTATTCCTTCATTTGAGGGGAGATCTACCAAAAATATGTCTTTCATGGTTC	4020
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Db	4021	TGTGCTTATTTAAATTTCTGTGATGCATATTCACAGGTACTTTAAACCTAGTCTATAGAT	4080
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Db	4081	TCAAGATATCCCGTGTCAAGTCTCTAAAAGTAAAAAGAAAAATGGGTACTTTGTGAAGGC	4140
QY	4141	TGATTCACAGTAAGTACTGTAGAGGGAGTGCCCTGTGTATTTCACAAATATCAACGTGA	4200
Db	4141	TGATTCACAGTAAGTACTGTAGAGGGAGTGCCCTGTGTATTTCACAAATATCAACGTGA	4200
QY	4201	GCATCAGATAAGATTTCTTTTAGTCACACACACTACCTTCTTACTAGGAAGATCCATAT	4260
Db	4201	GCATCAGATAAGATTTCTTTTAGTCACACACACTACCTTCTTACTAGGAAGATCCATAT	4260
QY	4261	ACTTGAATAATTTGCTGTGACCCAGGTTACTTATTCAGTCCCTTTATTAATAATTTTG	4320
Db	4261	ACTTGAATAATTTGCTGTGACCCAGGTTACTTATTCAGTCCCTTTATTAATAATTTTG	4320
QY	4321	TAAATATTGGGGCTCGAGAACCCAGCGAGCTGGTGTAGTCTTCAAGTCTCTAAACGTG	4380
Db	4321	TAAATATTGGGGCTCGAGAACCCAGCGAGCTGGTGTAGTCTTCAAGTCTCTAAACGTG	4380
QY	4381	CGCGCTGGGTTGAGGTTTATTTGATTTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAG	4440
Db	4381	CGCGCTGGGTTGAGGTTTATTTGATTTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAG	4440
QY	4441	AGAGCGCAGAGATGGAGATGGCCACACCGGATTCATTTCAGAGCTGCGGACAGGGCGCC	4500
Db	4441	AGAGCGCAGAGATGGAGATGGCCACACCGGATTCATTTCAGAGCTGCGGACAGGGCGCC	4500
QY	4501	TCTGATGTGAAAGAACTTGGCCCTGGACACACAGTCGGTTCGAATGAAGCGCAAACTCGAAGCC	4560
Db	4501	TCTGATGTGAAAGAACTTGGCCCTGGACACACAGTCGGTTCGAATGAAGCGCAAACTCGAAGCC	4560
QY	4561	CTCACAGATGAATTTGAAGACTGGAAATTCCTTAAGTAAAAATCAACGGAGGCCTCACTCA	4620
Db	4561	CTCACAGATGAATTTGAAGACTGGAAATTCCTTAAGTAAAAATCAACGGAGGCCTCACTCA	4620

Db 481 CATATCTCGACAGCTGTTACTGGGACCACAAAGAGGCCCTTACTCAGATATTGAGGACC 540
QY 4928 ACGTGGAGGCGCTGGATCACAGAGGAGGGTGAGCATGAGGAGGATGATGAAGATG 4987
Db 541 ACGTGGAGGCGCTGGATCACAGAGGAGGGTGAGCATGAGGAGGATGATGAAGATG 600
QY 4988 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
Db 601 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 5048 TGAGTGGAGGCGGAGGAGGATGAAGAGGTTATACGATGAGAGGATGAGTGGCGAGG 5107
Db 661 TGAGTGGAGGCGGAGGAGGATGAAGAGGTTATACGATGAGAGGATGAGTGGCGAGG 720
QY 5108 AAGATGAAGAAGAGCTGGTGAACAAGAAAGGGCTCAGACCGGAAATGAGAACCTGAAG 5167
Db 721 AAGATGAAGAAGAGCTGGTGAACAAGAAAGGGCTCAGACCGGAAATGAGAACCTGAAG 780
QY 5168 ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTGATT 5227
Db 781 ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTGATT 840
QY 5228 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 5276
Db 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 889

RESULT 3
US-10-273-334-15
; Sequence 15, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; CURRENT FILING DATE: 2002-10-18
; CURRENT APPLICATION NUMBER: US/10/273,334
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-10-273-334-15

Query Match 15.0%; Score 866.6; DB 6; Length 895;
Best Local Similarity 98.9%; Pred. No. 1e-83;
Matches 885; Conservative 0; Mismatches 4; Indels 6; Gaps 1;
QY 4388 GGGTTCGAGGTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTCAGACAGAGAGCGC 4447
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTCAGACAGAGAGCGC 60
QY 4448 GAGAGATGAGATGGGCAGACGGATTCAATCAGAGCTGGGAAACAGGGCGCCCTCTGATG 4507
Db 61 GAGAGATGAGATGGGCAGACGGATTCAATCAGAGCTGGGAAACAGGGCGCCCTCTGATG 120
QY 4508 TGAAGAACTTGGCTGGACAAAGTCGGTCGAATGAAGCAAACTCGAAGCCCTCACAG 4567
Db 121 TGAAGAACTTGGCTGGACAAAGTCGGTCGAATGAAGCAAACTCGAAGCCCTCACAG 180

QY 4568 ATCAATTTGAGAACTGGAAATCTTAAAGTAAATCAACGAGAGCCCTCACCTCAATCTCAG 4627
Db 181 ATCAATTTGAGAACTGGAAATCTTAAAGTAAATCAACGAGAGCCCTCACCTCAATCTCAG 240
QY 4628 ACTTACCAAAAGTTTAAAGTTGAGAAAGCTTGAACATAAGAGTCTCAGGGGCGCTTGAAGTAT 4687
Db 241 ACTTACCAAAAGTTTAAAGTTGAGAAAGCTTGAACATAAGAGTCTCAGGGGCGCTTGAAGTAT 300
QY 4688 TGCGAGAAAAGTGTCCAAACCTCACGCATCTATATTAAAGTGGCAACAAAATTAAGAGCC 4747
Db 301 TGCGAGAAAAGTGTCCAAACCTCACGCATCTATATTAAAGTGGCAACAAAATTAAGAGCC 360
QY 4748 TCAGCACAAATAGAGCCACCTGAACACAGTTTGAACAACTCAAGAGCTTAGACCTTTTCAATT 4807
Db 361 TCAGCACAAATAGAGCCACCTGAACACAGTTTGAACAACTCAAGAGCTTAGACCTTTTCAATT 420
QY 4808 GCAGAGTAACCAACCTTGAACAGCTACGGAGAAAACCTGTTCAAGCTTCTCCTGCAACTCA 4867
Db 421 GCAGAGTAACCAACCTTGAACAGCTACGGAGAAAACCTGTTCAAGCTTCTCCTGCAACTCA 480
QY 4868 CATATCTCGACAGCTGTTACTGGGACCAAGAGAGCCCTTACTCAGATATTGAGGACC 4927
Db 481 CATATCTCGACAGCTGTTACTGGGACCAAGAGAGCCCTTACTCAGATATTGAGGACC 540
QY 4928 ACGTGGAGGCGCTGGATGACGAGGAGGAGGGTGAGCATGAGGAGGATGATGAAGATG 4987
Db 541 ACGTGGAGGCGCTGGATGACGAGGAGGAGGGTGAGCATGAGGAGGATGATGAAGATG 600
QY 4988 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
Db 601 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 5048 TGAGTGGAGGCGGAGGAGGAGGATGAAGAGGTTATAACGATGGAGAGGTAGATGCGGAGG 5107
Db 661 TGAGTGGAGGCGGAGGAGGAGGATGAAGAGGTTATAACGATGGAGAGGTAGATGCGGAGG 720
QY 5108 AAGATGAACAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAAGAAATGAGAACCTGAAG 5167
Db 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAAGAAATGAGAACCTGAAG 780
QY 5168 ATGAGGAGAGAAGATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTGATT 5227
Db 781 ATGAGGAGAGAAGATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTGATT 840
QY 5228 TGACTGTTTTTACCATATC-----CCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 5276
Db 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 895

RESULT 4
US-10-273-334-21
; Sequence 21, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens

```
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
; US-10-273-334-21

Query Match      15.0%; Score 865; DB 6; Length 895;
Best Local Similarity 98.8%; Pred. No. 1.5e-83;
Matches 884; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy 4388 GGGTTCGAGGTTTATGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 4447
Db      1 GGGTTCGGGGTTTATGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60

Qy 4448 GAGAGATGAGATGGCAGACGGATTTCATTAGAGCTCGGAACAGAGCGGCCCTCTGATG 4507
Db      61 GAGAGATGAGATGGCAGACGGATTTCATTAGAGCTCGGAACAGAGCGGCCCTCTGATG 120

Qy 4508 TGAAGAAGACTTCCCTGGCAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG 4567
Db      121 TGAAGAAGACTTCCCTGGCAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG 180

Qy 4568 ATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 4627
Db      181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240

Qy 4628 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGGGGCCTGGAAGTAT 4687
Db      241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTAAAGTCTCAGGGGGCCTGGAAGTAT 300

Qy 4688 TGGCAGAAAGTGTCCAAACCTGACGACTACGGAGAAACGTGTTCAAGCTTCTCCTGCAACTCA 4867
Db      421 TGGCAGAAAGTGTCCAAACCTGACGACTACGGAGAAACGTGTTCAAGCTTCTCCTGCAACTCA 480

Qy 4868 CATATCTCAGACAGCTGTTACTGGGACCAACAGAGAGGCCCTTACTCAGATATTGAGGACC 4927
Db      5048 CATATCTCAGACAGCTGTTACTGGGACCAACAGAGAGGCCCTTACTCAGATATTGAGGACC 5107

Qy 5048 TGAGTGGAGGGACGAGAGAGGATGAAGAAGTTATAACGATGAGAGGTAGATGGCGAGG 5107
Db      661 TGAGTGGAGGGACGAGAGAGGATGAAGAAGTTATAACGATGAGAGGTAGATGGCGAGG 720

Qy 5108 AAGATGAGAGAGCTTGTGTGAGAGAGAGGGGTGAGAGCGGAAATCAGAACCTGGAAG 5167
Db      721 AAGATGAGAGAGCTTGTGTGAGAGAGAGGGGTGAGAGCGGAAATCAGAACCTGGAAG 780

Qy 5168 ATGAGGAGAGAGATGATGACTAGTGAATAACCTATTATTTGAAAAATTCCTATTGTGATT 5227
Db      781 ATGAGGAGAGAGATGATGACTAGTGAATAACCTATTATTTGAAAAATTCCTATTGTGATT 840

Qy 5228 TGACTGTTTTTACCCTATATC-----CCCTCCCCCTCCCAATCCTGCGCCCTCGAA 5276
Db      841 TGACTGTTTTTACCCTATATC-----CCCTCCCCCTCCCAATCCTGCGCCCTCGAA 895

RESULT 5
US-10-273-334-23
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|||||
Db 601 CTCAGGTAGTGAAGATGAGGAGCGGAGGAGGGGAGGAGGAGGTGACAGAGGAGCG 660
QY 5048 TGAGTGGAGGCGAGGAGGATGAAGAAGGTTTATACGATGGAGAGGTAGATGGCGAGG 5107
Db 661 TGAGTGGAGGCGAGGAGGATGAAGAAGGTTTATACGATGGAGAGGTAGATGACGAGG 720
QY 5108 AAGATGAAGAAGAGCTGGTGAACAAGAAAGGGGTGAGAGCGGAAATGAGAACCTGAAG 5167
Db 721 AAGATGAAGAAGAGCTGGTGAAGAAGAAAGGGGTGAGAGCGGAAATGAGAACCTGAAG 780
QY 5168 ATGAGGAGAAAGATGATGACTAAGTAACTAATATTTTGAATAATTCCTATTTGTGATT 5227
Db 781 ATGAGGAGAAAGATGATGACTAAGTAACTAATATTTTGAATAATTCCTATTTGTGATT 840
QY 5228 TGACTGTTTTTACCCTATATCCCT-----CCCCCTCCAAATCTGCCCTCGAA 5276
Db 841 TGACTGTTTTTACCCTATATCCCTCTCCCTCCCTCTAATCTGCTGCCCTCGAA 895

RESULT 6
US-10-273-334-6
; Sequence 6, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-6

Query Match 14.4%; Score 831.4; DB 6; Length 907;
Best Local Similarity 97.4%; Pred. No. 5e-80;
Matches 883; Conservative 0; Mismatches 6; Indels 18; Gaps 3;

QY 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGCGC 4447
Db 1 GGGTTCGGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGCGC 60
QY 4448 GAGAGATGGAGATGGGCGAGCGGATTCATTTCAGAGCTGCGGAACAGCGGCCCTCTGTATG 4507
Db 61 GAGAGCGGAGATGGGCGAGCGGATTCATTTCAGAGCTGCGGAACAGCGGCCCTCTGTATG 120
QY 4508 TGAAGAAGCTTGCCTGGACAACAGTCGGTCTGAATGAAGCAACCTGCAAGCCCTCACAG 4567
Db 121 TGAAGAAGCTTGCCTGGACAACAGTCGGTCTGAATGAAGCAACCTGCAAGCCCTCACAG 180
QY 4568 ATGAATTTGAAGAACTGGAATCTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 4627
Db 181 ATGAATTTGAAGAACTGGAATCTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
QY 4628 ACTTACCAAAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 4675
Db 241 ACTTACCAAAAGTTAACAAGTTGAGAAAGCTTGAACCTAACAAGTAAACAGTCTCAGGGG 300
QY 4676 GCCTGGGAAGTATGGCGAAGAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGGCAACA 4735
Db 301 GCCTGGGAAGTATGGCGAAGAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGGCAACA 360
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QY 4736 AAATTTAAAGACCTCAGCACAAATAGAGCCCACTGAAACAGTTAGAAAAACCTCAAGAGCTTAG 4795
Db 361 AAATTTAAAGACCTCAGCACAAATAGAGCCCACTGAAACAGTTAGAAAAACCTCAAGAGCTTAG 420
QY 4796 ACCTTTTCAATTCGAGAGGTAACCAACCTGAGAGCTACGAGAGAAACGTTGTTCAAGCTTC 4855
Db 421 ACCTTTTCAATTCGAGAGGTAACCAACCTGAGAGCTACGAGAGAAACGTTGTTCAAGCTTC 480
QY 4856 TCTGCAACTCACAATATCTCGACAGCTGTTACTGGGACCACAAAGGAGGCCCTTACTCTAG 4915
Db 481 TCTGCAACTCACAATATCTCGACAGCTGTTACTGGGACCACAAAGGAGGCCCTTACTCTAG 540
QY 4916 ATATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4975
Db 541 ATATTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 4976 ATGATCAAGATGCTCAGGTAGTGGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5035
Db 601 ATGATCAAGATGCTCAGGTAGTGGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 5036 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5095
Db 661 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
QY 5096 TAGATGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5155
Db 721 TAGATGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 5156 GAGAACCTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5215
Db 781 GAGAACCTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
QY 5216 CCTATTGTGATTGACTGTTTTTACCCTATCCCT-----CCCCCTCCAAATCTCTGCC 5269
Db 841 CCTATTGTGATTGACTGTTTTTACCCTATCCCTCTCTCCCTCCCTCTCTCTCTCTCTCTGCC 900
QY 5270 CCTCGAA 5276
Db 901 CCTCGAA 907

RESULT 7
US-10-273-334-13
; Sequence 13, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-10-273-334-13

Query Match 13.2%; Score 762.6; DB 6; Length 907;
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[illegible]

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; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathani R.
; APPLICANT: Kodkoi, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/36433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; JS-10-273-334-25

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Query Match	13.2%	Score 761;	DB 6;	Length 907;
Best Local Similarity	92.5%;	Pred. No. 1.2e-72;		
Matches 839;	Conservative 0;	Mismatches 50;	Indels 18;	Gaps
Qy 4388	GGGTTCCAGGCTTTATTGANTGAATTCGGCTGCACAGAGAGCCCTCTGCACAGAGAGAGCGC	4447		
Db 1	GGGTTCCGGGGTTTATTGATTGAATTCGGCGCGGGAGCCCTCTGCAGAGAGAGAGCGC	60		
Qy 4448	GAGAGATTGAGATTGGGCAGACGGGATTTCATTACAGAGCTGCGGAACAGGGCGCCCTCTGATG	4507		
Db 61	GAGAGATTGAGATTGGGCAGACGGGATTTCATTAGAGCTGCGGAACAGGGCGCCCTCTGATG	120		
Qy 4508	TGAAGAAGCTTGCCTCGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGGCCCTCACAG	4567		
Db 121	TGAAGAAGCTTGTCTGGCAACAGTCGGTCGAATGAAGGCAAACTCGAGGGCCCTCACAG	180		
Qy 4568	ATGAAATTGGAAGAACTTGGAAATCTTAACTAAATCAACGAGGCGCTCACCTCAATCTCAG	4627		
Db 181	ATGAAATTGGAAGAACTTGGAAATCTTAACTAAATCAACGAGGCGCTCACCTCAATCTCGGAA	240		
Qy 4628	ACTTACCAAAAGTTA---AAGTTGAGAAAGCTTTGAACCTA-----AGAGTCTCAGGGG	4679	57	4679
Db 241	ACTTACCAAAAGTTTAAACAAACTTAAAGAGCTTGAACCTAAGCGATAACAGAGTCTCAGGGG	300		
Qy 4676	GCCTGGAAGTATTGGCAGAAAAGTGTCRAAACCTCACGCACTATATTTAACTGAGCAACA	4739		
Db 301	GCCTGGAAGTATTGGCAGAAAAGTGTCGCAACCTCACGCACTATAAATTTAACTGAGCAACA	360		
Qy 4736	AAATTAAGACCTTCAGACAATAGAGCCACTGAAACAGTTTAGAAACCTTCAAGAGCTTAG	4799		
Db 361	AAATTAAGACCTTCAGACAATAGAGCCACTGAAAGGTTTGAAGAACCTTCAAGAGCTTAG	420		
Qy 4796	ACCTTTTCAATTGCGAGGTAAACCAACCTGAAACGACTACGGAGAAAACGTTTCAAGCTTC	4855		
Db 421	ACCTTTTCAATTGCGAGGTAAACCAACCTGAAACGACTACCGAGAAAATGTTTCAAGCTTC	480		
Qy 4856	TCCTGCAACTCACATATCTCGACAGCTGTTCTGGAACACAGAGGGCCCTTACTCAG	4915		
Db 481	TCCTGCAACTCACATATCTCGACGGGTATGACCGGGACACAGGAGGGCCCTGACTCGG	540		
Qy 4916	ATATTGAGGCCAGTGGAGGGCCTGGATCACAGGAGGAGGTGAGCATGAGGAGGT	4977		
Db 541	ATGCTGAGGGCTACGTGGAGGGCCTGGATGATGAGGAGGAGTATGAGGATGAGGAGGT	600		
Qy 4976	ATGATGAAGATGCTCAGGTATGGAAGATGAGGAGGGCGAGGAGGAGGAGGAGGTG	5033		
Db 601	ATGATGAAGATGCTCAGGTATGGAAGATGAGGAGGGCGAGGAGGAGGAGGAGGTG	660		
Qy 5036	AAGAGGAGGACGTGAGTGGAGGGACGACGAGGAGTGAAGAAGTTTATAACGATGAGGAGG	5098		
Db 661	AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGTGAAGAAGTTTATAACGATGAGGAGG	720		

RESULT 8
US-10-273-334-25
; Sequence 25, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.


```
Query Match      13.1%; Score 757.8; DB 6; Length 907;
Best Local Similarity 92.3%; Pred. No. 2.6e-72;
Matches 837; Conservative 0; Mismatches 52; Indels 18; Gaps 3;

QY 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGGAGAGCCTCTGCAGACAGAGAGCGC 4447
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGCCGGCGGGGAGCCTCTGCAGAGAGAGAGCGC 60

QY 4448 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGCGAAACAGGGCGCCCTCTGATG 4507
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGCGAAACAGGGCGCCCTCTGATG 120

QY 4508 TGAAGAACTTCGCCCTGGACACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 4567
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 TGAAGAACTTCCTCGTTCACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 180

QY 4568 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGGCTCACCTCAATCTCAG 4627
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGTAGGCTCACCTCAATCGCAA 240

QY 4628 ACTTACCAAGTTA---AAGTTGACAAAGCTTGAACCTA-----AGAGTCTCAGGGG 4675
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 ACTTACCAAGTTAACAACCTTAAGAGCTTGAACCTAAGCGATACAGAGTCTCAGGGG 300

QY 4676 GCCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACA 4735
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 GCCTAGAAGTATTGGCAGAAAAAGTGTCCGAACCTCACGCATCTAAATTTAAGTGGCAACA 360

QY 4736 AAATTAAGACCTCAGCACAAATAGACCACTGAAACAGATTAGAAAACCTCAAGAGCTTAG 4795
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 AAATTAAGACCTCAGCACAAATAGACCACTGAAAAAAGTTAGAAAACCTCAAGAGCTTAG 420

QY 4796 ACCTTTTCAATTCGAGGTAAACCAACCTGAACGACTACGGAGAGAAACCTGTTCAGGCTTC 4855
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 ACCTTTCCAATTCGAGGTAAACCAACCTGAACGACTACCGAGAGAAATGTGTTCAGGCTTC 480

QY 4856 TCCGTGCAACTCACATATCTCGACAGCTGTACTCGGACCAACAGGAGGCCCTTACTCAG 4915
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 TCCGCAACTCACATATCTCGACGGCTATGACCGGGACGACAAAGGAGGCCCTTACTCAGG 540

QY 4916 ATATTGAGGACCTGAGGGCCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGT 4975
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 ATGCTGAGGGCTACGTGGAGGGCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 600

QY 4976 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGT 5035
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660

QY 5036 AAGAGGAGACGTGAGTGGAGGGGAGGAGGAGGATGAAGAAGTTATACGATGGAGAGG 5095
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 661 AAGAGGAGACGTGAGTGGAGAGGAGGAGGAGGAGGATGAAGAAGTTATACGATGGAGAGG 720

QY 5096 TAGATGCGAGGAAGATGAAGAAGACCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAAT 5155
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 721 TAGATGACGAGGAAGATGAAGAAGACCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAAC 780

QY 5156 GAGAACCTGAAGATGAGGAGAGAGATGATGACTAAGTAGAATAAAGCTATTTTGAAGAAAT 5215
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 781 GAGAACCTGAAGATGAGGAGAGAGATGATGACTAAGTGAATAAAGCTATTTTGAAGAAAT 840

QY 5216 CCTATTGTGATTTGACTGTTTTTACCATATCCCTC-----CCCCCTCCCAATCCTGCC 5269
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 841 CCTATTGTGATTTGACTGTTTTTACCATATCCCTC-----CCCCCTCCCAATCCTGCC 900

QY 5270 CCCTGAA 5276
      ||||| |||||
Db 901 CCCTGAA 907
```

RESULT 11
US-10-273-334-9
; Sequence 9, Application US/10273334
; GENERAL INFORMATION:

```
; APPLICANT: Pasternack, Gary R.  
; APPLICANT: Kochevar, Gerald J.  
; APPLICANT: Brody, Jonathan R.  
; APPLICANT: Kodkol, Shrihari S.  
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY  
; FILE REFERENCE: 031787.0076  
; CURRENT APPLICATION NUMBER: US/10/273,334  
; CURRENT FILING DATE: 2002-10-18  
; PRIOR APPLICATION NUMBER: US/09/591,500  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: PCT/US98/26433  
; PRIOR FILING DATE: 1998-12-11  
; PRIOR APPLICATION NUMBER: US 60/069,677  
; PRIOR FILING DATE: 1997-12-11  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 907  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (66)..(812)  
; OTHER INFORMATION:  
; US-10-273-334-9  
  
Query Match      13.0%; Score 753; DB 6; Length 907;  
Best Local Similarity 92.0%; Pred. No. 8.4e-72;  
Matches 834; Conservative 0; Mismatches 55; Indels 18; Gaps 3;  
  
QY 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGAGCGC 4447  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGCCGGCGGGGAGCCTCTGCAGAGAGAGAGCGC 60  
  
QY 4448 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGCGAAACAGGGCGCCCTCTGATG 4507  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGCGAAACAGGGCGCCCTCTGATG 120  
  
QY 4508 TGAAGAACTTCGCCCTGGACACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 4567  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 121 TGAAGAACTTCCTCGTTCGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 180  
  
QY 4568 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGGCTCACCTCAATCTCAG 4627  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGTAGGCTCACCTCAATCGCAA 240  
  
QY 4628 ACTTACCAAAAGTTA---AAGTTGAGAAAAGCTTGAACCTA-----AGAGTCTCAGGGG 4675  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 241 ACTTCCCAAGTTAAACAACTTTAAGAAGCTTGAACCTGAACCTCAAGAGCTTAG 300  
  
QY 4676 GCCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACA 4735  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 301 GCCTAGAAGTATTGGCAGAAAAAGTGTCCGAACCTCACGCATCTAAATTTAAGTGGCAACA 360  
  
QY 4736 AAATTAAGACCTCAGCACAAATAGACCACTGAAACAGATTAGAAAACCTCAAGAGCTTAG 4795  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 361 AAATTAAGACCTCAGCACAAATAGACCACTGAAAAAAGTTAGAAAACCTCAAGAGCTTAG 420  
  
QY 4796 ACCTTTTCAATTCGAGGTAAACCAACCTGAACGACTACGGAGAGAAACCTGTTCAGGCTTC 4855  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 421 ACCTTTCCAATTCGAGGTAAACCAACCTGAACGACTACCGAGAGAAATGTGTTCAGGCTTC 480  
  
QY 4856 TCCGTGCAACTCACATATCTCGACAGCTGTACTCGGACCAACAGGAGGCCCTTACTCAG 4915  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 481 TCCGCAACTCACATATCTCGACGGCTATGACCGGGACGACAAAGGAGGCCCTTACTCAGG 540  
  
QY 4916 ATATTGAGGACCTGAGGGCCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGT 4975  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 541 ATGCTGAGGGCTACGTGGAGGGCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 600  
  
QY 4976 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGT 5035  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 601 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660  
  
QY 5036 AAGAGGAGACGTGAGTGGAGGGGAGGAGGAGGATGAAGAAGTTATACGATGGAGAGG 5095  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 661 AAGAGGAGACGTGAGTGGAGAGGAGGAGGAGGAGGATGAAGAAGTTATACGATGGAGAGG 720  
  
QY 5096 TAGATGCGAGGAAGATGAAGAAGACCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAAT 5155  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 721 TAGATGACGAGGAAGATGAAGAAGACCTTGGTGAAGAAGAAAGGGTCAAGAAGCGAAAC 780  
  
QY 5156 GAGAACCTGAAGATGAGGAGAGAGATGATGACTAAGTAGAATAAAGCTATTTTGAAGAAAT 5215  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 781 GAGAACCTGAAGATGAGGAGAGAGATGATGACTAAGTGAATAAAGCTATTTTGAAGAAAT 840  
  
QY 5216 CCTATTGTGATTTGACTGTTTTTACCATATCCCTC-----CCCCCTCCCAATCCTGCC 5269  
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 841 CCTATTGTGATTTGACTGTTTTTACCATATCCCTC-----CCCCCTCCCAATCCTGCC 900  
  
QY 5270 CCCTGAA 5276  
      ||||| |||||  
Db 901 CCCTGAA 907
```

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QY 5036 AAGAGGAGACGTGAGTGGAGGACGAGGAGGATGAAGAAGTTTATAACGATGAGAGG 5095
|||||
Db 661 AAGAGGAGACGTGAGTGGAGGAGGAGGAGGATGAAGAAGTTTATAACGATGAGAGG 720
|||||
QY 5096 TAGATGGCGAGAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAT 5155
|||||
Db 721 TAGATGACGAGAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAC 780
|||||
QY 5156 GAGAACCTGAAGATGAGGAGAAAGATGATGACTAAGTAGATACCTATTTTGAATAAT 5215
|||||
Db 781 GAGAACCTGAAGATGAGGAGAAAGATGATGACTAAGTAGATACCTATTTTGAATAAT 840
|||||
QY 5216 CCTATTGTGATTGACTGTTTTTACCATATCCCT-----CCCCCTCCCAATCCTGCC 5269
|||||
Db 841 CCTATTGTGATTGACTGTTTTTACCATATCCCTCTCCCCCCCCCTCTAATCCTGCC 900
|||||
QY 5270 CCCTGAA 5276
|||||
Db 901 CCCTGAA 907
|||||

RESULT 12
US-10-273-334-32
; Sequence 32, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR FILING DATE: 1998-12-11
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-32

Query Match 13.0%; Score 751.6; DB 6; Length 908;
Best Local Similarity 92.5%; Pred. No. 1.2e-71;
Matches 840; Conservative 0; Mismatches 49; Indels 19; Gaps 4;

QY 4388 GGGTTCGAGCTTATTCATTGAATTCGGCTGGCCAGCAGACGCTCTCGACAGAGAGCGC 4447
|||||
Db 1 GGGTTCGGGGTTATTGAATGAATTCGCGCGCGGGAGCCCTCTCGACAGAGAGAGCGC 60
|||||
QY 4448 -GAGAGATGAGATGGCAGACGAGTTCATTACAGAGCTGGGAAACAGGGCGCTCTGAT 4506
|||||
Db 61 GGAGAGATGAGATGGCAGACGAGTTCATTAGAGCTGGGAAACAGAGCGCCCTCTGAT 120
|||||
QY 4507 GTGAAGAAGTTCGCTGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACA 4566
|||||
Db 121 GTGAAGAAGTTCGCTGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACA 180
|||||
QY 4567 GATGAATTCGAAGTGGAACTTTAAGTAAATCAACGGAGGCTCAGCTCAATCTCA 4626
|||||
Db 181 GATGAATTCGAAGTGGAACTTTAAGTAAATCAACGGAGGCTCAGCTCAATCTCA 240
|||||
QY 4627 GACTTACCAAGTTA---AAGTTGAGAAAGCTTGAAGT-----AGAGTCTCAGG 4674
|||||
Db 241 AACTTACCAAGTTAACAAGTCTAGAGCTTGAAGTGAAGTGAAGTGAAGTCTCAGG 300
|||||
QY 4675 GGCTTGAAGTATGGCAGAAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAAC 4734
|||||
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Db 301 GGCTTGAAGTATGGCAGAAAAAGTGTCCGAACCTCACGCATCTAAATTTAAGTGGCAAC 360
|||||
QY 4735 AAAATTTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACTCAAGAGCTTA 4794
|||||
Db 361 AAAATTTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACTCAAGAGCTTA 420
|||||
QY 4795 GACCTTTTCAATTTGCCAGGTACCAACCTGACGACTACGGAGAAAAACCTGTTCAAGCTT 4854
|||||
Db 421 GACCTTTTCAATTTGCCAGGTACCAACCTGACGACTACGGAGAAAAACCTGTTCAAGCTT 480
|||||
QY 4855 CTCTCTCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCA 4914
|||||
Db 481 CTCTCTCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCG 540
|||||
QY 4915 GATATTGAGGACACCTGAGGAGGCTTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAG 4974
|||||
Db 541 GATGCTGAGGGCTACGTTGAGGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 600
|||||
QY 4975 TATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 5034
|||||
Db 601 TATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAG 660
|||||
QY 5035 GAAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAAGTTTATAACGATGAGAG 5094
|||||
Db 661 GAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGTTTATAACGATGAGAG 720
|||||
QY 5095 GTAGATGGCGAGGAGAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAA 5154
|||||
Db 721 GTAGATGACGAGGAGAGATGAAGAAGAGCTTGGTGAAGAAGAGGGGTGAGAAGCGAAAA 780
|||||
QY 5155 TGAGAACCTGAAGATGAGGAGGAGAGATGATGACTAAGTAGAATACCTATTTTGAATAAT 5214
|||||
Db 781 CGAGAACCTGAAGATGAGGAGGAGAGATGATGACTAAGTAGAATACCTATTTTGAATAAT 840
|||||
QY 5215 TCCTATTGTGATTGACTCTTTTACCCATATCCCT-----CCCCCTCCCAATCCTGCC 5268
|||||
Db 841 TCCTATTGTGATTGACTCTTTTACCCATATCCCTCTCCCCCCCCCTCTAATCCTGCC 900
|||||
QY 5269 CCCTGAA 5276
|||||
Db 901 CCCTGAA 908
|||||

RESULT 13
US-10-273-334-30
; Sequence 30, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(455)
; OTHER INFORMATION:
US-10-273-334-30
```

```
Query Match      12.6%; Score 727.4; DB 6; Length 907;
Best Local Similarity 90.2%; Pred. No. 4.1e-69;
Matches 818; Conservative 0; Mismatches 71; Indels 18; Gaps 3;

QY 4388 GGGTTCGAGGTTATGATGTAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 4447
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1 GGGTTCGGGGTTATGATGTAATTCGGCTGGCAGAGAGCCTCTGCAGAGAGAGAGCGC 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4448 GAGAGATGAGATGGCAGACGATTCATTCAGAGCTCGGGAACAGAGCGCCCTCTGATG 4507
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      61 GAGAGATGAGATGGCAGACGATTCATTCAGAGCTCGGGAACAGAGCGCCCTCTGATG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4508 TGAAGAACTTCCTCGGACACAGCTCGTGAATGAGGCAAACTCGAAGCCTCTCACAG 4567
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      121 TGAAGAACTTCCTCGGACACAGCTCGTGAATGAGGCAAACTCGAAGCCTCTCACAG 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4568 ATGAATTTGAAGAACTGGAATTTTAAATCAAGAGGCGCTACCTCAATCTCAG 4627
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      181 ATGAATTTGAAGAACTGGAATTTTAAATCAAGAGGCGCTACCTCAATCTCAG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4628 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 4675
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      241 ACTTACCAAGTTAAGAAAGCTTGAAGAGCTTGAAGAGTAAACAGAGTCTCAGGG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4676 GCGTGAAGTATTGGCAGAAAGTGTCCAAACCTTCACGCATCTATATTTAAGTGGCAACA 4735
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      301 GCGTGAAGTATTGGCAGAAAGTGTCCAAACCTTCATACATCTAATTTAAGTGGCAACA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4736 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTGTAGAAAACCTCAAGAGCTTAG 4795
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAGTGTAGAAAACCTCGAGAGCTTAG 420
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4796 ACCTTTTCAATTCGGAGGTACCAACCTGAACAGTGTGATGAGGAAACGTTTCAAGCTTC 4855
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      421 ACCTTTTCAATTCGGAGGTACCAACCTGAACAGTGTGATGAGGAAAGATGTTCAGCTCC 480
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4856 TCCTGCAACTCACATCTCAGACAGCTGTACTGGGACCAAGAGGAGGAGGAGGAGGAGGAGG 4915
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      481 TCCTGCAACTCACATCTCAGACAGCTGTACTGGGACCAAGAGGAGGAGGAGGAGGAGGAGG 540
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4916 ATATTGAGGACCGTGGAGGCGCTGGATGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGT 4975
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      541 ATGGTGGAGGCGCTGGATGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 600
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4976 ATGATGAAGTCTCAGGTAGTGAAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 5035
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      601 ATGATGAAGTCTCAGGTAGTGAAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 5036 AAGAGGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 5095
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      661 AAGAGGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 720
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 5096 TAGATGGCAGGAGAGATGAAGAGAGCTTGGTGAAGAAAGAGGAGGAGGAGGAGGAGGAGT 5155
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      721 TAGATGGCAGGAGAGATGAAGAGAGCTTGGTGAAGAAAGAGGAGGAGGAGGAGGAGGAGT 780
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 5156 GAGAACTGAAGATGAGGAGAGAGATGATGACTTAAGTGAATAAATCTATTTTGAATAAT 5215
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      781 GAGAACTGAAGATGAGGAGAGAGATGATGACTTAAGTGAATAAATCTATTTTGAATAAT 840
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 5216 CCTATTGTGATTTGACTGTTTTTACCCATATCCCTT-----CCGCCCTCCCAATCCTGCC 5269
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      841 CCTATTGTGATTTGACTGTTTTTACCCATATCCCTTCCGCCCTCCCAATCCTGCC 900
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 5270 CCCTGAA 5276
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      901 CCCTGAA 907
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-10-273-334-4
; Sequence 4, Application US/10273334
```

```
GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-273-334-4
```

```
Query Match      12.4%; Score 716; DB 6; Length 907;
Best Local Similarity 89.2%; Pred. No. 6.4e-68;
Matches 799; Conservative 0; Mismatches 85; Indels 12; Gaps 2;

QY 4388 GGGTTCGAGGTTATGATGTAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 4447
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      1 GGGTTCGGGGTTATGATGTAATTCGGCTGGCAGAGAGCCTCTGCAGAGAGAGAGCGC 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4448 GAGAGATGAGATGGCAGACGATTCATTCAGAGCTGCGGAACAGAGGCGCCCTCTGATG 4507
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      61 GAGAGATGAGATGGCAGACGATTCATTCAGAGCTGCGGAACAGAGGCGCCCTCTGATG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4508 TGAAGAACTTCCTCGGACACAGTGTGATGAGGCAAACTCGAAGCCTCTCACAG 4567
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      121 TGAAGAACTTCCTCGGACACAGTGTGATGAGGCAAACTCGAAGCCTCTCACAG 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4568 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACAGGAGGCGCTCACCTCAATCTCAG 4627
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACAGTGTGAGGCAAACTCACCTCAATCTCAG 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4628 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 4675
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      241 ACTTACCAAGTTAAGAAAGCTTGAAGAGCTTGAAGAGTAAACAGAGCCTCAGTGG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 4676 GCGTGAAGTATTGGCAGAAAGTGTCCAAACCTTCACGCATCTATATTTAAGTGGCAACA 4735
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      301 GCGTGAAGTATTGGCAGAAAGTGTCCAAACCTTCATACATCTAATTTAAGTGGCAACA 360
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QY 4916 ATATTGAGGACCGTGGAGGCGCTGGATGAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGT 4975
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QY 4976 ATGATGAAGTCTCAGGTAGTGAAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 5035
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QY 5156 GAGAACTGAAGATGAGGAGAGAGATGATGACTTAAGTGAATAAATCTATTTTGAATAAT 5215
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Qy 5216 CCTATTGTGATTTGACTGTTTTTACCATATCCCTCCCTCCCAATCCCTGCC 5271

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RESULT 15

US-10-273-334-11

; Sequence 11, Application US/10273334

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kocheavar, Gerald J.

; APPLICANT: Brody, Jonathan R.

; APPLICANT: Kodkol, Shriharis S.

; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

; FILE REFERENCE: 031787.0076

; CURRENT APPLICATION NUMBER: US/10/273,334

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: US/09/591,500

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: PCT/US98/26433

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 11

; LENGTH: 905

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (64)..(810)

; OTHER INFORMATION:

US-10-273-334-11

Query Match 12.3%; Score 711.8; DB 6; Length 905;

Best Local Similarity 89.9%; Pred. No. 1.8e-67;

Matches 815; Conservative 0; Mismatches 72; Indels 20; Gaps 4;

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Qy 4448 GAGAGATGGAGATGGGACAGCGATTTCATTCAGATCGGGAACAGGGCGCCCTCGATG 4507

Db 59 GAGAGATGGAGATGGGCAATGGAATTCATTTAGAGCTGGGACAGAGCGCCCTCGATG 118

Qy 4508 TGAAGAACTTCGCCCTGGACACAGTCGGTCCGAATGAAGCAACCTGCAAGCCCTCACAG 4567

Db 119 TGAAGAACTTTTCCTGGACACAGTCAGTCAATGAAGCAAAATTTGGAAGCCCTCACAG 178

Qy 4568 ATGAATTTGAAGAACTTGAATTTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 4627

Db 179 ATGAATTTGAAGAACTTGAATTTTAAATCAATCAATAGGCCCTCACCTCAATTCGAA 238

Qy 4628 ACTTACCAAGTTA---AAGTTCAGAAAGCTTGAACTA-----AGAGTCTCAGGGG 4675

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Qy 4856 TCCGTCAACTCAATATCTCGACAGCTGTTACTTGGGACCACAAAGAGGCCCTTACTCAG 4915

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Search completed: December 8, 2002, 21:29:45

Job time : 294 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 21:38:13 : Search time 2141.32 Seconds
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Title: US-09-591-500-3

Perfect score: 889

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 24791104 seqs, 12571243825 residues

Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	889	100.0	5785	22	US-09-591-500-1	Sequence 1, Appli
3	866.6	97.5	895	22	US-09-591-500-15	Sequence 15, Appli
4	865	97.3	895	22	US-09-591-500-21	Sequence 21, Appli
5	839.4	94.4	895	22	US-09-591-500-23	Sequence 23, Appli
6	831.4	93.5	907	22	US-09-591-500-6	Sequence 6, Appli
7	764.2	86.0	1197	30	US-09-760-469-94	Sequence 94, Appli
8	764.2	86.0	1197	42	US-10-216-583-94	Sequence 94, Appli
9	764.2	86.0	1595	25	US-09-644-871-8887	Sequence 8887, Ap
10	764.2	86.0	1595	25	US-09-649-164-9117	Sequence 9117, Ap
11	764.2	86.0	1595	25	US-09-652-913-10130	Sequence 10130, A
12	764.2	86.0	1595	27	US-09-699-998-8868	Sequence 8868, Ap
13	764.2	86.0	1595	27	US-09-699-999-6021	Sequence 6021, Ap
14	764.2	86.0	1595	28	US-09-710-281-4371	Sequence 4371, Ap
15	764.2	86.0	1595	28	US-09-710-286-2968	Sequence 2968, Ap
16	764.2	86.0	1595	28	US-09-716-973-2254	Sequence 2254, Ap
17	764.2	86.0	1595	29	US-09-726-172-2050	Sequence 2050, Ap
18	764.2	86.0	1595	29	US-09-726-788-6017	Sequence 6017, Ap
19	764.2	86.0	1595	29	US-09-726-810-3350	Sequence 3350, Ap
20	764.2	86.0	1595	29	US-09-726-811-4774	Sequence 4774, Ap
21	764.2	86.0	2447	17	US-09-359-922-2129	Sequence 2129, Ap

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24 764.2 86.0 2449 30 US-09-760-469-601 Sequence 601, Ap
25 764.2 86.0 2449 42 US-10-216-583-601 Sequence 601, Ap
26 762.6 85.8 907 22 US-09-591-500-13 Sequence 13, Appl
27 762.2 85.7 3955 36 US-09-976-594-207 Sequence 207, Ap
28 762.2 85.7 3955 68 US-60-240-409-207 Sequence 207, Ap
29 761 85.6 907 22 US-09-591-500-25 Sequence 25, Appl
30 761 85.6 1052 1 PCT-US02-25766-3866 Sequence 3866, Ap
31 761 85.6 2398 16 US-09-205-070-14975 Sequence 14975, A
32 761 85.6 2398 17 US-09-340-623-14975 Sequence 14975, A
33 761 85.6 2398 33 US-09-898-888-14975 Sequence 14975, A
34 761 85.6 2398 33 US-09-898-888A-14975 Sequence 33, Appl
35 760.2 85.5 906 22 US-09-591-500-33 Sequence 33, Appl
36 757.8 85.2 907 22 US-09-591-500-28 Sequence 28, Appl
37 756.2 85.1 916 14 US-09-038-847A-2 Sequence 2, Appl
38 756.2 85.1 916 17 US-09-393-302-25 Sequence 25, Appl
39 756.2 85.1 916 31 US-09-825-886-25 Sequence 9, Appl
40 753 84.7 908 22 US-09-591-500-9 Sequence 32, Appl
41 751.6 84.5 908 22 US-09-591-500-32 Sequence 12193, A
42 742 83.5 1155 1 PCT-US01-08631-12193 Sequence 13384, A
43 735.6 82.7 6753 61 US-60-172-373-13384 Sequence 30, Appl
44 727.4 81.8 907 22 US-09-591-500-30 Sequence 245, Ap
45 720.2 81.0 925 37 US-09-997-722-245

ALIGNMENTS

RESULT 1
US-09-591-500-3
; Sequence 3, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-591-500-3

Query Match 100.0%; Score 889; DB 22; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.4e-158;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GGTTTCAGGTTTATTGATTGATTCGGCTGGCAGAGAGCCCTCTGCACAGAGAGCGC 60
QY 61 GAGAGATGAGATGGCAGACGATTTCATTACAGAGCTGGGAAACAGGGCGCCCTCTGATG 120
DB 61 GAGAGATGAGATGGCAGACGATTTCATTACAGAGCTGGGAAACAGGGCGCCCTCTGATG 120
QY 121 TGAAGAAGCTTCCCTGGACACAGTCGGTCCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
DB 121 TGAAGAAGCTTCCCTGGACACAGTCGGTCCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGGAATCTTAAAGTAAATCAACGAGGCGCTCACTCAATCTCAG 240
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QY 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTTGAACTAAGAGTCTCAGGGGCGCTGGAAGTAT 300
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QY 541 ACCTGGAGGCGCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGTATGATGAAGATG 600
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QY 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 889
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RESULT 2
US-09-591-500-1
; Sequence 1, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5785
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (4453)..(5154)
; OTHER INFORMATION:
US-09-591-500-1

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DB				
QY	61	GAGAGATGGAGATGGGCAGACGAGATTCAATTCAGAGCTGCGGAACAGGGCGCCCTCTGATG	120	
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QY	301	TGCGAGAAAAGTCTCCAAACCTCAACGATCTATATTAACTGGCAACAAAATTAAGACC	360	
DB				
QY	301	TGCGAGAAAAGTCTCCAAACCTCAACGATCTATATTAACTGGCAACAAAATTAAGACC	360	
DB				
QY	361	TCAGCACAATFAGGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTTAGACCTTTTCAATT	420	
DB				
QY	361	TCAGCACAATFAGGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTTAGACCTTTTCAATT	420	
DB				
QY	421	GCAGGTAACCAACCTGAAGGACTACGGAGAAAACGTGTTCAAGCTTTCCTGCAACTCA	480	
DB				
QY	421	GCAGGTAACCAACCTGAAGGACTACGGAGAAAACGTGTTCAAGCTTTCCTGCAACTCA	480	
DB				
QY	481	CATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAGATATTGAGGACC	540	
DB				
QY	481	CATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAGATATTGAGGACC	540	
DB				
QY	541	ACGTGGAGGCCCTGGATGACGAGGAGGAGGGTGAGCATGAGGAGGAGTATGATGAAGATG	600	
DB				
QY	541	ACGTGGAGGCCCTGGATGACGAGGAGGAGGGTGAGCATGAGGAGGAGTATGATGAAGATG	600	
DB				
QY	601	CTCAGGTAGTGGAAATGAGGAGGGCGAGAGGAGGAGGAAGGTGAAGAGGAGGACG	660	
DB				
QY	601	CTCAGGTAGTGGAAATGAGGAGGGCGAGAGGAGGAGGAAGGTGAAGAGGAGGACG	660	
DB				
QY	661	TGAGTGGAGGGGACGAGGAGGATGAAGAAGTTATACCATGCGAGAGGTAGATGCCGAG	720	
DB				
QY	661	TGAGTGGAGGGGACGCGGAGGATGAAGAAGTTATACCATGCGAGAGGTAGATGCCGAG	720	
DB				
QY	721	AAGATGAAGAAGAGCTTGTTGAAGAAGAAGGGGCTCAGAAGCGGAAAATCAGAACCTGAAG	780	

[illegible]

Db 721 RAGATGAAGAGAGCTTGGTGAAGAGAAAGGGTCAAGACGAAATGAGAACCTGAAG 780
QY 781 ATGAGGGAGAGATGATGACTAAAGTAGAATAACCTATTTTGAAGAAATTCCTATTGTGATT 840
Db 781 ATGAGGGAGAGATGATGACTAAAGTAGAATAACCTATTTTGAAGAAATTCCTATTGTGATT 840
QY 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCC 873
Db 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCC 873

RESULT 4
US-09-591-500-21
; Sequence 21, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-09-591-500-21

Query Match 97.3%; Score 865; DB 22; Length 895;
Best Local Similarity 99.3%; Pred. No. 5.le-154;
Matches 867; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGSTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCAGAGAGCTCTGCAGACAGAGAGCGC 60
QY 61 GAGAGATGAGATGGCAGACGAGATTTCATTCAGAGCTGCGGAACAGGCGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGCAGACGAGATTTCATTCAGAGCTGCGGAACAGGCGCCCTCTGATG 120
QY 121 TGAAGAACTTGCCTGGACACAGTCGGTCAATTAAGGCAAACTCGAAGCCCTCAG 180
Db 121 TGAAGAACTTGTCTGGACACAGTCGGTCAATTAAGGCAAACTCGAAGCCCTCAG 180
QY 181 ATCAATTTGAAGAACTTGAATTTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAACTTGAATTTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
QY 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAACACTAAGAGTCTCAGGGGCGCTGGAAGTAT 300
Db 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAACACTAAGAGTCTCAGGGGCGCTGGAAGTAT 300
QY 301 TGGCAGAAAGTGTCCAAACCTCAGGCATCTATATTAAAGTGGCAACAAATTAAGACC 360
Db 301 TGGCAGAAAGTGTCCAAACCTCAGGCATCTATATTAAAGTGGCAACAAATTAAGACC 360
QY 361 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACTCAAGAGCTTAGACCTTTTCAATT 420
Db 361 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACTCAAGAGCTTAGACCTTTTCAATT 420
QY 421 GCGAGGTAAACCACTGAAACGACTACGGAGAAAACGTTGTTCAAGCTTCTCTGCAACTCA 480

Db 421 GCGAGGTAAACCACTGAAACGACTACGGAGAAAACGTGTTCAAGCTTCTCTGCAACTCA 480
QY 481 CATATCTCGACACTCTTACTGGACCAAGAGAGCCCTTACTCAGATATTGAGGACC 540
Db 481 CATATCTCGACACTCTTACTGGACCAAGAGAGCCCTTACTCAGATATTGAGGACC 540
QY 541 ACCTGGAGGCGCTTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATG 600
Db 541 ACCTGGAGGCGCTTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATG 600
QY 601 CTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 601 CTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 661 TGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATTAACGATGGAGAGTAGATGGCGAGG 720
Db 661 TGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATTAACGATGGAGAGTAGATGGCGAGG 720
QY 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAGGCGGAAATGAGAACCTGAAG 780
Db 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAGGCGGAAATGAGAACCTGAAG 780
QY 781 ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTTTGAAGAAATTCCTATTGTGATT 840
Db 781 ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTTTGAAGAAATTCCTATTGTGATT 840
QY 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCC 873
Db 841 TGACTGTTTTTACCCTATCCCTCCCTCCCTCC 873

RESULT 5
US-09-591-500-23
; Sequence 23, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-09-591-500-23

Query Match 94.4%; Score 839.4; DB 22; Length 895;
Best Local Similarity 97.5%; Pred. No. 3.6e-149;
Matches 851; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGACAGAGCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCGCGCGGAGAGCCTCTGCAGAGAGGAGCGC 60
QY 61 GAGAGATGGAGATGGCAGAGCGGATTTCATTTCAGAGCTTCGGGAACAGAGCGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGCAGAGCGGATTTCATTTCAGAGCTTCGGGAACAGAGCGCCCTCTGATG 120
QY 121 TGAAGAACTTGCCTCGGACAGACAGTGGTCAATTAAGGCAAACTCGAAGCCCTCAG 180

||||| 121 TGAAGAAGAACTTGTCCTGACAAACAGTCGGTCGATGAAGGCAAACTCGAAGGCTCACAG 180
Qy 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCTCACCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCTCACCTCAATCGCAA 240
Qy 241 ACTTACCAAAAGTTAAAGTTGAGAAGCTTGAACCTAAGAGTCTCAGGGGCTCGAAGTAT 300
Db 241 ACTTACCAAAAGTTAAAGTTGAGAAGCTTGAACCTAAGAGTCTCAGGGGCTCGAAGTAT 300
Qy 301 TGGCAGAAAAGTGTCACAACTCACGACTATATATTTAAGTGGCAACAAAATTAAGAGACC 360
Db 301 TGGCAGAAAAGTGTCACAACTCACGACTATATATTTAAGTGGCAACAAAATTAAGAGACC 360
Qy 361 TCAGCAATAAGAGCCACTGAACAGTTAGAAACCTCAAGAGCTTAGAGCTTTTCAATT 420
Db 361 TCAGCAATAAGAGCCACTGAACAGTTAGAAACCTCAAGAGCTTAGAGCTTTTCAATT 420
Qy 421 GCGAGGTAACCAACCTGAAGGACTTACGAGAAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Db 421 GCGAGGTAACCAACCTGAAGGACTTACGAGAAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Qy 481 CATATCTCGACAGCTGTTACTTGGGACCAAGAGGCCCCCTTACTCAGATATTGAGGACC 540
Db 481 CATATCTCGACAGCTGTTACTTGGGACCAAGAGGCCCCCTTACTCAGATATTGAGGACC 540
Qy 541 ACGTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGATGATGAAGATG 600
Db 541 ACGTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGATGATGAAGATG 600
Qy 601 CTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGTGAAGAGGAGGAGC 660
Db 601 CTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGTGAAGAGGAGGAGC 660
Qy 661 TGAGTGAGGCGGAGGAGGAGGATGAAGAAGGTTATTAACGATGGAGAGGTAGATGATG 720
Db 661 TGAGTGAGGCGGAGGAGGAGGATGAAGAAGGTTATTAACGATGGAGAGGTAGATGATG 720
Qy 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTGAAGAAGGAGGAGGAGGAGGAG 780
Db 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTGAAGAAGGAGGAGGAGGAGGAG 780
Qy 781 ATGAGGAGAGGATGATGACTAAGTGAATAACCTATTTTGAATAATTCCTATTGTGATT 840
Db 781 ATGAGGAGAGGATGATGACTAAGTGAATAACCTATTTTGAATAATTCCTATTGTGATT 840
Qy 841 TGACTGTTTTACCCATATCCCTCCCTCCCTCC 873
Db 841 TGACTGTTTTACCCATATCCCTCCCTCCCTCC 873

RESULT 6
US-09-591-500-6
; Sequence 6, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkoi, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 907
; TYPE: DNA

i ORGANISM: Homo sapiens
US-09-591-500-6

Query Match 93.5%; Score 831.4; DB 22; Length 907;
Best Local Similarity 97.4%; Pred. No. 1.2e-147;
Matches 883; Conservative 0; Mismatches 6; Indels 18; Gaps 3;

Qy 1 GGGTTCGAGGTTTATTGATTGGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGAGGTTTATTGATTGGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
Qy 61 GAGAGATGAGATGGCAGACGSAATTCATTAGAGCTCGGAACAGGGCGCCCTCTGATG 120
Db 61 GAGAGACGAGATGGCAGACGSAATTCATTAGAGCTCGGAACAGGGCGCCCTCTGATG 120
Qy 121 TGAAGAAGCTTCCCTTGGACACAGTCGCTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 121 TGAAGAAGCTTCCCTTGGACACAGTCGCTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Qy 181 ATCAATTTGAAGAACTTGAATTTCTTAAGTAAATCAACGGAGGCTCACCCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAACTTGAATTTCTTAAGTAAATCAACGGAGGCTCACCCTCAATCTCAG 240
Qy 241 ACTTACCAAAAGTTA--AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
Db 241 ACTTACCAAAAGTTAACAAGTTGAGAAAGCTTGAAGAGCTTAACAGAGTCTCAGGG 300
Qy 289 GCTTGGAGATTTGGCAGAAAAGTGTCCAACCTCAGCATCTATATTTAAGTGGCAACA 348
Db 301 GCTTGGAGATTTGGCAGAAAAGTGTCCAACCTCAGCATCTATATTTAAGTGGCAACA 360
Qy 349 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 361 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 420
Qy 409 ACCTTTTCAATTCGAGGTAAACCAACCTGAAGGACTAGGAGAAACGTTTCAAGCTTC 468
Db 421 ACCTTTTCAATTCGAGGTAAACCAACCTGAAGGACTAGGAGAAACGTTTCAAGCTTC 480
Qy 469 TCCTGCAACTACATATCTCGACAGCTGTACTGGGACCACAAGAGGCCCTTACTCAG 528
Db 481 TCCTGCAACTACATATCTCGACAGCTGTACTGGGACCACAAGAGGCCCTTACTCAG 540
Qy 529 ATATTGAGGACCACTGGAGGCGCTGGATGACGAGGAGGAGGCTCAGCATGAGGAGGAGT 588
Db 541 ATATTGAGGCGCCACCTGGAGGCGCTGGATGACGAGGAGGAGGCTCAGCATGAGGAGGAGT 600
Qy 589 ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGT 648
Db 601 ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGT 660
Qy 649 AAGAGGAGCAGTGTAGTGGAGGACGAGGAGGATGAAGAAGGTTTAAACGATGAGAGG 708
Db 661 AAGAGGAGCAGTGTAGTGGAGGACGAGGAGGATGAAGAAGGTTTAAACGATGAGAGG 720
Qy 709 TAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAGGAGGCTCAGAAAGGAGT 768
Db 721 TAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAGGAGGCTCAGAAAGGAGT 780
Qy 769 GAGAACCTGAAGATGAGGAGGAAGATGACTAAGTGAATAACCTATTTTGAATAAT 828
Db 781 GAGAACCTGAAGATGAGGAGGAAGATGACTAAGTGAATAACCTATTTTGAATAAT 840
Qy 829 CCTATTGTGATTGACTGTTTTACCCTATATCCCT-----CCCCCTCCTCCTGCC 882
Db 841 CCTATTGTGATTGACTGTTTTACCCTATATCCCTCCTCCTCCTCCTCCTCCTCCTGCC 900
Qy 883 CCCTGAA 889
Db 901 CCCTGAA 907

RESULT 7

Db	334	AC	TTACCAAAAGTTAAACAAACTTAAGAAGCTTGAACATAAGCGATAACAGAGTCTCAGGGG	393
QY	289	GC	CTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCACTATATTTAAAGTGGCAACA	348
Db	394	GC	CTGGAAGTATTGGCAGAAAAAGTGTCCGAACCTCAGCACTTAATTTAAAGTGGCAACA	453
QY	349	AA	ATTAAGACCTCAGCACAAATAGAGCCACTGAACAGTTTAGAANAACCTCAAGAGCTTAG	408
Db	454	AA	ATTAAGACCTCAGCACAAATAGAGCCACTGAANAAGTTAGAAAACCTCAAGAGCTTAG	513
QY	409	AC	CTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGGAGAAAAAGTGTTCAAGCTTC	468
Db	514	AC	CTTTTCAATTGCGAGGTAAACCAACCTGAACGACTACCGAGAAAATGTGTTCAAGCTCC	573
QY	469	TC	CTGCAACTCACATATCTCGACAGCTGTACTGGACCAACAGGAGGCCCTTACTCAG	528
Db	574	TC	CGCAACTCACATATCTCGACGGCTATGACCGGACGACAAAGGAGGCCCTGACTCGG	633
QY	529	AT	ATTGAGGACCACTGGAGGGCCTGGATCACGAGCAGGAGGCTGACATGAGGAGGAGT	588
Db	634	AT	CTGAGGGCTACGTTGAGGGCCTGGATGATGAGGAGGAGTGAAGATGAGGAGGAGT	693
QY	589	AT	GATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGAGGAGGAGGAGGAGGAGTG	648
Db	694	AT	GATGAAGATGCTCAGGTAGTGGAAAGCAGGAGGAGGAGGAGGATGAGGAGGAGGAGTG	753
QY	649	AA	GAGGAGCAGCTGAGTGGAGGGACGAGGAGGATGAAGAAGTTATACGATGGAGAGG	708
Db	754	AA	GAGGAGCAGCTGAGTGGAGAGGAGGAGGAGGATGAAGAAGTTATACGATGGAGAGG	813
QY	709	TAG	TGCGAGGAGGAAGATGAAGAAGACTTGGTCAACAAGAAAGGGCTCAGAACCGAAAT	768
Db	814	TAG	TGACGAGGAAGATGAAGAAGACTTGGTGAAGAAGAAGGGCTCAGAACCGAAAC	873
QY	769	GAG	AACTGGAAGATGAGGGGAGAAGATGATGACTAAGTAGAATAACCTATTTTGAATAATT	828
Db	874	GAGA	AACTGGAAGATGAGGGGAGAAGATGATGACTAAGTGAATAACCTATTTTGAATAATT	933
QY	829	CC	TATTGTGATTTGACTGTTTTTACCACATATCCCCCT-----CCCCCTCCAACTCTGCC	882
Db	934	CC	TATTGTGATTTGACTGTTTTTACCACATATCCCCCTCCCCCCCCCTCCAACTCTGCC	993
QY	883	CC	CTGAA 889	
Db	994	CC	CTGAA 1000	

```

RESULT 9
US-09-644-871-8887
; Sequence 8887, Application US/09644871
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1167-001
; CURRENT APPLICATION NUMBER: US/09/644, 871
; CURRENT FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: 60/151,059
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 9739
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8887
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-644-871-8887

```

Query Match 86.0%; Score 764.2; DB 25; Length 1595;

	Best Local Similarity	92.7%;	Pred. NO. 7e-135;	Mismatches	0;	Mismatches	48;	Indels	18;	Gaps	3;
	Matches	841;	Conservative	0;	Mismatches	48;	Indels	18;	Gaps	3;	
QY	1	GGGTTTCGAGGTTTATTTGAATTTCGGCTGCACGACGAGCCCTCTGCAGACAGCAGCGC	60								
Dd	257	GGGTTTCGGGTTTTATTGATTGAATTCGCCGCCGCGGNAGCCTCTGCAGAGAGAGCGC	316								
QY	61	GAGAGATGAGATGGCGACAGCGATTCATTCAGACTCGGAAACAGGCGCCCTCTGTATG	120								
Dd	317	GAGAATGGAGTGGCGACAGCGATTCATTTAGACTCGGAAACAGGACGCCCTCTGTATG	376								
QY	121	TCAAGAACTTCCTCGCATCGTGACAACAGTTCGTCGAATTAAGGCAAACCTCGAAGCCCACAG	180								
Dd	377	TGAAGAATCTCTCTGACAAACAGTTCGGTTCGATTAAGGCAAACTCGAAGCCCTCACAG	436								
QY	181	ATGAATTTGAAGAACTGGAATCTTTAAGTAAAATAAACGGAGGCCCTCACCTCAATCTCAG	240								
Dd	437	ATGAATTTGAAGAACTGGAATCTTTAAGTAAAACTCAACGTAGGCCCTCACCTCAATCGCAA	496								
QY	241	ACTTACCRAAGTAA-- -- AAGTTGAGAAAGCTTGAACTA----- AGAGTCTCAGGGG	288								
Dd	497	ACTTACCRAAGTTAAACAACTTAAGAAGCTTGAACTAAGCGATTAACGAGTCTCAGGGG	556								
QY	289	GCTTGGAAAGTATTTGGCAGAAAGTAGTGTCCAACCTCACGCATCTATATTTAAGTGGCAACA	348								
Dd	557	GCTTGGAAAGTATTTGGCAGAAAGTGTCCGAACCTCACGCATCTAATTTAAGTGGCAACA	616								
QY	349	AAATTAAGAACTTCAGCAACATAGAGCCACCTGAAACAGTTGAAAAACCTCAAGACCTTAG	408								
Dd	617	AAATTTAAAGAACTTCAGCAACATAGAGCCACCTGAAAAAGTTGAAAAACCTCAAGACCTTAG	676								
QY	409	ACCTTTTCAATTCGCAGAGTTAACCAACCTGAACGACTACGGAGAAACCTGTGTCAAGCTTC	468								
Dd	677	ACCTTTTCAATTCGCAGAGTTAACCAACCTGAACGACTACGGAGAAATGTGTCAAGCTTC	736								
QY	469	TCCTGCAACTCACATATCTCGACAGCTGTACTGGGACCAAGGAGGCCCTTACTCAG	528								
Dd	737	TCCCCCAACTCACATATCTCGACGCTATGACCGGAGACAAAGGAGGCCCTGACTCGG	796								
QY	529	ATATTGAGGACCCAGCTGGAGGCCCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGT	588								
Dd	797	ATGCTGAGGCTACGTGGAGGCCCTGGATGATGAGAGGAGGTGAGCATGAGGAGGAGT	856								
QY	589	ATGATGAAGATGCTCAGTAGTGGAAAGATGAGAGGGCGAGGAGGAGGAGGAAGGTG	648								
Dd	857	ATGATGAAGATGCTCAGTAGTGGAAAGACGAGGAGGAGGAGGAGGAAGGTG	916								
QY	649	AAGAGGAGAGCTGAGTGGAGGGACGAGGAGGATGAAGAGGTTATACNATGGAGAGG	708								
Dd	917	AAGAGGAGAGCTGAGTGGAGGAGGAGGAGGATGAAGAGGTTATACNATGGAGAGG	976								
QY	709	TAGATGGCGAGGAAGATGAAGAAGCTTGGTGAAGAAAGAGGGGTGAGAAAGCGAAAT	768								
Dd	977	TAGATGACGAGGAAGATGAAGAAGCTTGGTGAAGAAAGAGGGGTGAGAAAGCGAAAC	1036								
QY	769	GAGAACCTTGAAGATCAGGAGGAAGATGACTAAGTGAATAACCTATTTTGAAAAATT	828								
Dd	1037	GAGAACCTTGAAGATCAGGAGGAAGATGACTAAGTGAATAACCTATTTTGAAAAATT	1096								
QY	829	CCTATTGTGATTGACTGTTTACCATAATCCCT---- - CCCCCCTCAATCCTGCC	882								
Dd	1097	CCTATTGTGATTGACTGTTTACCATAATCCCT---- - CCCCCCTCAATCCTGCC	1156								
QY	883	CCCTGAA	889								
Dd	1157	CCCTGAA	1163								

RESULT 10
US-09-649-164-9117
; Sequence 9117, Application US/09649164
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.

; APPLICANT: Kingsbury, Gillian A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600 1165 001
; CURRENT APPLICATION NUMBER: US/09/649,164
; PRIOR FILING DATE: 2000-08-25
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 9995
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9117
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-649-164-9117

Query Match 86.0%; Score 764.2; DB 25; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
DB 257 GGGTTCGGGGTTTATTGATGAATTCGGCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 316
QY 61 GAGAGATGGAGTGGCAGACGGATTTCAGAGCTCGGAACAGAGCGCCCTCTGATG 120
DB 317 GAGAGATGGAGTGGCAGACGGATTTCAGAGCTCGGAACAGAGCGCCCTCTGATG 376
QY 121 TGAAGAAGCTTCGCCCTGGCAACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 180
DB 377 TGAAGAAGCTTCGCCCTGGCAACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 436
QY 181 ATGAATTTGAAGAAGCTGGAATTTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
DB 437 ATGAATTTGAAGAAGCTGGAATTTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 496
QY 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
DB 497 ACTTACCAAGTTAAGCAAACTTAAAGAAAGCTTGAAGAGCTTGAACCTAAGCGATACAGAGTCTCAGGGG 556
QY 589 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGG 648
DB 857 ATGATGAAGATGCTCAGGTAGTGGAGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 916
QY 649 AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 708
DB 917 AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 976
QY 709 TAGATGGCGAGGAAGTGAAGAGAGCTTGGTGAAGAGAGAAAGGGGTTCAGAGCGAAAT 768

DB 977 TAGATGACGAGGAAGATGAAGAGAGCTTGGTCAAGAAAGAGGGGTCAAGAGCGGAAAC 1036
QY 769 GAGAACTGAAGATGAGGAGAGATGATGACTAAGTAACTAAGTAACCTATTTTGAAGAAAT 828
DB 1037 GAGAACTGAAGATGAGGAGAGATGATGACTAAGTAACTAAGTAACCTATTTTGAAGAAAT 1096
QY 829 CCTATTGTGATTTGACTGTGTTTACCCATATCCCT-----CCCCCTCCCAATCCTGCC 882
DB 1097 CCTATTGTGATTTGACTGTGTTTACCCATATCCCTCTCCCGCCCTCCCAATCCTGCC 1156
QY 883 CCTGTAA 889
DB 1157 CCTGTAA 1163
RESULT 11
US-09-652-913-10130
; Sequence 10130, Application US/09652913
; GENERAL INFORMATION:
; APPLICANT: Falb, Dean R.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1174-001
; CURRENT APPLICATION NUMBER: US/09/652,913
; PRIOR FILING DATE: 2000-08-31
; PRIOR FILING DATE: 60/152,107
; NUMBER OF SEQ ID NOS: 10833
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10130
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-652-913-10130

Query Match 86.0%; Score 764.2; DB 25; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;
QY 1 GGGTTCGAGGTTTATTGATGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
DB 257 GGGTTCGGGGTTTATTGATGAATTCGGCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 316
QY 61 GAGAGATGGAGTGGCAGACGGATTTCAGAGCTCGGAACAGAGCGCCCTCTGATG 120
DB 317 GAGAGATGGAGTGGCAGACGGATTTCAGAGCTCGGAACAGAGCGCCCTCTGATG 376
QY 121 TGAAGAAGCTTCGCCCTGGCAACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 180
DB 377 TGAAGAAGCTTCGCCCTGGCAACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 436
QY 181 ATGAATTTGAAGAAGCTGGAATTTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
DB 437 ATGAATTTGAAGAAGCTGGAATTTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 496
QY 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
DB 497 ACTTACCAAGTTAAGCAAACTTAAAGAAAGCTTGAAGAGCTTGAACCTAAGCGATACAGAGTCTCAGGGG 556
QY 289 GCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348
DB 557 GCCTGGAAGTATTGGCAGAAAGTGTCCGAACTCAGCATCTAATTTAAGTGGCAACA 616
QY 349 AAATTAAGACCTCAGCACCAATAGAGCCACTGAAACAGATTGAAAAACCTCAAGAGCTTAG 408
DB 617 AAATTAAGACCTCAGCACCAATAGAGCCACTGAAACAGATTGAAAAACCTCAAGAGCTTAG 676
QY 409 ACCTTTTCAATTGCGAGGTTAACCAACCTGACGACTACGAGAAAGCTGTTCAAGCTTC 468

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Db 677 ACCITTTCAATTCGAGTACCAACCTGAACGACTACCGAGAAAATGTGTTCAAGCTCC 736
Qy 469 TCCTGCAACTCACATATCTGCAGAGCTGTACTGGGACCAAGAGGAGCCCTTACTCAG 528
Db 737 TCCGCAACTCACATATCTGCAGGCTATGACCGGGACGACAGGAGGCCCTGACTCGG 796
Qy 529 ATATTGAGGACCACTGAGGAGGCTGATGACGAGGAGGAGGCTGACATGAGGAGGAGT 588
Db 797 ATGCTGAGGCTACGTGAGGAGGCTGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 856
Qy 589 ATGATGAGGATCTCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 648
Db 857 ATGATGAGGATCTCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 916
Qy 649 AAGAGGAGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 708
Db 917 AAGAGGAGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 976
Qy 709 TAGATGCGGAGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 768
Db 977 TAGATGCGGAGGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 1036
Qy 769 GAGAACCTTGAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 828
Db 1037 GAGAACCTTGAAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGT 1096
Qy 829 CCTATTGTGATTTGACTGTGTTTACCATAATCCCT-----CCCCCTCCAAATCCTGCC 882
Db 1097 CCTATTGTGATTTGACTGTGTTTACCATAATCCCTCTCCCCCTCCAAATCCTGCC 1156
Qy 883 CCCTGAA 889
Db 1157 CCCTGAA 1163
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RESULT 12
US-09-699-998-8868
; Sequence 8868, Application US/09699999
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2008-001
; CURRENT APPLICATION NUMBER: US/09/699,998
; CURRENT FILING DATE: 2000-10-30
; PRIOR FILING DATE: 60/162,362
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 10905
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8868
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-699-998-8868
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Query Match 86.0%; Score 764.2; DB 27; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;

Qy 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCCTGCGAGACAGAGAGCGC 60
Db 257 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCCTGCGAGACAGAGAGCGC 316
Qy 61 GAGAGATGAGATGGGCGAGAGGATTCATTGAGCTGCGGAACAGGCGCCCTCTGATG 120
Db 317 GAGAGATGAGATGGGCGAGAGGATTCATTGAGCTGCGGAACAGAGAGAGGCGCCCTCTGATG 376
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QY 121 TGAAGAACTTGCCTGGACACACAGTCGGTCCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 377 TGAAGAACTTGCCTGGACACACAGTCGGTCCGAATGAAGGCAAACTCGAAGCCCTCACAG 436
QY 181 ATGAATTTGAAGAACTTGAATTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Db 437 ATGAATTTGAAGAACTTGAATTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 496
QY 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTTGAACATA-----AGAGTCTCAGGGG 288
Db 497 ACTTACCAAGTTA---AAGTTGAGAAAGCTTTGAACATA-----AGAGTCTCAGGGG 556
QY 289 GCCTGAAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348
Db 557 GCCTGAAAGTATTGGCAGAAAAGTGTCCGAACTCTCAGCATCTAAATTTAAGTGGCAACA 616
QY 349 AAATTAAGAACCTTCAGCACACATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 617 AAATTAAGAACCTTCAGCACACATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 676
QY 409 ACCTTTTCAATTGCGAGGTAAACCACTGAACGACTACGAGAAACACGTTTCAAGCTTC 468
Db 677 ACCTTTTCAATTGCGAGGTAAACCACTGAACGACTACGAGAAACACGTTTCAAGCTTC 736
QY 469 TCCTGCAACTCACATATCTCGACAGCTGTACTGGGACACAGAGGCGCCCTTACTCAG 528
Db 737 TCCTGCAACTCACATATCTCGACAGCTGTACTGGGACACAGAGGCGCCCTTACTCAG 796
QY 529 ATATTGAGGACCACTGAGGAGGCTGATGATGAGGAGGAGGCTGAGCATGAGGAGGAGT 588
Db 797 ATGCTGAGGAGGCTGATGATGAGGAGGAGGCTGATGATGAGGAGGAGGAGT 856
QY 589 ATGATGAAGATGCTCAGTGTAGTGTAGGAGTGTAGGAGGCGGAGGAGGAGGAGGAGT 648
Db 857 ATGATGAAGATGCTCAGTGTAGTGTAGGAGTGTAGGAGGCGGAGGAGGAGGAGGAGT 916
QY 649 AAGAGGAGGAGTGTAGTGTAGGAGGAGGAGGAGGAGTGTAGGAGGAGGAGGAGGAGT 708
Db 917 AAGAGGAGGAGTGTAGTGTAGGAGGAGGAGGAGGAGTGTAGGAGGAGGAGGAGGAGT 976
QY 709 TAGATGCGGAGGAGTGTAGTGTAGGAGGAGTGTAGTGTAGGAGGAGGAGGAGGAGT 768
Db 977 TAGATGCGGAGGAGTGTAGTGTAGGAGGAGTGTAGTGTAGGAGGAGGAGGAGGAGT 1036
QY 769 GAGAACCTTGAAGATGAGGAGGAGGAGGAGTGTAGTGTAGGAGGAGGAGGAGGAGT 828
Db 1037 GAGAACCTTGAAGATGAGGAGGAGGAGGAGTGTAGTGTAGGAGGAGGAGGAGGAGT 1096
QY 829 CCTATTGTGATTTGACTGTGTTTACCATAATCCCT-----CCCCCTCCAAATCCTGCC 882
Db 1097 CCTATTGTGATTTGACTGTGTTTACCATAATCCCTCTCCCCCTCCAAATCCTGCC 1156
QY 883 CCCTGAA 889
Db 1157 CCCTGAA 1163
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RESULT 13
US-09-699-999-6021
; Sequence 6021, Application US/09699999
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Vasicek, Thomas
; APPLICANT: Wang, Youzhan
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2032-001
; CURRENT APPLICATION NUMBER: US/09/699,999
; CURRENT FILING DATE: 2000-10-30
; PRIOR FILING DATE: 60/162,361
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 7488
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6021
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-699-999-6021

Query Match 86.0%; Score 764.2; DB 27; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;

QY 1 GGGTTCGAGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAGAGAGCGC 60
DB 257 GGGTTTCGGGGTTTATGATTGAATTCGCCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 316

QY 61 GAGAGATGGAGATGGCAGACGATTTCATTAGAGCTCGGAACAGGCGCCTCTGATG 120
DB 317 GAGAGATGGAGATGGCAGACGATTTCATTAGAGCTCGGAGACAGAGCGCCTCTGATG 376

QY 121 TGAAGAAGTTCGCCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG 180
DB 377 TGAAGAAGTTCGCCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG 436

QY 181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCTCACCCTCAATCTCAG 240
DB 437 ATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCTCACCCTCAATCTCAG 496

QY 241 ACTTACCAAGTTA---AAGTTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
DB 497 ACTTACCAAGTTA---AAGTTTGAGAACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 556

QY 289 GCGTGAAGTATGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAACA 348
DB 557 GCGTGAAGTATGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAACA 616

QY 349 AAATTAAGAACTTCGCCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG 408
DB 617 AAATTAAGAACTTCGCCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG 676

QY 409 ACCTTTTCAATTTGGCAGGTAAACCACTGAACGACTACGAGAGAAACCTGTTCAAGCTTC 468
DB 677 ACCTTTTCAATTTGGCAGGTAAACCACTGAACGACTACGAGAGAAACCTGTTCAAGCTTC 736

QY 469 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCAACAGGAGGCGCCCTTACTCAG 528
DB 737 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCAACAGGAGGCGCCCTTACTCAG 796

QY 529 ATATTGAGGACCACTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGGATGAGGAGGAGT 588
DB 797 ATATTGAGGACCACTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGGATGAGGAGGAGT 856

QY 589 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 648
DB 857 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 916

QY 649 AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGGATGAGAAGGTTATACGATGAGGAGG 708
DB 917 AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGGAGGATGAGAAGGTTATACGATGAGGAGG 976

QY 709 TAGATGCGGAGGAGATGAAGAGAGCTTGGTGAAGAGAAAGGGTTCAGAGGCGCAAAAT 768
DB 977 TAGATGCGGAGGAGATGAAGAGAGCTTGGTGAAGAGAAAGGGTTCAGAGGCGCAAAAT 1036

QY 769 GAGAAGCTGAAGATGAGGAGGAGATGATGACTAAGTAACTAATTTTGAAGAAAT 828
DB 1037 GAGAAGCTGAAGATGAGGAGGAGATGATGACTAAGTAACTAATTTTGAAGAAAT 1096

QY 829 CCTATTGATTTGACTGTTTTTACCATATCCCT------CCGCCCTTCCAAATCCTGCC 882
DB 1096 CCTATTGATTTGACTGTTTTTACCATATCCCT------CCGCCCTTCCAAATCCTGCC 940

DB 1097 CCTATTGATTTGACTGTTTTTACCATATCCCTTCCCCCCCCCTCCCAATCTCTGCC 1156

QY 883 CCCTGAA 889
DB 1157 CCCTGAA 1163

RESULT 14
US-09-710-281-4371
; Sequence 4371, Application US/09710281
; GENERAL INFORMATION:
; APPLICANT: Hunter, John J.
; APPLICANT: Shyjan, Andrew W.
; APPLICANT: Sbdal, Hilde
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2036-001
; CURRENT APPLICATION NUMBER: US/09/710, 281
; CURRENT FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 60/164, 254
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 5803
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4371
; LENGTH: 1595
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1595)
; OTHER INFORMATION: n = A,T,C or G
US-09-710-281-4371

Query Match 86.0%; Score 764.2; DB 28; Length 1595;
Best Local Similarity 92.7%; Pred. No. 7e-135;
Matches 841; Conservative 0; Mismatches 48; Indels 18; Gaps 3;

QY 1 GGGTTCGAGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAGAGAGCGC 60
DB 257 GGGTTTCGGGGTTTATGATTGAATTCGCCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 316

QY 61 GAGAGATGGAGATGGGAGAGCGGATTCATTTCAGAGCTGCGGAACAGAGGCGCCTCTGATG 120
DB 317 GAGAGATGGAGATGGGAGAGCGGATTCATTTCAGAGCTGCGGAACAGAGGCGCCTCTGATG 376

QY 121 TGAAGAAGTTCGCCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG 180
DB 377 TGAAGAAGTTCGCCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG 436

QY 181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCGCTCACCCTCAATCTCAG 240
DB 437 ATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGGAGGCGCTCACCCTCAATCTCAG 496

QY 241 ACTTACCAAGTTA---AAGTTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
DB 497 ACTTACCAAGTTA---AAGTTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 556

QY 289 GCGTGAAGTATGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAACA 348
DB 557 GCGTGAAGTATGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAACA 616

QY 349 AAATTAAGAACTTCGCCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCAGAGCTT 408
DB 617 AAATTAAGAACTTCGCCCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCAGAGCTT 676

QY 409 ACCTTTTCAATTTGGCAGGTAAACCACTGAACGACTACGAGAGAAACCTGTTCAAGCTTC 468
DB 677 ACCTTTTCAATTTGGCAGGTAAACCACTGAACGACTACGAGAGAAACCTGTTCAAGCTTC 736

QY 469 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCAACAGGAGGCGCCCTTACTCAG 528
DB 737 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCAACAGGAGGCGCCCTTACTCAG 796

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 21:58:38 ; Search time 55.4388 Seconds
(without alignments)
11105.648 Million cell updates/sec

Title: US-09-591-500-3

Perfect score: 889

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 361435 seqs, 346278564 residues

Total number of hits satisfying chosen parameters: 722870

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	889	100.0	889	6	US-10-273-334-3
2	889	100.0	5785	6	US-10-273-334-1
3	866.6	97.5	895	6	US-10-273-334-15
4	865	97.3	895	6	US-10-273-334-21
5	839.4	94.4	895	6	US-10-273-334-23
6	831.4	93.5	907	6	US-10-273-334-6
7	762.6	85.8	907	6	US-10-273-334-13
8	761	85.6	907	6	US-10-273-334-25
9	760.2	85.5	906	6	US-10-273-334-33
10	757.8	85.2	907	6	US-10-273-334-28
11	753	84.7	907	6	US-10-273-334-9
12	751.6	84.5	908	6	US-10-273-334-32
13	727.4	81.8	907	6	US-10-273-334-30
14	716	80.5	907	6	US-10-273-334-4
15	711.8	80.1	905	6	US-10-273-334-11
16	702	79.0	905	6	US-10-273-334-17
17	681.2	76.6	905	6	US-10-273-334-7
18	679.6	76.4	905	6	US-10-273-334-19
19	679.6	76.4	905	6	US-10-273-334-26
20	318.4	35.8	1937	5	US-09-724-676-18913
21	318.4	35.8	1937	5	US-09-724-676A-18913
22	132.6	14.9	147	5	US-09-513-999C-24429
23	110	12.4	3489	6	US-10-194-046-1
24	103.2	11.6	648	6	US-10-152-319A-2106
c 25	101	11.4	659158	5	US-09-771-208A-20
26	100.2	11.3	318	5	US-09-513-999C-14277

RESULT 1

US-10-273-334-3

; Sequence 3, Application US/10273334

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kochevar, Gerald J.

; APPLICANT: Brody, Jonathan R.

; APPLICANT: Kodkol, Shrihari S.

; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

; FILE REFERENCE: 031787.0076

; CURRENT APPLICATION NUMBER: US/10/273,334

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: US/09/591,500

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: PCT/US98/26433

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 889

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-273-334-3

Query Match . 100.0%; Score 889; DB 6; Length 889;

Best Local Similarity 100.0%; Pred. No. 1.1e-177;

Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GGTTTCGAGTTTATTGATTGATTCGGCTGGCAGAGAGCCCTTCGACAGAGAGCGCC	50
Db	1	GGTTTCGAGTTTATTGATTGATTCGGCTGGCAGAGAGCCCTTCGACAGAGAGCGCC	60
Qy	61	GAGAGATGGAGATGGSCAGACAGATTCATTTCAGAGCTGGGAACAGGGCCCTCTGATG	120
Db	61	GAGAGATGGAGATGGSCAGACAGATTCATTTCAGAGCTGGGAACAGGGCCCTCTGATG	120
Qy	121	TGAAGAAGTTCGCTTGGACACAGTCGGTGCAGTGAAGGCAAACTCGAAGCCCTCAG	180
Db	121	TGAAGAAGTTCGCTTGGACACAGTCGGTGCAGTGAAGGCAAACTCGAAGCCCTCAG	180
Qy	181	ATGAATTTCAAGAACTGGGAATTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTAG	240
Db	181	ATGAATTTCAAGAACTGGGAATTTAAAGTAAATCAACGAGGCGCTCACCTCAATCTAG	240
Qy	241	ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAGGGGCGCTCGGAAGTAT	300
Db	241	ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAGGGGCGCTCGGAAGTAT	300

Qy	301	TGC	GAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAAGTGGCAACAAATTTAAAGACC	360
Db	301	TGC	GAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAAGTGGCAACAAATTTAAAGACC	360
Qy	361	TCAGC	ACAATAGAGCCACTGAAACAGTTTGAANAACCTCAAGAGCTTAGACCTTTTCAATT	420
Db	361	TCAGC	ACAATAGAGCCACTGAAACAGTTTGAANAACCTCAAGAGCTTAGACCTTTTCAATT	420
Qy	421	GCAGG	TAAACACCTGAACGACTACGGAGAAAACGTGTTCAAGCTTCCTCTGCAACTCA	480
Db	421	GCAGG	TAAACACCTGAACGACTACGGAGAAAACGTGTTCAAGCTTCCTCTGCAACTCA	480
Qy	481	CATATC	TCGACAGCTGTTACTGGGACCAAGGAGGCCCTTACTCAGATATTGAGGACC	540
Db	481	CATATC	TCGACAGCTGTTACTGGGACCAAGGAGGCCCTTACTCAGATATTGAGGACC	540
Qy	541	ACGTG	GAGGGCCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATG	600
Db	541	ACGTG	GAGGGCCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATG	600
Qy	601	CTCAGG	TAGTGGGAAGATGAGGAGGGCGAGGAGGAGGAGGTGAAGAGGAGGAGG	660
Db	601	CTCAGG	TAGTGGGAAGATGAGGAGGGCGAGGAGGAGGAGGTGAAGAGGAGGAGG	660
Qy	661	TGAGT	GCAGGGGACGAGGAGGATGAAGAAGTTTATACCATGGAGAGGTAGATGCGCAGG	720
Db	661	TGAGT	GCAGGGGACGAGGAGGATGAAGAAGTTTATACCATGGAGAGGTAGATGCGCAGG	720
Qy	721	AAGAT	GAAAGAGAGCTTGGTGGAAGAAGAGGGGTGAGAAGCGAAATCAGAACCTGAAG	780
Db	721	AAGAT	GAAAGAGAGCTTGGTGGAAGAAGAGGGGTGAGAAGCGAAATCAGAACCTGAAG	780
Qy	781	ATGAGG	GAGAAGATGATGACTTAAGTAGAATAACCTATTTTGAATAATTCCTATTGTTATT	840
Db	781	ATGAGG	GAGAAGATGATGACTTAAGTAGAATAACCTATTTTGAATAATTCCTATTGTTATT	840
Qy	841	TGACTG	TTTTTACCCATATCCCTTCCCTCCCTCCCAATCTGCCCCCTCGAA	889
Db	841	TGACTG	TTTTTACCCATATCCCTTCCCTCCCTCCCAATCTGCCCCCTCGAA	889

RESULT 2

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US-10-273-334-1
; Sequence 1, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: KodkoI, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5785
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4453)..(5154)
; OTHER INFORMATION:
US-10-273-334-1

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Query Match

100.0%: Score 889: DB 6: Length 5785;

Best Local Similarity 100.08; Pred. No. 1.7e-177; Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps			
Qy	1	GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC	60
Db	4388	GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC	4447
Qy	61	GAGAGATGGAGATGGCGCAGCGGATTCATTAGAGCTCGGAAACAGGGGCCCTCTGATG	120
Db	4448	GAGAGATGGAGATGGCGCAGCGGATTCATTAGAGCTCGGAAACAGGGGCCCTCTGATG	4507
Qy	121	TGAAAGAACTTGCCTGGACACAGTCGGTGGAAATGAAGGCAAACTCGAAGCCCTCACAG	180
Db	4508	TGAAAGAACTTGCCTGGACACAGTCGGTGGAAATGAAGGCAAACTCGAAGCCCTCACAG	4567
Qy	181	ATGAATTTGAAGAACTTGAATTTCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG	240
Db	4568	ATGAATTTGAAGAACTTGAATTTCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG	4627
Qy	241	ACTTACCAAAGTTAAAGTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGGCTTGAAGTAT	300
Db	4628	ACTTACCAAAGTTAAAGTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGGCTTGAAGTAT	4687
Qy	301	TGCGAGAAAAGTCTCCAAACCTCAGCATCTATATTTAAAGTGGCAACAAAATTAAGAGCC	360
Db	4688	TGCGAGAAAAGTCTCCAAACCTCAGCATCTATATTTAAAGTGGCAACAAAATTAAGAGCC	4747
Qy	361	TCAGCACAATTAGAGCCACTGAACAGTTTGAAGAAACCTCAAGAGCTTAGACCTTTTCAATT	420
Db	4748	TCAGCACAATTAGAGCCACTGAACAGTTTGAAGAAACCTCAAGAGCTTAGACCTTTTCAATT	4807
Qy	421	GCGAGTTAACCAACCTGAACGACTACGGAGAGAAAAGTGTTCAGAGCTTCTCTGCAACTCA	480
Db	4808	GCGAGTTAACCAACCTGAACGACTACGGAGAGAAAAGTGTTCAGAGCTTCTCTGCAACTCA	4867
Qy	481	CATATCTCGACAGCTGTTACTTGGGACCACAGGAGGCCCTTACTCAGATATTGAGGACC	540
Db	4868	CATATCTCGACAGCTGTTACTTGGGACCACAGGAGGCCCTTACTCAGATATTGAGGACC	4927
Qy	541	ACGTGGAGGGCCTGGATGACGAGGAGGGGTGAGCATGAGAGGAGTATGATGAAGATG	600
Db	4928	ACGTGGAGGGCCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGTATGATGAAGATG	4987
Qy	601	CTCAGGTAGTGGAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	660
Db	4988	CTCAGGTAGTGGAGATGAGGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	5047
Qy	661	TGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATAACGATGGAGAGGTAGATGGCAGG	720
Db	5048	TGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATAACGATGGAGAGGTAGATGGCAGG	5107
Qy	721	AAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCAGAGCGAAATGAGAACTGAAG	780
Db	5108	AAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCAGAGCGAAATGAGAACTGAAG	5167
Qy	781	ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTTTGAAGAAATTCCTATTGTGATT	840
Db	5168	ATGAGGAGAGAGATGATGACTAAGTAGAATAACCTATTTTGAAGAAATTCCTATTGTGATT	5227
Qy	841	TGACTGTTTTTACCATATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA	889
Db	5228	TGACTGTTTTTACCATATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA	5276

RESULT 3

```

US-10-273-334-15
:
: Sequence 15, Application US/10273334
:
: GENERAL INFORMATION:
:
: APPLICANT: Pasternack, Gary R.
: APPLICANT: Kocheavar, Gerald J.
: APPLICANT: Brody, Jonathan R.
: APPLICANT: Kodkol, Shrihari S.
:
: TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

```

FILE REFERENCE: 031787.0076
CURRENT APPLICATION NUMBER: US/10/273,334
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: US/05/591,500
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: PCT/US98/26433
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: US 60/069,677
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 895
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (66)..(767)
OTHER INFORMATION:
US-10-273-334-15

Query Match 97.5%; Score 866.6; DB 6; Length 895;
Best Local Similarity 99.4%; Pred. No. 5.4e-173;
Matches 868; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGCGC 60
DB 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGCGC 60
QY 61 GAGAGATGGAGATGGGCAGACGGATTCAATTCAGAGCTGCGGAACAGGGCCCTCTGATG 120
DB 61 GAGAGATGGAGATGGGCAGACGGATTCAATTCAGAGCTGCGGAACAGGGCCCTCTGATG 120
QY 121 TGAAGAAGCTTGCCTGGACACAGCTCGTGAATGAAGCCAACTCGAAGCCCTCACAG 180
DB 121 TGAAGAAGCTTGCCTGGACACAGCTCGTGAATGAAGCCAACTCGAAGCCCTCACAG 180
-QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCCCTCACTCAATCTCAG 240
DB 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCCCTCACTCAATCTCAG 240
QY 241 ACTTACCAAAAGTTAAAGTTGAGAAAGCTTGAACCTAAGAGCTTCAGGGGGCTTGAAGTAT 300
DB 241 ACTTACCAAAAGTTAAAGTTGAGAAAGCTTGAACCTAAGAGCTTCAGGGGGCTTGAAGTAT 300
QY 301 TGGCAGAAAAGTTGCCAAACCTCAGCATCTATTTAAGTGAACACACAAATTTAAAGACC 360
DB 301 TGGCAGAAAAGTTGCCAAACCTCAGCATCTATTTAAGTGAACACACAAATTTAAAGACC 360
QY 361 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420
DB 361 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420
QY 421 GCGAGGTAAACCACTGAAAGCTTACGAGAAACCTGTTCAAGCTTCTCTGCAACTCA 480
DB 421 GCGAGGTAAACCACTGAAAGCTTACGAGAAACCTGTTCAAGCTTCTCTGCAACTCA 480
QY 481 CATATCTCGACAGCTGTACTGGACACCAAGAGGCCCTTACTCAGATATTGAGGACC 540
DB 481 CATATCTCGACAGCTGTACTGGACACCAAGAGGCCCTTACTCAGATATTGAGGACC 540
QY 541 ACCTGGAGGGCCCTGGATGACGAGGAGGAGGTTGAGCATGAGGAGGAGTATGATGAAGATG 600
DB 541 ACCTGGAGGGCCCTGGATGACGAGGAGGAGGTTGAGCATGAGGAGGAGTATGATGAAGATG 600
QY 601 CTCAGGTAGTGGAAAGATGAGGAGGGCAGGAGGAGGAGGAGGAGTGAAGAGGAGGACG 660
DB 601 CTCAGGTAGTGGAAAGATGAGGAGGGCAGGAGGAGGAGGAGGAGTGAAGAGGAGGACG 660
QY 661 TGAGTGGAGGGGACGAGGAGGATGAGAAAGGTTATTAACCATGGAGAGGTAGATGGCGAGG 720
DB 661 TGAGTGGAGGGGACGAGGAGGATGAGAAAGGTTATTAACCATGGAGAGGTAGATGGCGAGG 720

QY 721 AAGATCAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAGAAAGCGAAATAGAACCTGAAG 780
DB 721 AAGATCAAGAAGAGCTTGGTGAAGAAGAAAGGGTCAGAAAGCGAAATAGAACCTGAAG 780
QY 781 ATGAGGGAAGAAGATGATGACTAAGTAGAATAACCTATTATTTGAAAAATTCCTATTGTGATT 840
DB 781 ATGAGGGAAGAAGATGATGACTAAGTAGAATAACCTATTATTTGAAAAATTCCTATTGTGATT 840
QY 841 TGACTCTTTTACCCCATATCCCTCCCTCCCTCC 873
DB 841 TGACTCTTTTACCCCATATCCCATCTCCCTCC 873

RESULT 4

US-10-273-334-21
Sequence 21, Application US/10273334
GENERAL INFORMATION:
APPLICANT: Pasternack, Gary R.
APPLICANT: Kochevar, Gerald J.
APPLICANT: Brody, Jonathan R.
APPLICANT: Kodkol, Shrihari S.
TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
FILE REFERENCE: 031787.0076
CURRENT APPLICATION NUMBER: US/10/273,334
CURRENT FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: US/09/591,500
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: PCT/US98/26433
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: US 60/069,677
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 895
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (66)..(767)
OTHER INFORMATION:
US-10-273-334-21

Query Match 97.3%; Score 865; DB 6; Length 895;
Best Local Similarity 99.3%; Pred. No. 1.2e-172;
Matches 867; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGCGC 60
DB 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGCGC 60
QY 61 GAGAGATGGAGATGGGCAGACGGATTCAATTCAGAGCTGCGGAACAGGGCCCTCTGATG 120
DB 61 GAGAGATGGAGATGGGCAGACGGATTCAATTCAGAGCTGCGGAACAGGGCCCTCTGATG 120
QY 121 TGAAGAAGCTTGCCTGGACACAGCTCGTGAATGAAGCCAACTCGAAGCCCTCACAG 180
DB 121 TGAAGAAGCTTGCCTGGACACAGCTCGTGAATGAAGCCAACTCGAAGCCCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCCCTCACTCAATCTCAG 240
DB 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCCCTCACTCAATCTCAG 240
QY 241 ACTTACCAAAAGTTAAAGTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGGCTTGAAGTAT 300
DB 241 ACTTACCAAAAGTTAAAGTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGGCTTGAAGTAT 300
QY 301 TGGCAGAAAAGTTGCCAAACCTCAGCATCTATTTAAGTGGCAACAAAATTTAAAGACC 360
DB 301 TGGCAGAAAAGTTGCCAAACCTCAGCATCTATTTAAGTGGCAACAAAATTTAAAGACC 360
QY 361 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420

Db 361 TCAGCAACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420
Qy 421 GCGAGGTAAACCAACCTGACAGCTACGAGAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Db 421 GCGAGGTAAACCAACCTGACAGCTACGAGAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Qy 481 CATATCTCGACAGCTGTTACTTGGGACCACAAAGAGGCCCCCTTACTCAGATATTGAGGACC 540
Db 481 CATATCTCGACAGCTGTTACTTGGGACCACAAAGAGGCCCCCTTACTCAGATATTGAGGACC 540
Qy 541 ACCTGGAGGGCCTGGATGACAGAGAGAGGCTGAGCATGAGAGGAGTATGATGAGATG 600
Db 541 ACCTGGAGGGCCTGGATGACAGAGAGAGGCTGAGCATGAGAGGAGTATGATGAGATG 600
Qy 601 CTCAGGTAGTGAAGATGAGAGGGCCGAGGAGGAGGAGGAGGTTGAAGAGGAGGAGC 660
Db 601 CTCAGGTAGTGAAGATGAGAGGGCCGAGGAGGAGGAGGAGGAGGTTGAAGAGGAGGAGC 660
Qy 661 TCAGTGGAGGGGACGAGGAGGATGAAGAAGGTTTAAACGATGGAGAGGTAGATGGCGAGG 720
Db 661 TCAGTGGAGGGGACGAGGAGGATGAAGAAGGTTTAAACGATGGAGAGGTAGATGGCGAGG 720
Qy 721 AAGATGAAGAGACCTGGTGAAGAAAGAGGGGTGAGAGCGGAAATGAGAACCTGAAG 780
Db 721 AAGATGAAGAGACCTGGTGAAGAAAGAGGGGTGAGAGCGGAAATGAGAACCTGAAG 780
Qy 781 ATGAGGGAGAAGATGATGACTAAGTGAATAACCTATTTTGAATAATTCCTATTGTGATT 840
Db 781 ATGAGGGAGAAGATGATGACTAAGTGAATAACCTATTTTGAATAATTCCTATTGTGATT 840
Qy 841 TGACTGTTTTTACCCTATATCCCTCCCTCCCTCC 873
Db 841 TGACTGTTTTTACCCTATATCCCTCCCTCCCTCC 873

RESULT 5
US-10-273-334-23
; Sequence 23, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-10-273-334-23

Query Match 94.4%; Score 839.4; DB 6; Length 895;
Best Local Similarity 97.5%; Pred. No. 2.7e-167;
Matches 851; Conservative 0; Mismatches 22; Indels 0; Gaps 0;
Qy 1 GGGTTCGAGGTTATTGATTGAATTCGGCTGCGACGAGAGGCTCTGACAGACAGAGAGCGC 60
Db 1 GGGTTCGAGGTTATTGATTGAATTCGGCTGCGAGGAGGCTCTGACAGAGGAGCGC 60

Qy 61 GAGAGATGAGATGGGCAGACGGATTTCATTTCAGAGCTCGGAAACAGGCGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGGCAGACGGATTTCATTTCAGAGCTCGGAAACAGGCGCCCTCTGATG 120
Qy 121 TGAAGAAGCTTCCCTTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 121 TGAAGAAGCTTCTCTGGACAAACAGTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Qy 181 ATGAATTTCAAGAAGCTTGAATTTTAAAGTAAATCAAGCGAGGCGCTCACCTCAATCTCAG 240
Db 181 ATGAATTTCAAGAAGCTTGAATTTTAAAGTAAATCAAGCGAGGCGCTCACCTCAATCTCAG 240
Qy 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAAGTCTCAGGGGCGCTGGAAGTAT 300
Db 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAAGTCTCAGGGGCGCTGGAAGTAT 300
Qy 301 TGGCAGAAAAGTGTCCAAACCTCAGGCATCTATATTTAGTGGCAACAAAATTAAGAGCC 360
Db 301 TGGCAGAAAAGTGTCCAAACCTCAGGCATCTATATTTAGTGGCAACAAAATTAAGAGCC 360
Qy 361 TCAGCAACAATAGAGCCACCTGAAACAGCTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420
Db 361 TCAGCAACAATAGAGCCACCTGAAACAGCTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT 420
Qy 421 GCGAGTAAACCAACCTGAAACAGCTACGAGAGAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Db 421 GCGAGTAAACCAACCTGAAACAGCTACGAGAGAAACGTTTCAAGCTTCTCCTGCAACTCA 480
Qy 481 CATATCTCGACAGCTGTTACTTGGGACCACAAAGAGGCGCCCTTACTCAGATATTGAGGACC 540
Db 481 CATATCTCGACAGCTGTTACTTGGGACCACAAAGAGGCGCCCTTACTCAGATATTGAGGACC 540
Qy 541 ACCTGAGGGCCTGGATGACGAGGAGGAGGTTTAAACGATGGAGGTAGATGCGGAGG 600
Db 541 ACCTGAGGGCCTGGATGACGAGGAGGAGGTTTAAACGATGGAGGTAGATGCGGAGG 600
Qy 601 CTCAGTGTGGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGTTGAAGAGGAGGAGC 660
Db 601 CTCAGTGTGGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGTTGAAGAGGAGGAGC 660
Qy 661 TGAGTGGAGGGACGAGGAGGATGAAGAAGTTTAAACGATGGAGGTAGATGCGGAGG 720
Db 661 TGAGTGGAGGGACGAGGAGGATGAAGAAGTTTAAACGATGGAGGTAGATGCGGAGG 720
Qy 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAGCGGAAATGAGAACCTGAAG 780
Db 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAGCGGAAATGAGAACCTGAAG 780
Qy 781 ATGAGGAGAAGATGATGACTAAGTGAATAACCTATTTTGAATAATTCCTATTGTGATT 840
Db 781 ATGAGGAGAAGATGATGACTAAGTGAATAACCTATTTTGAATAATTCCTATTGTGATT 840
Qy 841 TGACTGTTTTTACCCTATATCCCTCCCTCCCTCC 873
Db 841 TGACTGTTTTTACCCTATATCCCTCCCTCCCTCC 873

RESULT 6
US-10-273-334-6
; Sequence 6, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-6

Query Match 93.5%; Score 831.4; DB 6; Length 907;
Best Local Similarity 97.4%; Pred. No. 1.3e-165;
Matches 883; Conservative 0; Mismatches 16; Indels 18; Gaps 3;

QY 1 GGGTTTCAGAGTTTATTCATTGAATTCGGCTGGCAGCAGAGCCCTCTCAGACAGAGCGC 60
DB 1 GGGTTCGGGGTTATTGATTAATTCGGCTGGCAGCAGAGCCCTCTCAGACAGAGCGC 60

QY 61 GAGAGATGGAGATGGCGAGACGGATTCAATTCAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120
DB 61 GAGAGACGGAGATGGCGAGACGGATTCACTAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120

QY 121 TGAAGAACTTGCCTGGCAACAGTCGGTCGAATGAAGCCAACTCGAAGCCCTCACAG 180
DB 121 TGAAGAACTTGCCTGGCAACAGTCGGTCGAATGAAGCCAACTCGAAGCCCTCACAG 180

QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGCGCTCACCTCAATCTCAG 240
DB 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGCGCTCACCTCAATCTCAG 240

QY 241 ACTTACCAAAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
DB 241 ACTTACCAAAAGTTAAGTAACTTGAGAAAGCTTGAACCTAAGCAGTAAACAGAGTCTCAGGGG 300

QY 289 GCCTGGAAGTATGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348
DB 289 GCCTGGAAGTATGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348

QY 349 AAATTAAGACCTTCAGCACAATAGAGCCACTGAAACAGTGTAGAAACCTCAAGAGCTTAG 408
DB 349 AAATTAAGACCTTCAGCACAATAGAGCCACTGAAACAGTGTAGAAACCTCAAGAGCTTAG 408

QY 409 ACCTTTTCAATTGCGAGGTACCAACCTGAACGACTACGGAGAAACCGTGTTCAAAGCTTC 468
DB 409 ACCTTTTCAATTGCGAGGTACCAACCTGAACGACTACGGAGAAACCGTGTTCAAAGCTTC 468

QY 469 TCCTGCAACTCACATATCTCGACAGCTGTGTTACTGGGACCACAAAGGCTTACTCAG 528
DB 469 TCCTGCAACTCACATATCTCGACAGCTGTGTTACTGGGACCACAAAGGCTTACTCAG 528

QY 529 ATATTGAGGACCAGTGGAGGGCTGGATCAGCAGGAGGAGGTGAGCATGAGGAGGAGT 588
DB 529 ATATTGAGGACCAGTGGAGGGCTGGATCAGCAGGAGGAGGTGAGCATGAGGAGGAGT 588

QY 541 ATATTGAGGCCCAGTGGAGGGCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGT 600
DB 541 ATATTGAGGCCCAGTGGAGGGCTGGATGACGAGGAGGAGGTGAGCATGAGGAGGAGT 600

QY 589 ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAAGGTG 648
DB 589 ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAAGGTG 648

QY 601 ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAAGGTG 660
DB 601 ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAAGGTG 660

QY 649 AAGAGGAGGACCTGACGTGGAGGGGACGAGGAGGATGAAGAGGTTATACCATGGAGAGG 708
DB 649 AAGAGGAGGACCTGACGTGGAGGGGACGAGGAGGATGAAGAGGTTATACCATGGAGAGG 708

QY 709 TAGATGCGGAGGAGATGAAGAGAGCTTGGTGAAGAAGAAAGGGGTCAAGACGCAAAAT 768
DB 709 TAGATGCGGAGGAGATGAAGAGAGCTTGGTGAAGAAGAAAGGGGTCAAGACGCAAAAT 768

QY 721 TAGATGCGGAGGAGATGAAGAGAGCTTGGTGAAGAAGAAAGGGGTCAAGACGCAAAAT 780
DB 721 TAGATGCGGAGGAGATGAAGAGAGCTTGGTGAAGAAGAAAGGGGTCAAGACGCAAAAT 780

QY 769 GAGAACTGAAGATGAGGGGAGAGATGACTAAGTGAATAACCTATTTTGAAGAAAT 828
DB 769 GAGAACTGAAGATGAGGGGAGAGATGACTAAGTGAATAACCTATTTTGAAGAAAT 828

QY 781 GAGAACTGAAGATGAGGGGAGAGATGACTAAGTGAATAACCTATTTTGAAGAAAT 840
DB 781 GAGAACTGAAGATGAGGGGAGAGATGACTAAGTGAATAACCTATTTTGAAGAAAT 840

QY 829 CCTATTGTGATTGACTGTGTTTACCATAATCCCT-----CCGCCCTCAATCTGCC 882
DB 829 CCTATTGTGATTGACTGTGTTTACCATAATCCCT-----CCGCCCTCAATCTGCC 882

QY 841 CCTATTGTGATTGACTGTGTTTACCATAATCCCTCTCCGCCCTCAATCTGCC 900
DB 841 CCTATTGTGATTGACTGTGTTTACCATAATCCCTCTCCGCCCTCAATCTGCC 900

QY 883 CCTGAA 889
DB 901 CCTGAA 907

RESULT 7
US-10-273-334-13
; Sequence 13, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 03187.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-10-273-334-13

Query Match 85.8%; Score 762.6; DB 6; Length 907;
Best Local Similarity 92.6%; Pred. No. 3.5e-151;
Matches 840; Conservative 0; Mismatches 49; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTATTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTCAGACAGAGCGC 60
DB 1 GGGTTCGGGGTTATTGATTGAATTCGCGCGCGGGAGCCCTCTCAGAGAGAGCGC 60

QY 61 GAGAGATGGAGATGGCGAGACGGATTCAATTCAGAGCTCGGGAACAGGCGCCCTCTGATG 120
DB 61 GAGAGATGGAGATGGCGAGACGGATTCAATTCAGAGCTCGGGAACAGGCGCCCTCTGATG 120

QY 121 TGAAGAACTTGCCTGGCAACAGTCGGTCGAATGAAGCCAACTCGAAGCCCTCACAG 180
DB 121 TGAAGAACTTGCCTGGCAACAGTCGGTCGAATGAAGCCAACTCGAAGCCCTCACAG 180

QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGCGCTCACCTCAATCGCA 240
DB 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGCGCTCACCTCAATCGCA 240

QY 241 ACTTACCAAAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
DB 241 ACTTACCAAAAGTTAAGTAACTTGAGAAAGCTTGAACCTAAGCAGTAAACAGAGTCTCAGGGG 300

QY 289 GCCTGGAAGTATGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348
DB 289 GCCTGGAAGTATGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348

QY 349 AAATTAAGACCTTCAGCACAATAGAGCCACTGAAACAGTGTAGAAACCTCAAGAGCTTAG 408
DB 349 AAATTAAGACCTTCAGCACAATAGAGCCACTGAAACAGTGTAGAAACCTCAAGAGCTTAG 408

QY 409 ACCTTTTCAATTGCGAGGTACCAACCTGAACGACTACGGAGAAACCGTGTTCAAAGCTTC 468
DB 409 ACCTTTTCAATTGCGAGGTACCAACCTGAACGACTACGGAGAAACCGTGTTCAAAGCTTC 468

QY 421 ACCTTTTCAATTGCGAGGTACCAACCTGAACGACTACGGAGAAACCGTGTTCAAAGCTTC 480
DB 421 ACCTTTTCAATTGCGAGGTACCAACCTGAACGACTACGGAGAAACCGTGTTCAAAGCTTC 480

QY 469 TCCTGCAACTCACATATCTCGACAGCTGTGTTACTGGGACCACAAAGGCTTACTCAG 528
DB 469 TCCTGCAACTCACATATCTCGACAGCTGTGTTACTGGGACCACAAAGGCTTACTCAG 528

Db 481 TCCGCAACTCACATATCTCAGCGCTATGACCGGGACGACAAGGAGGCCCTGACTCGG 540
Qy 529 ATATTGAGGACACGCTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGT 588
Db 541 ATGCTGAGGCGTACGTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 600
Qy 589 ATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT 648
Db 601 ATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT 660
Qy 649 AAGAGGAGGAGCTGAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708
Db 661 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 720
Qy 709 TAGATGGCGAGGAGATGAGAGAGCTGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGT 768
Db 721 TAGATGGCGAGGAGATGAGAGAGCTGTGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGT 780
Qy 769 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 828
Db 781 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Qy 829 CCTATTGTGATTGACTGTGTTTACCATATCCCT-----CCCCCTCCATFCCCTGCC 882
Db 841 CCTATTGTGATTGACTGTGTTTACCATATCCCTCTCCCTCCCTCTCTAATCCTGCC 900
Qy 883 CCCTGAA 889
Db 901 CCCTGAA 907

RESULT 8

US-10-273-334-25

; Sequence 25, Application US/10273334

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kocheavar, Gerald J.

; APPLICANT: Brody, Jonathan R.

; APPLICANT: Kodkol, Shrihari S.

; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

; FILE REFERENCE: 031787.0076

; CURRENT APPLICATION NUMBER: US/10/273,334

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: US/09/591,500

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: PCT/US98/26433

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 25

; LENGTH: 907

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-273-334-25

Query Match 85.68; Score 761; DB 6; Length 907;

Best Local Similarity 92.58; Pred. No. 7.5e-151;

Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

Qy 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGGAGGCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGGAGGCTCTGCAGACAGAGAGCGC 60
Qy 61 GAGAGATGAGATGGCAGACGAGTATTCAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGCAGACGAGTATTCAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120
Qy 121 TGAAGAAGACTTCCCTGACACACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 121 TGAAGAAGACTTCTCTGGACACACAGTCGGTGAATGAAGGCAAACTCGAAGGCGCTCACAG 180

Qy 181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Qy 241 ACTTACCAAGTTA--AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
Db 241 ACTTACCAAGTTA--AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 300
Qy 289 GCTTGAAGTATTTGGCAGAAAAGTGTCCAAAGCTCAGCATCTATATTAAGTGGCAACA 348
Db 301 GCTTGAAGTATTTGGCAGAAAAGTGTCCAAAGCTCAGCATCTATATTAAGTGGCAACA 360
Qy 349 AAATTAAGACCTTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 361 AAATTAAGACCTTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 420
Qy 409 ACCTTTTCAATTTGCGAGGTAAACCACTGAAAGCTACGAGGAGGAGGAGGAGGAGGAGT 468
Db 421 ACCTTTTCAATTTGCGAGGTAAACCACTGAAAGCTACGAGGAGGAGGAGGAGGAGGAGT 480
Qy 469 TCCTGCAACTCACATATCTCGACAGCTGTACTGGACCAAGAGGAGGAGGAGGAGGAGT 528
Db 481 TCCGCAACTCACATATCTCGACAGCTGTACTGGACCAAGAGGAGGAGGAGGAGGAGT 540
Qy 529 ATATTGAGGACACGCTGGAGGCGCTGGATGATGAGGAGGAGGAGGAGGAGGAGGAGT 588
Db 541 ATGCTGAGGCGTACGTGGAGGCGCTGGATGATGAGGAGGAGGAGGAGGAGGAGT 600
Qy 589 ATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 648
Db 601 ATGATGAAGATGCTCAGTGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 660
Qy 649 AAGAGGAGGAGCTGAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708
Db 661 AAGAGGAGGAGCTGAGTGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 720
Qy 709 TAGATGGCGAGGAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCAGAACGCAAAAT 768
Db 721 TAGATGACGAGGAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCAGAACGCAAAAT 780
Qy 769 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 828
Db 781 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Qy 829 CCTATTGTGATTGACTGTGTTTACCATATCCCT-----CCCCCTCCATFCCCTGCC 882
Db 841 CCTATTGTGATTGACTGTGTTTACCATATCCCTCTCCCTCTCCCTCTAATCCTGCC 900
Qy 883 CCCTGAA 889
Db 901 CCCTGAA 907

RESULT 9

US-10-273-334-33

; Sequence 33, Application US/10273334

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kocheavar, Gerald J.

; APPLICANT: Brody, Jonathan R.

; APPLICANT: Kodkol, Shrihari S.

; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

; FILE REFERENCE: 031787.0076

; CURRENT APPLICATION NUMBER: US/10/273,334

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: US/09/591,500

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: PCT/US98/26433

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 51

SOFTWARE: PatentIn version 3.1

SEQ ID NO 33

LENGTH: 906

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (66)..(812)

OTHER INFORMATION:

US-10-273-334-33

Query Match 85.5%; Score 760.2; DB 6; Length 906;

Best Local Similarity 93.2%; Pred. No. 1.1e-150;

Matches 845; Conservative 0; Mismatches 43; Indels 19; Gaps 4;

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QY 1 GGGTTCGAGGTTTATTGATGTAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGCTGGCGGGGAGCCCTCTGCAGAGAGAGAGCGC 60
QY 61 GAGAGATGGAGATGGCGAGAGCGGATTTCATTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGCGAGAGCGGATTTCATTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 120
QY 121 TGAAGAAGCTTGCCTCGACACACAGTCGTCGTAATGAAGCAACTCGAAGCGCTCACAG 180
Db 121 TGAAGAAGCTTGCCTCGACACACAGTCGTCGTAATGAAGCAACTCGAAGCGCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCGCAA 240
QY 241 ACTTTACAAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
Db 241 ACTTTACAAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
QY 289 GCCTGGAAGTATTTGCGAGAGAGTCTCCAAACCTCAGCAGCTATATTTAAAGTGGCAACA 348
Db 289 GCCTGGAAGTATTTGCGAGAGAGTCTCCAAACCTCAGCAGCTATATTTAAAGTGGCAACA 348
QY 301 GCCTGGAAGTATTTGCGAGAGAGTCTCCAAACCTCAGCAGCTATATTTAAAGTGGCAACA 360
Db 301 GCCTGGAAGTATTTGCGAGAGAGTCTCCAAACCTCAGCAGCTATATTTAAAGTGGCAACA 360
QY 349 AAATTAAGACCTCAGACAACTAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAG 408
Db 349 AAATTAAGACCTCAGACAACTAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAG 408
QY 361 AAATTAAGACCTCAGACAACTAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAG 420
Db 361 AAATTAAGACCTCAGACAACTAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAG 420
QY 409 ACCTTTTCAATTTGCGAGGTACCAACCTGAAACGACTACGAGAGAAACGTTTCAAGCTTC 468
Db 409 ACCTTTTCAATTTGCGAGGTACCAACCTGAAACGACTACGAGAGAAACGTTTCAAGCTTC 468
QY 421 ACCTTTTCAATTTGCGAGGTACCAACCTGAAACGACTACGAGAGAAACGTTTCAAGCTTC 480
Db 421 ACCTTTTCAATTTGCGAGGTACCAACCTGAAACGACTACGAGAGAAACGTTTCAAGCTTC 480
QY 469 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCAACAGAGAGGCCCTTACTCAG 528
Db 469 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCAACAGAGAGGCCCTTACTCAG 528
QY 481 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCAACAGAGAGGCCCTTACTCAG 540
Db 481 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCAACAGAGAGGCCCTTACTCAG 540
QY 529 ATATTGAGGACCACTGAGGAGGCTGATGACGAGGAGGAGGCTGACGATGAGGAGGAGT 588
Db 529 ATATTGAGGACCACTGAGGAGGCTGATGACGAGGAGGAGGCTGACGATGAGGAGGAGT 588
QY 541 ATGCTGAGGAGCTACGTTGAGGAGGCTGATGACGAGGAGGAGGATGAGGAGGAGT 600
Db 541 ATGCTGAGGAGCTACGTTGAGGAGGCTGATGACGAGGAGGAGGATGAGGAGGAGT 600
QY 589 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT 648
Db 589 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGT 648
QY 601 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
Db 601 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
QY 649 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAGGTTATACGATGGAGAGG 708
Db 649 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAGGTTATACGATGGAGAGG 708
QY 661 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAGGTTATACGATGGAGAGG 720
Db 661 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAGGTTATACGATGGAGAGG 720
QY 709 TAGATGCGAGGAGGATGAAGAGGCTTGGTGAAGAGGAGGAGGCTGAGAGCGGAGGAGT 768
Db 709 TAGATGCGAGGAGGATGAAGAGGCTTGGTGAAGAGGAGGAGGCTGAGAGCGGAGGAGT 768
QY 721 TAGATGCGAGGAGGATGAAGAGGCTTGGTGAAGAGGAGGAGGCTGAGAGCGGAGGAGT 779
Db 721 TAGATGCGAGGAGGATGAAGAGGCTTGGTGAAGAGGAGGAGGCTGAGAGCGGAGGAGT 779
QY 769 GAGAACTGAGGATGAGGAGGAGGATGATGACTTAAGTAAATCAACCTATTTTGAAGAAAT 828
Db 769 GAGAACTGAGGATGAGGAGGAGGATGATGACTTAAGTAAATCAACCTATTTTGAAGAAAT 828
QY 780 GAGAACTGAGGATGAGGAGGAGGATGATGACTTAAGTAAATCAACCTATTTTGAAGAAAT 839
Db 780 GAGAACTGAGGATGAGGAGGAGGATGATGACTTAAGTAAATCAACCTATTTTGAAGAAAT 839
QY 829 CCTATTGTGATTGACTGTTTTTACCCTATCCCT-----CCCCCTTCAATCTCGC 882
Db 829 CCTATTGTGATTGACTGTTTTTACCCTATCCCT-----CCCCCTTCAATCTCGC 882
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Db 840 CCTATTGTGATTGACTGTTTTTACCCTATCCCTCTCCCTCCCTCTCTAATCTGCTGCC 899
QY 883 CCCTGAA 889
Db 900 CCCTGAA 906

RESULT 10
US-10-273-334-28
; Sequence 28, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-10-273-334-28
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Query Match 85.2%; Score 757.8; DB 6; Length 907;

Best Local Similarity 92.3%; Pred. No. 3.5e-150;

Matches 837; Conservative 0; Mismatches 52; Indels 18; Gaps 3;

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QY 1 GGGTTCGAGGTTTATTGATGTAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGCGCGCGGAGGAGCCCTCTGCAGAGAGAGAGCGC 60
QY 61 GAGAGATGAGATGGCGAGAGCGGATTTCATTCAGAGCTGCGGAACAGGCGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGCGAGAGCGGATTTCATTCAGAGCTGCGGAACAGGAGCGCCCTCTGATG 120
QY 121 TGAAGAAGCTTGCCTCGGACAACTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 121 TGAAGAAGCTTGCCTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAAGGAGGCGCTCACCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAAGGAGGCGCTCACCTCAATCGCAA 240
QY 241 ACTTTACAAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
Db 241 ACTTTACAAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
QY 289 GCCTGGAAGTATTTGCGAGAGAGTCTCCAAACCTCAGCAGCTATATTTAAAGTGGCAACA 348
Db 289 GCCTGGAAGTATTTGCGAGAGAGTCTCCAAACCTCAGCAGCTATATTTAAAGTGGCAACA 348
QY 301 GCCTGGAAGTATTTGCGAGAGAGTCTCCAAACCTCAGCAGCTATATTTAAAGTGGCAACA 360
Db 301 GCCTGGAAGTATTTGCGAGAGAGTCTCCAAACCTCAGCAGCTATATTTAAAGTGGCAACA 360
QY 349 AAATTAAGACCTCAGACAACTAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAG 408
Db 349 AAATTAAGACCTCAGACAACTAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAG 408
QY 361 AAATTAAGACCTCAGACAACTAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAG 420
Db 361 AAATTAAGACCTCAGACAACTAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAG 420
QY 409 ACCTTTTCAATTTGCGAGGTACCAACCTGAAACGACTACGAGAGAAACGTTTCAAGCTTC 468
Db 409 ACCTTTTCAATTTGCGAGGTACCAACCTGAAACGACTACGAGAGAAACGTTTCAAGCTTC 468
QY 421 ACCTTTTCAATTTGCGAGGTACCAACCTGAAACGACTACGAGAGAAACGTTTCAAGCTTC 480
Db 421 ACCTTTTCAATTTGCGAGGTACCAACCTGAAACGACTACGAGAGAAACGTTTCAAGCTTC 480
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; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-32

Query Match      84.5%; Score 751.6; DB 6; Length 908;
Best Local Similarity 92.5%; Pred. No. 7e-149;
Matches 840; Conservative 0; Mismatches 49; Indels 19; Gaps 4;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCGCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 60
QY 61 -GAGAGATGGAGATGGCAGACGATTCATTTCAGAGCTGCGGACAGAGAGAGAGAGAGAG 119
Db 61 GGAGAGATGGAGATGGCAGACGATTCATTTCAGAGCTGCGGACAGAGAGAGAGAGAGAG 120
QY 120 GTGAAGAACTTGCCTGGACACAGTCGGTTCGAATCAAGGCAAACTCGAAGCCCTCACA 179
Db 121 GTGAAGAACTTGCCTGGACACAGTCGGTTCGAATCAAGGCAAACTCGAAGCCCTCACA 180
QY 180 GATGAATTTGAAGAACTGGAATCTTAAGTAAATCAACGAGGCGCTCACTCAATCTCA 239
Db 181 GATGAATTTGAAGAACTGGAATCTTAAGTAAATCAACGAGTTCAGGCTCACTCAATCTCA 240
QY 240 GACTTACCAGATTA---AAGTTCAGAAAGCTTGAACATA-----AGAGTCTCAGGG 287
Db 241 AACTTACCAGATTA---AAGTTCAGAAAGCTTGAACATA-----AGAGTCTCAGGG 300
QY 288 GGCCTGGAAGTATTGGCAGAAAGCTTCCAAACCTCAGCATCTATATTTAAGTGGCAAC 347
Db 301 GGCCTGGAAGTATTGGCAGAAAGCTTCCAAACCTCAGCATCTATATTTAAGTGGCAAC 360
QY 348 AAAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGCTTAGAAAACCTTCAAGAGCTTA 407
Db 361 AAAATTAAGACCTCAGCACAATAGAGCCACTGAAAAAAGTTAGAAAACCTTCAAGAGCTTA 420
QY 408 GACCTTTTCAATTCGAGAGTAAACCACTGAACGACTACGAGAGAGAGAGAGAGAGCTT 467
Db 421 GACCTTTTCAATTCGAGAGTAAACCACTGAACGACTACGAGAGAGAGAGAGAGAGCTT 480
QY 468 CTCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCGCCCTTACTCA 527
Db 481 CTCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCGCCCTGACTCG 540
QY 528 GATATTGAGACACAGTGGAGGCGCTGGATGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 587
Db 541 GATGCTGAGGCGCTACGTTGAGGCGCTGGATGATGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 588 TATGATCAAGATGCTCAGTGTAGTGGAGATGAGAGGCGGAGGAGGAGGAGGAGAGAGT 647
Db 601 TATGATCAAGATGCTCAGTGTAGTGGAGATGAGAGGCGGAGGAGGAGGAGGAGAGT 660
QY 648 GAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGCTTATACGATGAGAGAG 707
Db 661 GAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGCTTATACGATGAGAGAG 720
QY 708 GTAGATGGCAGAGAGATGAAGAAGAGCTTGGTGAAGAGAGAGAGAGAGAGAGAGAGAG 767
Db 721 GTAGATGGCAGAGAGATGAAGAAGAGCTTGGTGAAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 768 TGAGAACTTCAAGATGAGGAGAGAGATGATGACTAAGTAACTTATTTGAAAAAT 827
Db 781 CGAGAACTTCAAGATGAGGAGAGAGATGATGACTAAGTAACTTATTTGAAAAAT 840
QY 828 TCCTATTGTGATTGACTGTTTTTAACCATATATCCCT-----CCCCCTCCAACTCCTGC 881
Db 841 TCCTATTGTGATTGACTGTTTTTAACCATATATCCCT-----CCCCCTCCAACTCCTGC 900
QY 882 CCCTGAA 889
Db 901 CCCTGAA 908

RESULT 13
US-10-273-334-30
; Sequence 30, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(455)
; OTHER INFORMATION:
US-10-273-334-30

Query Match      81.8%; Score 727.4; DB 6; Length 907;
Best Local Similarity 90.2%; Pred. No. 8.4e-144;
Matches 818; Conservative 0; Mismatches 71; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGAGCCCTGCGACAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCGCGCGGAGCCTCTGCAGAGAGAGAGCGC 60
QY 61 GAGAGATGAGATGGCAGACGGAATTCATTTCAGAGCTGCGGACAGAGGCGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGCAGACGGAATTCATTTCAGAGCTGCGGACAGAGGCGCCCTCTGATG 120
QY 121 TGAAGAAGCTTCCCTGGACACACAGTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 121 TGAAGAAGCTTCCCTGGACACACAGTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
QY 181 ATGAATTTCAAGAACTTGAATTCCTTAAGTAAATCAACGAGGAGGCGCTCACCCTCAATCTCAG 240
Db 181 ATGAATTTGAAGAACTTGAATTCCTTAAGTAAATCAACGAGGAGGCGCTCACCCTCAATCTCAG 240
QY 241 ACTTACCAAGTTA---AAGTTGAGAAAAGCTTGAACATA-----AGAGTCTCAGGG 288
Db 241 ACTTACCAAGTTA---AAGTTGAGAAAAGCTTGAACATA-----AGAGTCTCAGGG 300
QY 289 GCCTGGAAGTATTTGCGAGAAAAGTGTCCAAAACCTCAGCAGCTATATATTTAAGTGGCAACA 348
Db 301 GCCTGGAAGTATTTGCGAGAAAAGTGTCCAAAACCTCAGCAGCTATATATTTAAGTGGCAACA 360
QY 349 AAAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 361 AAAATTAAGACCTCAGCACAATAGAGCCACTGAAAAAAGTTAGAAAACCTCAGAGCTTAG 420
QY 409 ACCTTTTCAATTTGCGAGGTAAACCAACCTGAACTGAGGAGAAACCTGTTTCAAGCTTC 468
Db 421 ACCTTTTCAATTTGCGAGGTAAACCAACCTGAACTGAGGAGAAACCTGTTTCAAGCTTC 480
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Search completed: December 9, 2002, 00:34:18
Job time : 63.4368 secs

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; LENGTH: 905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(810)
; OTHER INFORMATION:
US-10-273-334-11

Query Match      80.1%; Score 711.8; DB 6; Length 905;
Best Local Similarity 90.2%; Pred. No. 1.6e-140;
Matches 798; Conservative 0; Mismatches 73; Indels 14; Gaps 3;

Qy 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCACGAGAGCCTCTGCAGACAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGTTGAATTCGGCTGGCTCAGAGCCCTCGAG--AGAAAGCGT 58

Qy 61 GAGAGATGGAGATGGGAGAGCGGATTTCATTCAGAGCTGCGGAACAGGGCGCCCTCTGATG 120
Db 59 GAGAGATGGAGATGGGAAATGGATTTCATTTAGAGCTGCGGAACAGGACGCCCTCCGATG 118

Qy 121 TGAAGAACTTGCCTCGACACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 119 TGAAGAACTTTCTCGACACAGTCAGTCAAAATGAAGGCAAAATGGAAGGCCCTCACAG 178

Qy 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAG 240
Db 179 ATGAATTTGAAGAACTGGAATTTAATAATACATCAACATAGGCCCTCACCTCAATTCGCA 238

Qy 241 ACTTACCAAAAGTTA---AAGTTGAGAAGCTTGAACATA-----AGAGTCTCAGGGG 288
Db 239 ACTTGCACAAAGTTAAACAAACTTAAAGAAAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGG 298

Qy 289 GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGGCATCTATATTTAAGTGGCAACA 348
Db 299 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACTACATCTAAATTTAAGTGGCAACA 358

Qy 349 AAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGGCTTAG 408
Db 359 AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG 418

Qy 409 ACCTTTTCAATTCGGAGGTAACCAACTGAACGACTACGGAGAAAACGTGTTCAAGCTTC 468
Db 419 ACCTTTTCACTTCGGAGGTAACCAACTGAACGACTACCGAGAAAATGTGTTCAAGCTCC 478

Qy 469 TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACACAGAGAGGCCCTTACTCTAG 528
Db 479 TCCCGCAACTCACATATCTCGACGGCTATGACCGGGACGACAAAGGAGGCCCTGACTCGG 538

Qy 529 ATATTGAGGACCACTGAGGGGCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGT 588
Db 539 ATGCTGAGGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 598

Qy 589 ATGATGAAGATGCTCAGGTAGTGAAGATGAGAGGGCGGAGGAGGAGGAGGAGGAGG 648
Db 599 ATGATGAAGATGCTCAGGTAGTGAAGATGAGAGGGAGGAGGAGGAGGAGGAGGAGG 658

Qy 649 AAGAGGAGGACGTGAGTGGAGGGGAGGAGGAGGATGAAGAAGCTTATAACGATGGAGAGG 708
Db 659 AAGAGGAGGACGTGAGTGGAGGGAGGAGGAGGATGAAGAAGCTTATAACGATGGAGAGG 718

Qy 709 TAGATGGCAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGGAAAAT 768
Db 719 TAGATGACGAGGAAGATGAAGAAGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGGAAAAC 778

Qy 769 GAGAACTGAGATGAGGAGGAAGATGATGACTAAGTAACCTATTTTGAATAATT 828
Db 779 GAGAACTGAGATGAGGAGGAAGATGATGACTAAGTGAATAAACCTATTTTGAATAATT 838

Qy 829 CCTATTGTGATTGACTGTTTTTACCCTATATCCCTCCCCCTCC 873
Db 839 CCTATTGTGATTGACTGTTTTTACCCTATATCCCTCCCCCTCC 883
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OM nucleic - nucleic search, using sw model

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(without alignments)
10438.259 Million cell updates/sec

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Perfect score: 907
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Scoring table: IDENTITY_NUC
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	857.8	94.6	905	22	US-09-591-500-19
4	857.8	94.6	905	22	US-09-591-500-26
5	856.2	94.4	905	22	US-09-591-500-7
6	833.4	91.9	907	22	US-09-591-500-33
7	827.8	91.3	906	22	US-09-591-500-9
8	825.4	91.0	1052	1	PCT-US02-25766-3866
9	825.4	91.0	2398	16	US-09-205-070-14975
10	825.4	91.0	2398	17	US-09-340-623-14975
11	825.4	91.0	2398	33	US-09-898-888-14975
12	825.4	91.0	2398	33	US-09-898-888A-14975
13	823.8	90.8	907	22	US-09-591-500-13
14	822.2	90.7	907	22	US-09-591-500-25
15	822.2	90.7	907	22	US-09-591-500-28
16	822.2	90.7	1197	30	US-09-760-469-94
17	822.2	90.7	1197	42	US-10-216-363-94
18	822.2	90.7	1595	25	US-09-644-871-8887
19	822.2	90.7	1595	25	US-09-649-164-9117
20	822.2	90.7	1595	25	US-09-652-913-10130
21	822.2	90.7	1595	27	US-09-699-998-8868

22	822.2	90.7	1595	27	US-09-699-999-6021	Sequence 6021, Ap
23	822.2	90.7	1595	28	US-09-710-281-4371	Sequence 4371, Ap
24	822.2	90.7	1595	28	US-09-710-286-2968	Sequence 2968, Ap
25	822.2	90.7	1595	28	US-09-716-973-2254	Sequence 2254, Ap
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28	822.2	90.7	1595	29	US-09-726-810-3350	Sequence 3350, Ap
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33	822.2	90.7	2447	34	US-09-919-003-2129	Sequence 2129, Ap
34	822.2	90.7	2449	30	US-09-760-469-601	Sequence 601, App
35	822.2	90.7	2449	32	US-10-216-583-601	Sequence 601, App
36	821.8	90.6	3955	36	US-09-576-594-207	Sequence 207, App
37	817.8	90.6	3955	68	US-60-240-409-207	Sequence 207, App
38	812.8	89.6	908	22	US-09-591-500-17	Sequence 17, Appl
39	801.8	88.4	905	22	US-09-591-500-32	Sequence 32, Appl
40	801.6	88.4	905	22	US-09-591-500-11	Sequence 11, Appl
41	796.4	87.8	916	14	PCT-US01-08631-12193	Sequence 12193, A
42	796.4	87.8	916	17	US-09-038-847A-2	Sequence 2, Appli
43	796.4	87.8	916	31	US-09-393-302-25	Sequence 25, Appl
44	795.2	87.5	6753	61	US-09-825-886-25	Sequence 25, Appl
45	782.2	86.2	907	22	US-09-172-373-13384	Sequence 13384, A
46	782.2	86.2	907	22	US-09-591-500-6	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-09-591-500-4
; Sequence 4, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-591-500-4

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RESULT 2
US-09-591-500-30
; Sequence 30, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

; LOCATION: (66)..(455)
; OTHER INFORMATION:
US-09-591-500-30

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Query Match      97.5%; Score 884.6; DB 22; Length 907;
Best Local Similarity 98.5%; Pred. No. 1.3e-164;
Matches 893; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 GGGTCCGGGTTTATTGATCAATTCGGCTGGCCGGGAGCCCTCTGCAGAGAGAGAGCGC 60
Db 1 GGGTCCGGGTTTATTGATCAATTCGGCTGGCCGGGAGCCCTCTGCAGAGAGAGAGCGC 60

Qy 61 CAGAGATGGAGATGGCAGACCGGATTCATTTAGAGCTGCGGAACGGGACGCCCTCTGATG 120
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Qy 121 TGAAGAACTTGTCTCGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGGCTCACAG 180
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Qy 181 ATGAATTTGAGAACTGGAATTCCTTAAGTACATCAACGTAGGCTCACCTCAATCGCAA 240
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Qy 541 ATGGTGAGGGCTTTGTGGAGTGCCTGGATGACAGGAGGAGGATGAGGATGAGGAGGAGT 600
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Qy 661 AAGAGGAGGAGCTGAGTGGAGACGAGAGAGAGAGATGAGGATGAGGATGAGGAGGAGGAGT 720
Db 661 AAGAGGAGGAGCTGAGTGGAGACGAGAGAGAGAGATGAGGATGAGGATGAGGAGGAGGAGT 720

Qy 721 TAGATGATGAGGAAGATGAAGAGAGCTTGGTGAAGAAAGAGGGTTCAGAACCGGAAAT 780
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Qy 781 AAGAACTGAAGATGAGGAGAGACAGATGCCCTAAGTGGAAATTAATCTATTTTGAAGAAAT 840
Db 781 AAGAACTGAAGATGAGGAGAGACAGATGCCCTAAGTGGAAATTAATCTATTTTGAAGAAAT 840

Qy 841 CCTTTCTGATTTTACTGTTTTTACCGGTACCCCTCTCCCCCCCCACCTCAATCTCTGCC 900
Db 841 CCTATTGTGATTTGACTGTTTTTACCATATCCCTCTCCCCCCCCCTCTCAATCTCTGCC 900

Qy 901 CCCTGAA 907
Db 901 CCCTGAA 907
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RESULT 3
US-09-591-500-19
; Sequence 19, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(453)
; OTHER INFORMATION:
US-09-591-500-19

Query Match 94.6%; Score 857.8; DB 22; Length 905;
Best Local Similarity 97.4%; Pred. No. 2.6e-159;
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Qy	61	GAGAGATGAGATGGCAGACAGGATTCATTTAGAGCTGCGGAACGGGAGGCCCTCTGATG	120
Db	59	GAGAGATGAGATGGGCAATGGAATTCATTTAGAGCTGCGGAACGGGAGGCCCTCGGATG	118
Qy	121	TGAAGAACTTGTCTCGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGGCCCTCACAG	180
Db	119	TGAAGAACTTGTCTCGGACAAACAGTCAGTCAATGAAGGCAAACTGGAAGGCCCTCACAG	178
Qy	181	ATGAATTTGAAGAACTGGAATTCCTTAAGTACAACTCAACGTAGGCTCACCTCAATCGAA	240
Db	179	ATGAATTTGAAGAACTGGAATTTAAATACAACTCAACGTAGGCTCACCTCAATTTGCAA	238
Qy	241	ACTTACCAAAAGTTAAACAACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA	300
Db	239	ACTTACCAAAAGTTAAACAACTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA	298
Qy	301	GCCTAGAAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA	360
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Qy	361	AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAACCTCGAGAGCTTAG	420
Db	359	AAATTAAGACCTCAGCACAAATAGAGCCCTGAAAAAGTTAGAAACCTCGAGAGCTTAG	418
Qy	421	ACCTTTTCACTTGGAGGTAAACCACTGAACAACTACTGAGAGAGATGTTCAAGCTCC	480
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Qy	481	TCCTGCAACTCACATCTCAACGGCTGTGACCCGGATGACAAAGGAGGCCCTTAACCTCGG	540
Db	479	TCCTGCAACTCACATCTCAACGGCTGTGACCCGGATGACAAAGGAGGCCCTTAACCTCGG	538
Qy	541	ATGGTGAGGGCTTTGTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGAGGAGT	600
Db	539	ATGGTGAGGGCTTTGTGGAGTGCCTGGATGACAAAGGAGGAGGATGAGGAGGAGT	598
Qy	601	ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT	660

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US-09-591-500-7

Query Match 94.4%; Score 856.2; DB 22; Length 905;
Best Local Similarity 97.2%; Pred. No. 5.3e-159;
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DB 1 GGGTTCGGGGTTTATTGATTCGAATTCGGCTGGCGGAGCCCTCTGCAGAGAGAGCGT 58
QY 61 GAGAGATGAGATGGCAGACGCGATTCATTTAGAGCTTCGGAGCGGAGCCCTCTGATG 120
DB 59 GAGAGATGAGATGGCAATGATTCATTTAGAGCTTCGGAGCAGACGCGCCCTCCGATG 118
QY 121 TGAAGAACTTTCCTGGACACAGTCGGTGAATGAAGGCAACTCGAAGGCTCACAG 180
DB 119 TGAAGAACTTTCCTGGACACAGTCAGTCAATGAAGGCAATTCGAAGGCTCACAG 178
QY 181 ATGAATTTGAAGAACTTGAATTCCTTAAGTACAATCAACGTAGGCTCACTCAATCCAA 240
DB 179 ATGAATTTGAAGAACTTGAATTCCTTAAGTACAATCAACGTAGGCTCACTCAATCCAA 238
QY 241 ACTTACCAGAGTTAAACAACTTAAAGAGCTTGAACCTTAAGCAGTAAAGGCTCAGTGG 300
DB 239 ACTTACCAGAGTTAAACAACTTAAAGAGCTTGAACCTTAAGCAGTAAAGGCTCAGTGG 298
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DB 299 GCCTAGAGATTTGGCAGAAAGTGTCCAACTCATACTACATCTAAATTTAAGTGGCAACA 358
QY 361 AAATTAAGAGCTCAGCACAAATGAGCCCTGAAAGAGTTAGAAAGCTCGAGAGCTTAG 420
DB 359 AAATTAAGAGCTCAGCACAAATGAGCCCTGAAAGAGTTAGAAAGCTCGAGAGCTTAG 418
QY 421 ACCTTTTCACTTGGAGGTAAACAACTGAACTACTCAGAGAGATGTTCAAGCTCC 480
DB 419 ACCTTTTCACTTGGAGGTAAACAACTGAACTACTCAGAGAGATGTTCAAGCTCC 478
QY 481 TCCTGCAACTCACAATATCTCAAGGCTGTACCCGGATGACAGAGGCGCCCTAACTCGG 540
DB 479 TCCTGCAACTCACAATATCTCAAGGCTGTACCCGGATGACAGAGGCGCCCTAACTCGG 538
QY 541 ATGGTGAAGGCTTGTGAGTGGCTGGATGACAGAGGAGGATGAGGATGAGGAGGAGGAGT 600
DB 539 ATGGTGAAGGCTTGTGAGTGGCTGGATGACAGAGGAGGATGAGGATGAGGAGGAGT 598
QY 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGCAGAGATGAGGAGGAGGAGGAGT 660
DB 599 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGCAGAGATGAGGAGGAGGAGGAGT 658
QY 661 AAGAGGAGGAGCTGAGTGGAGACGAGGAGAGAGGATGAGGTTATACAAATGGAGAGG 720
DB 659 AAGAGGAGGAGCTGAGTGGAGACGAGGAGAGAGGATGAGGTTATACAAATGGAGAGG 718
QY 721 TAGATGATGAGGAGATGAAGAGAGCTTGGTGAAGAGAGAGGCTGAGAGCGGAGGAGT 780
DB 719 TAGATGATGAGGAGATGAAGAGAGCTTGGTGAAGAGAGAGGCTGAGAGCGGAGGAGT 778
QY 781 AAGAACTGAAGATGAGGAGAGAGAGTGCCTTAAGTGAATATCTATTTTGAAGAAAT 840
DB 779 AAGAACTGAAGATGAGGAGAGAGAGTGCCTTAAGTGAATATCTATTTTGAAGAAAT 838
QY 841 CCTTTTGTGATTTTACTGTTTTTGTAGCGGTACCCCTCTCCCTCCCTCTATCTCTGCGC 900
DB 839 CCTTTTGTGATTTTACTGTTTTTGTAGCGGTATCCCTCTCCCTCCCTCTATCTCTGCGC 898
QY 901 CCTGAA 907
DB 899 CCTGAA 905

RESULT 6

US-09-591-500-9
; Sequence 9, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-09-591-500-9

Query Match 91.9%; Score 833.4; DB 22; Length 907;
Best Local Similarity 94.9%; Pred. No. 1.7e-154;
Matches 861; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 GGGTTCGGGGTTTATTGATTCGAATTCGGCTGGCGGAGCCCTCTGCAGAGAGAGCGC 60
DB 1 GGGTTCGGGGTTTATTGATTCGAATTCGGCTGGCGGAGCCCTCTGCAGAGAGAGCGC 60
QY 61 GAGAGATGAGATGGCAGACGAGTTCATTTAGAGCTCGGAGCGGAGCGCCCTCTGATG 120
DB 61 GAGAGATGAGATGGCAGACGAGTTCATTTAGAGCTCGGAGCGGAGCGCCCTCTGATG 120
QY 121 TGAAGAACTTCTCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGGCTTCACAG 180
DB 121 TGAAGAACTTCTCTGGACACAGTCGGTGAATGAAGGCAAACTCGAAGGCTTCACAG 180
QY 181 ATCAATTTTGAAGAACTGGAATTCCTTAAGTACAATCAAGTAGGCTCACCCTCAATCGCA 240
DB 181 ATGAATTTTGAAGAACTGGAATTCCTTAAGTACAATCAAGTAGGCTCACCCTCAATCGCA 240
QY 241 ACTTACCAAGTTTAAACAACTTAAAGAGCTTGAAGTAAAGCAAGTAAAGAGCTCAGTGG 300
DB 241 ACTTACCAAGTTTAAACAACTTAAAGAGCTTGAAGTAAAGCAAGTAAAGAGCTCAGTGG 300
QY 301 GCCTGAGAGTATGGCAGAAAAGTGTCCAAAGCTCATACATCTAAATTTAAGTGGCAACA 360
DB 301 GCCTGAGAGTATGGCAGAAAAGTGTCCAAAGCTCATACATCTAAATTTAAGTGGCAACA 360
QY 361 AAATTAAGAGCTCAGCAATAGAGCCCTGAAAAAGTTAGAAAACCTCGAGAGCTTAG 420
DB 361 AAATTAAGAGCTCAGCAATAGAGCCCTGAAAAAGTTAGAAAACCTCGAGAGCTTAG 420
QY 421 ACCTTTTCACTTGGAGGTAAACAACTTGAACAACTTACTGAGAGAGGATGTTCAAGCTCC 480
DB 421 ACCTTTTCACTTGGAGGTAAACAACTTGAACAACTTACTGAGAGAGGATGTTCAAGCTCC 480
QY 481 TCCTGCAACTCACAATCTCAAGGCTGTGACCGGATGACAAGGAGGCGCCCTAACTCGG 540
DB 481 TCCTGCAACTCACAATCTCAAGGCTGTGACCGGATGACAAGGAGGCGCCCTGACTCGG 540
QY 541 ATGGTGAAGGCTTGTGAGTGGCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600
DB 541 ATGGTGAAGGCTTGTGAGTGGCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600
QY 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 660
DB 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 660

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Db 601 ATGATGAAGATGCTCAGCTAGTAGTAAGATGAGGAGGACGAGGATCAGGAGGAGGAAGTG 660
QY 661 AAGAGGAGGACCTGAGTGGAGACGAGGAGGAGGAGGATGAAGGTTATAACAATGAGAGG 720
Db 661 AAGAGGAGGACCTGAGTGGAGAGGAGGAGGAGGATGAAGGTTATAACAATGAGAGG 720
QY 721 TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGAGGAAAT 780
Db 721 TAGATGAGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGAGGAAAT 780
QY 781 AAGAACTGAAGATGAGGAGGAGGAGGATGCTTAAGTGAAGTAAATCTTAATTTGAAAAT 840
Db 781 GAGAACTGAAGATGAGGAGGAGGAGGATGCTTAAGTGAAGTAAATCTTAATTTGAAAAT 840
QY 841 CCTTTTGTGATTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTT 900
Db 841 CCTATTGTGATTGACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTT 900
QY 901 CCCTGAA 907
Db 901 CCCTGAA 907

RESULT 7
US-09-591-500-33
; Sequence 33, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-09-591-500-33

Query Match 91.3%; Score 827.8; DB 22; Length 906;
Best Local Similarity 95.3%; Pred No. 2.2e-153;
Matches 864; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGGAGCCTCTGCAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGGAGCCTCTGCAGAGAGAGAGCGC 60
QY 61 GAGAGATGAGATGGGACAGCGATTTCATTAGAGCTGCGGAACGGAGCGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGGACAGCGATTTCATTAGAGCTGCGGAACGGAGCGCCCTCTGATG 120
QY 121 TGAAGAAGCTTCCTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCCCTCACAG 180
Db 121 TGAAGAAGCTTCCTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCCCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAATCTTAAAGTACAATCAACGTAGCGCTCACTCAATCGCAA 240
Db 181 ATGAATTTGAAGAACTGGAATCTTAAAGTACAATCAACGTAGCGCTCACTCAATCGCAA 240
QY 241 ACTTACCAAGTTAAACAACCTTAAGAGCTTGAAGTAAAGCAAGTAAAGCAAGCTCAGTGG 300
Db 241 ACTTACCAAGTTAAACAACCTTAAGAGCTTGAAGTAAAGCAAGTAAAGCAAGCTCAGTGG 300
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Db 241 ACTTACCAAGTTAAACAACCTTAAGAGCTTGAAGTAAAGCAAGTAAAGCAAGCTCAGGGG 300
QY 301 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTTAAATTTAAAGTGGCAACA 360
Db 301 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTAAATTTAAAGTGGCAACA 360
QY 361 AAATTTAAGACCTCAGCACAATAGAGCCCTGAAAAGTTAGAAAACCTCAGAGGCTTAG 420
Db 361 AAATTTAAGACCTCAGCACAATAGAGCCCTGAAAAGTTAGAAAACCTCAGAGGCTTAG 420
QY 421 ACCTTTTCACCTTCGGAGGTAACCAACCTGAACAACCTACTGAGAGAGAGATGTTCAACCTCC 480
Db 421 ACCTTTTCACCTTCGGAGGTAACCAACCTGAACAACCTACTGAGAGAGAGATGTTCAACCTCC 480
QY 481 TCCTGCAACTCACAATATCTCAACGGCTGTGACCCGGTGTGACCAAGAGAGGCGCCCTAACTCG 540
Db 481 TCCTGCAACTCACAATATCTCAACGGCTGTGACCCGGTGTGACCAAGAGAGGCGCCCTGACTCG 540
QY 541 ATGCTGAGGGCTTGTGAGTGCCTGATGACAAGAGGAGGATGAGGATGAGGAGGAGT 600
Db 541 ATGCTGAGGGCTTGTGAGTGCCTGATGACAAGAGGAGGATGAGGATGAGGAGGAGT 600
QY 601 ATGATGAAGATGCTCAGGTAATGSAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Db 601 ATGATGAAGATGCTCAGGTAATGSAAGATGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
QY 661 AAGAGGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAAGCTTATAACAATGGAGAGG 720
Db 661 AAGAGGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAAGCTTATAACAATGGAGAGG 720
QY 721 TAGATGATGAGGAAGATGAACAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGAGGAAAT 780
Db 721 TAGATGATGAGGAAGATGAACAAGAGCTTGGTGAAGAAGAAGGGGTGAGAGGAGGAAAT 780
QY 781 AAGAACTGAAGATGAGGAGGAGGAGGATGCTTAAGTGAAGTAAATCTTATTTTGAAGAAAT 840
Db 780 GAGAACTGAAGATGAGGAGGAGGAGGATGCTTAAGTGAAGTAAATCTTATTTTGAAGAAAT 840
QY 841 CCTTTTGTGATTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTT 900
Db 840 CCTATTGTGATTGACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTTACTGTTT 899
QY 901 CCCTGAA 907
Db 901 CCCTGAA 906

RESULT 8
PCT-US02-25766-3866
; Sequence 3866, Application PC/TUS0225766
; GENERAL INFORMATION:
; APPLICANT: GENE LOGIC, INC.
; APPLICANT: MUNGER, William E.
; APPLICANT: FAULK, Ronald
; APPLICANT: SUN, Hongwei
; APPLICANT: SASAI, Hitoshi
; APPLICANT: WAGA, Iwao
; APPLICANT: YAMAMOTO, Jun
; TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
; FILE REFERENCE: 44921-5068-WO
; CURRENT APPLICATION NUMBER: PCT/US02/25766
; CURRENT FILING DATE: 2002-08-14
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 13946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3866
; LENGTH: 1052
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. U73477
PCT-US02-25766-3866
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Query Match	91.0%;	Score 925.4;	DB 1;	Length 1052;
Best Local Similarity	94.4%;	Pred. No. 6.6e-153;		
Matches 856;	Conservative 0;	Mismatches 51;	Indels 0;	Gaps 0;
Qy	1	GGGTTCCGGGTTTATTTGATTGAATTCGGCTGGCGGGAGCCCTCTGCAGACAGAGAGCGC	60	
Db	32	GGGTTCCGGGTTTATTTGATTGAATTCGCCCGCGGGAGCCCTCTGCAGAGAGAGAGCGC	91	
Qy	61	GAGAGATGGAGATGGGCAGACGGATTTCATTTAGAGCTCGGAAACGGGACGCCCTCTGATG	120	
Db	92	GAGAGATGGAGATGGGCAGACGGATTTCATTTAGAGCTCCGGAACAGGACGCCCTCTGATG	151	
Qy	121	TGAAGAACCTTGTCTCTGCACACACAGTCGGTCGANTGAAGGCAAACTCGAAGGCCCTCACAG	180	
Db	152	TGAAGAACCTTGTCTCTGCACACACAGTCGGTCGANTGAAGGCAAACTCGAAGGCCCTCACAG	211	
Qy	181	ATGAATTTGAAGAACCTGGAATTCCTTAAGTCAAACTCAAGCTAGGCTCACCTCAATTCGAA	240	
Db	212	ATGAATTTGAAGAACCTGGAATTCCTTAAGTCAAACTCAAGCTAGGCTCACCTCAATTCGAA	271	
Qy	241	ACTTACCAAAGTTAAACAAACTTTAAGAAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGG	300	
Db	272	ACTTACCAAAGTTAAACAAACTTTAAGAAGCTTGAACCTAAGCAGTAACAGAGCTCTCAGGG	331	
Qy	301	GCCTAGAAGTATTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAGTGGCAACA	360	
Db	332	GCCTAGAAGTATTGGCAGAAAAGTGTCCGAACCTCACGATCTAAATTTAGTGGCAACA	391	
Qy	361	AAATTTAAAGACCTCAGACCAATAGAGCCCTGAAAAAGTTGAAAACCTCCAGAGCTTAG	420	
Db	392	AAATTTAAAGACCTCAGACCAATAGAGCCCTGAAAAAGTTGAAAACCTCCAGAGCTTAG	451	
Qy	421	ACCTTTTCACCTTGGGAGGTAAACCAACCTGAAACACTACTTGAGAGAAGATGTTCAAGTCC	480	
Db	452	ACCTTTTCACCTTGGGAGGTAAACCAACCTGAAACACTACCGAGAAATGTGTTCAAGTCC	511	
Qy	481	TCCTGCAACTCACATATCTCAACGGCTGTGACCGGATGACAAGGAGGCCCTTAACTCGG	540	
Db	512	TCCGCAACTCACATATCTCAACGGCTGTGACCGGATGACAAGGAGGCCCTTAACTCGG	571	
Qy	541	ATGCTGAGGGCTTTGTGGAGTGCCTGGATGACAAGGAGGAGGATCAGGATGAGGAGAGT	600	
Db	572	ATGCTGAGGGCTACGTGGAGGCCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGAGT	631	
Qy	601	ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGAACTGT	660	
Db	632	ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGAACTGT	691	
Qy	661	AAGAGGAGGAGCTCAGTGGAGACCGAGGAGGAGGAGGATGAAGGTTATTAACAATCGAGGG	720	
Db	692	AAGAGGAGGAGCTCAGTGGAGAGGAGGAGGAGGATGAAGAGGTTATTAACAATCGAGGG	751	
Qy	721	TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAAGAAAGGGGTGAGAAGCGAAAAT	780	
Db	752	TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAAGAAAGGGGTGAGAAGCGAAAAC	811	
Qy	781	AAGAACTGAGATGAGGGGAGAAACAGATGCCTAAGTGGAAATATCTATTTTGAATAATT	840	
Db	812	GAGAACTGAGATGAGGGGAGAAAGATGATGACTAAGTGGAAATACCTATTTTGAATAATT	871	
Qy	841	CCTTTGTGATTTTACTGTTTTTTAGCCGTCACCCCTCTCCCGCCCGCCCTCTAATTCCTGCC	900	
Db	872	CCTATTGTGATTTGACTGTTTTTTACCAATATCCCTCTCCCGCCCGCCCTCTAATTCCTGCC	931	
Qy	901	CCCTGAA	907	
Db	932	CCCTGAA	938	

RESULT 9
US-09-205-070-14975
; Sequence 14975, Application US/09205070

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: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc.
: TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
: TITLE OF INVENTION: LIBRARIES
: FILE REFERENCE: 20411-748
: CURRENT APPLICATION NUMBER: US/09/205,070
: CURRENT FILING DATE: 1998-12-03
: NUMBER OF SEQ ID NOS: 45207
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 14975
: LENGTH: 2398
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-205-070-14975

```

Query Match. 91.0%; Score 825.4; DB 16; Length 2398;									
Best Local Similarity 94.4%; Pred. No. 7.6e-153;									
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps									
Qy	1	GGGTTCGGGGTTTATTCAATGAATTCGGCTGGCGGGAGCCCTCGAGAGAGAGAGCCG	60						
Db	32	GGGTTCGGGGTTTATTGAATTCGCCGGCGGGAGCCCTCTCGAGAGAGAGAGCCG	91						
Qy	61	GAGAGATGGAGATGGGCAGACGGATTCAATTAGAGCTGCGGAACGGAGCCCTCTGATG	120						
Db	92	GAGAGATGGAGATGGGCAGACGGATTCAATTAGAGCTGCGGAACGGAGCCCTCTGATG	151						
Qy	121	TGAAGAACCTTGCTCTGGCAACAGTCGGTCGAATGAAGCAAACTCGAAGGCCTCACAG	180						
Db	152	TGAAGAACCTTGCTCTGGCAACAGTCGGTCGAATGAAGCAAACTCGAAGGCCTCACAG	211						
Qy	181	ATGAATTTGAAGAACTGGAATTCCTTAAGTACAATCAACGTAGGCCCTCACTCAATCGCAA	240						
Db	212	ATGAATTTGAAGAACTGGAATTCCTTAAGTACAATCAACGTAGGCCCTCACTCAATCGCAA	271						
Qy	241	ACTTACCAAAAGTTAAACAAACTTTAAGAAGCTTGAACCTTAAGCAGTAACAGAGCCTCAGTGG	300						
Db	272	ACTTACCAAAAGTTAAACAAACTTTAAGAAGCTTGAACCTTAAGCAGTAACAGAGCCTCAGTGG	331						
Qy	301	GCCTAGAAGTATTTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA	360						
Db	332	GCCTAGAAGTATTTGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA	391						
Qy	361	AAATTTAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG	420						
Db	392	AAATTTAAGACCTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTCGAGAGCTTAG	451						
Qy	421	ACCTTTTCACTTCGGAGGTAAACCAACTGAACAACTACTGAGAGAAGATGTTCAAGCTCC	480						
Db	452	ACCTTTTCAATTCGAGGTAAACCAACTGAACCACTACCGAGAAAATGTGTTCAAGCTCC	511						
Qy	481	TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAGGAGGCCCTTAAGTCGG	540						
Db	512	TCCGCAACTCACATATCTCGAGGGTATGACCCGGACGACAGGAGGCCCTGAGCTCGG	571						
Qy	541	ATGCTGAGGGCTTTGTGGAGTGCTGGATCACAAAGGAGGAGGATGAGGATGAGGAGGAGT	600						
Db	572	ATGCTGAGGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	631						
Qy	601	ATGATGAAGATGCTCAGGTAATGGAAAGATGAGGAGGACGAGGATGAGGAGGAGCAACCTG	660						
Db	632	ATGATGAAGATGCTCAGGTAAGTGGAAAGACGAGGAGGACGAGGATGAGGAGGAGGAGTGG	691						
Qy	661	AAGAGGAGGACGTGAGTGGAGACGAGGAGGAGGAGGATCAAGGTTATACATGAGAGG	720						
Db	692	AAGAGGAGGACGTGAGTGGAGAGGAGGAGGAGGATGAAGAAGTTATACGATGAGAGG	751						
Qy	721	TAGATGATGAGGAAGATGAAGAAGAGCTTGGTCAAGAAGAAAGGGGTGAGAAGCGAAAT	780						
Db	752	TAGATGACGAGGAGATGAGAGAGCTTGGTGAAGAAAGAGGGGTGAGAAGCGGAAC	811						
Qy	781	AAGAACTGAAGATGAGGAGAGACGATGCCCTAAGTGGAAATATCTATTTTGAATAATT	840						

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Db 812 GAGAACTGAAGATGAGGAGGAAGATGATGACTAAGTGAATAACCTATTTTGAATAATT 871
QY 841 CTTTTGTGATTTACTCTTTTGTAGCCCTACCCCTCTCCGCCCCCACTCTAATCCTGCC 900
Db 872 CCTATTGTGATTTGACTGTTTATACCCATATCCCTCTCCGCCCCCACTCTAATCCTGCC 931
QY 901 CCCTGAA 907
Db 932 CCCTGAA 938

RESULT 10
US-09-340-623-14975
; Sequence 14975, Application US/09340623
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748CON1
; CURRENT APPLICATION NUMBER: US/09/340,623
; CURRENT FILING DATE: 1999-06-28
; EARLIER APPLICATION NUMBER: US 09/205,070
; EARLIER FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14975
; LENGTH: 2398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-340-623-14975

Query Match 91.0%; Score 825.4; DB 17; Length 2398;
Best Local Similarity 94.4%; Pred. No. 7.6e-153;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGGCCTCTGCAGAGAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTGAATTCGGCGGGGAGGCCTCTGCAGAGAGAGAGCGC 91
QY 61 GAGAGATGAGATGGCAGACGGATTCTATTAGAGCTGCGGAACGGAGCGCCTCTGATG 120
Db 92 GAGAGATGAGATGGCAGACGGATTCTATTAGAGCTGCGGNACAGAGAGCGCCTCTGATG 151
QY 121 TGAAGAAGCTTCTCTGGACACAGTCGGTGAAGCTGCGGAACGGAGCGCTCAAGTCGCA 180
Db 152 TGAAGAAGCTTCTCTGGACACAGTCGGTGAAGCTGCGGAACGGAGCGCTCAAGTCGCA 211
QY 181 ATGAATTTGAAGAACTGGAATTTTAAGTACAACTCAAGCTAGGCCTCACTCAATCGCAA 240
Db 212 ATGAATTTGAAGAACTGGAATTTTAAGTACAACTCAAGCTAGGCCTCACTCAATCGCAA 271
QY 241 ACTTACCAAGCTTAAACAACTTAAAGAGCTTGAACCTGCGGAACGGAGCGCTCAAGTC 300
Db 272 ACTTACCAAGCTTAAACAACTTAAAGAGCTTGAACCTGCGGAACGGAGCGCTCAAGTC 331
QY 361 AATTTAAGACCTTCAGCAATAGAGCCCTGAAAGAGTTAGAAAACCTTCAGAGAGCTTAG 420
Db 392 AATTTAAGACCTTCAGCAATAGAGCCCTGAAAGAGTTAGAAAACCTTCAGAGAGCTTAG 451
QY 421 ACCTTTTCACTTCGAGAGTAAACAACTTGAACAACTACTGAGAGAGAGATGTTTCAAGCTCC 480
Db 452 ACCTTTTCACTTCGAGAGTAAACAACTTGAACAACTTACCGAGAGAGATGTTTCAAGCTCC 511
QY 481 TCCTGCAACTACATATCTCAAGGGCTGTGACCCGGATGACAGAGAGGCCCTCACTACG 540
Db 512 TCCTGCAACTACATATCTCAAGGGCTGTGACCCGGATGACAGAGAGGCCCTCACTACG 571
QY 541 ATGGTGAAGGCTTTTGGAGTGCTCGATGACAGAGAGGAGGATGAGGAGGAGT 600
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Db 572 ATCCTGAGGCTTACGTGGAGGCCCTGGATGATGAGGAGGAGGATGAGGAGGAGT 631
QY 601 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 660
Db 632 ATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 691
QY 661 AAGAGGAGGAGTGTGAGTGGAGGAGGAGGAGGAGGATGAAGGTTATACATATGAGAGG 720
Db 692 AAGAGGAGGAGTGTGAGTGGAGGAGGAGGAGGAGGATGAAGGTTATACGATGGAGAGG 751
QY 721 TAGATGATGAGGAAGATGAAGAGAGCTTGGTGAAGAAAGAGGGTCAAGACGCAAAAT 780
Db 752 TAGATGAGGAGGAAGATGAAGAGAGCTTGGTGAAGAAAGAGGGTCAAGACGCAAAAT 811
QY 781 AAGAACTGAAGATGAGGAGGAGGAGGATGAGGAGGAGGATGAAGGTTATACATATGAG 840
Db 812 GAGAACTGAAGATGAGGAGGAGGAGGATGAGGAGGAGGATGAAGGTTATACATATGAG 871
QY 841 CTTTGTGATTTTACTGTTTGTAGCGGTACCCCTCTCCGCCCCCACTCTAATCCTGCC 900
Db 872 CTTTGTGATTTTACTGTTTGTAGCGGTACCCCTCTCCGCCCCCACTCTAATCCTGCC 931
QY 901 CCCTGAA 907
Db 932 CCCTGAA 938

RESULT 11
US-09-898-888-14975
; Sequence 14975, Application US/09898888
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-748CON1
; CURRENT APPLICATION NUMBER: US/09/898,888
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/340,623
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14975
; LENGTH: 2398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-898-888-14975

Query Match 91.0%; Score 825.4; DB 33; Length 2398;
Best Local Similarity 94.4%; Pred. No. 7.6e-153;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGAGGCCTCTGCAGAGAGAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTGAATTCGGCGGGGAGGCCTCTGCAGAGAGAGAGCGC 91
QY 61 GAGAGATGAGATGGGAGGAGGAGGATTCATTAGAGCTGCGGAACGGAGCGCCTCTGATG 120
Db 92 GAGAGATGAGATGGGAGGAGGAGGATTCATTAGAGCTGCGGAACGGAGCGCCTCTGATG 151
QY 121 TGAAGAAGCTTGTCTCTGGACACAGTCGGTGAAGCTGCGGAACGGAGCGCTCAAGTCAG 180
Db 152 TGAAGAAGCTTGTCTCTGGACACAGTCGGTGAAGCTGCGGAACGGAGCGCTCAAGTCAG 211
QY 181 ATGAATTTGAAGAACTGGAATTTTAAGTACAACTCAAGCTAGGCCTCACTCAATCGCAA 240
Db 212 ATGAATTTGAAGAACTGGAATTTTAAGTACAACTCAAGCTAGGCCTCACTCAATCGCAA 271
QY 241 ACTTACCAAGCTTAAACAACTTAAAGAGCTTGAACCTGCGGAACGGAGCGCTCACTG 300
Db 272 ACTTACCAAGCTTAAACAACTTAAAGAGCTTGAACCTGCGGAACGGAGCGCTCACTG 331
QY 301 GCCTAGAGAGTATGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
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Db 332 GCCTAGAAAGTATTGGCAGAAAAGTGTCCGAACCTCACGCATCTAAATTTAAGTGGCAACA 391
Qy 361 AAATTAAGAGCTCAGCACATAGAGCCCTGAAAGATTAGAAAACCTCGAGAGCTTAG 420
Db 392 AAATTAAGAGCTCAGCACATAGAGCCACTGAAAAGATTAGAAAACCTCAAGAGCTTAG 451
Qy 421 ACCTTTTCACTTGGAGGTAAACCAACCTGAACAACCTACTCAGAGAAAGATGTTCAAGCTCC 480
Db 452 ACCTTTTCAATTCGAGTAGTACCAACCTGAACGACTACCGAGAAATGTTGTTCAAGCTCC 511
Qy 481 TCCTGCAACTCACATATCTAACCGCTGTGACCCGGATGACAAGAGGCCCCCTAACTCGG 540
Db 512 TCCCGCAACTCACATATCTCAGCGCTATGACCGGGACGACAAGGAGGCCCTGACTCGG 571
Qy 541 ATGCTGAGGGCTTTGTGAGTGCCTGGATGACAGAGGAGGAGGTGAGGATGAGGAGGAGT 600
Db 572 ATGCTGAGGGCTACGTGAGGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631
Qy 601 ATGATGAAGATGCTCAGGTAAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Db 632 ATGATGAAGATGCTCAGGTAAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 691
Qy 661 AAGAGGAGGAGCTGAGTGGAGACAGAGAGGAGGAGGATGAGGATGAGGAGGAGGAGT 720
Db 692 AAGAGGAGGAGCTGAGTGGAGAGGAGGAGGAGGATGAGGATGAGGAGGAGGAGT 751
Qy 721 TAGATGATGAGGAGATGAAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGT 780
Db 752 TAGATGAGGAGAGATGAAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGT 811
Qy 781 AAGAACTGAAGATGAGGAGAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGT 840
Db 812 GAGAACTGAAGATGAGGAGAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGT 871
Qy 841 CCTTTTCTGATTTTACTGTTTATGCGGTACCCCTCTCCCGCCCACTTAATCTCGTGC 900
Db 872 CCTATTGATTTGACTGTTTATACCATATCCCTCTCCCGCCCACTTAATCTCGTGC 931
Qy 901 CCCTGAA 907
Db 932 CCCTGAA 938

RESULT 12

US-09-898-888A-14975
; Sequence 14975, Application US/09898888A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
; FILE OF INVENTION: LIBRARIES
; FILE REFERENCE: 20411-748CON1
; CURRENT APPLICATION NUMBER: US/09/898,888A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/340,623
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: US 09/205,070
; PRIOR FILING DATE: 1998-12-03
; NUMBER OF SEQ ID NOS: 45207
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14975
; LENGTH: 2398
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-898-888A-14975

Query Match 91.0%; Score 825.4; DB 33; Length 2398;
Best Local Similarity 94.4%; Pred. No. 7.6e-153;
Matches 856; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 1 GGGTCCGGGTTTATTGATTGATTCGGCTGCGCGGGAGGCTCTGCAGAGAGAGAGCGC 60
Db 32 GGGTCCGGGTTTATTGATTGATTCGGCTGCGCGGGAGGCTCTGCAGAGAGAGAGCGC 91

Qy 61 GAGAGATGGAGATGGGCAGACGGATTCAATTTAGAGCTGGGAAACGGGAGCCCTCTGTAGT 120
Db 92 GAGAGATGGAGATGGGCAGACGGATTCAATTTAGAGCTGGGAAACGGGAGCCCTCTGTAGT 151
Qy 121 TGAAGAACTTGTCTTGGACACAGTCGGTCGTAATGAAGCAAACTCGAAGGCGCTCACAG 180
Db 152 TGAAGAACTTGTCTTGGACACAGTCGGTCGTAATGAAGCAAACTCGAAGGCGCTCACAG 211
Qy 181 ATGAATTTGAAGAACTTGAATTTCTTAAGTACAATCAACCTAGGCGCTCACCTCAATCGCAA 240
Db 212 ATGAATTTGAAGAACTTGAATTTCTTAAGTACAATCAACCTAGGCGCTCACCTCAATCGCAA 271
Qy 241 ACTTACCAAGTTAAACAACCTTTAGAAGCTTGAACCTAAGCAGTAAACAGAGCTTCAGGG 300
Db 272 ACTTACCAAGTTAAACAACCTTTAGAAGCTTGAACCTAAGCAGTAAACAGAGCTTCAGGG 331
Qy 301 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAAGCTCATACATCTAAATTTAAGTGGCAACA 360
Db 332 GCCTAGAAGTATTGGCAGAAAAGTGTCCAAAGCTCATACATCTAAATTTAAGTGGCAACA 391
Qy 361 AAATTAAGACCTTCAGCACAAATAGAGCCCTGAAAAGTTAGAAAACCTTCGAGAGCTTAG 420
Db 392 AAATTAAGACCTTCAGCACAAATAGAGCCACTGAAAAGTTAGAAAACCTTCAGAGCTTAG 451
Qy 421 ACCTTTTCACTTTCGAGGTAAACCAACCTGAACAACCTACTCTGAGAGAGATGTTCAAAGCTCC 480
Db 452 ACCTTTTCAATTTGCGAGGTAAACCAACCTGAACGACTTACCGAGAAAATGTGTTCAAAGCTCC 511
Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGATGACAAAGGAGGCGCCCTACTCGG 540
Db 512 TCCCGCAACTCACATATCTCGAGCGCTATGACCGGAGCACAAGGAGGCGCCCTGACTCGG 571
Qy 541 ATGCTGAGGGCTTTTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAGT 600
Db 572 ATGCTGAGGGCTACGTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631
Qy 601 ATGATGAAGATCCTCAGGTAAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 660
Db 632 ATGATGAAGATCCTCAGGTAAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGT 691
Qy 661 AAGAGGAGGAGTGTGAGTGGAGACGAGGAGGAGGAGGATGAGGTTAATCAATGGAGAGG 720
Db 692 AAGAGGAGGAGTGTGAGTGGAGAGGAGGAGGAGGATGAGGAGGAGGAGGAGGAGG 751
Qy 721 TAGATGATGAGGAGATGAAGAGAGCTTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGT 780
Db 752 TAGATGAGGAGAGATGAAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGT 811
Qy 781 AAGAACTGAAGATGAGGAGAGAGAGCTTGAAGTGAATTAATCTATTGTAATAATT 840
Db 812 GAGAACTGAAGATGAGGAGAGAGAGATGATGACTAAGTGAATTAATCTATTGTAATAATT 871
Qy 841 CCTTTTGTGATTTTACTGTTTATAGCCGTACCCCTCTCCCGCCCACTTAATCTCTGCC 900
Db 872 CCTATTGATTTGACTGTTTATACCATATCCCTCTCCCGCCCACTTAATCTCTGCC 931
Qy 901 CCCTGAA 907
Db 932 CCCTGAA 938

RESULT 13

US-09-591-500-13
; Sequence 13, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodoli, Shihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06

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; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-09-591-500-13

Query Match      90.8%; Score 823.8; DB 22; Length 907;
Best Local Similarity 94.3%; Pred. No. 1.3e-152;
Matches 855; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATGATGTAATTCGGCTGCGCGGGAGGCTCTGCAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATGATGTAATTCGCGCGGGAGGCTCTGCAGAGAGAGAGCGC 60

QY 61 GAGAGATGAGATGGGACAGCGATTCTTTAGAGCTGCGGAACGGGACGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGGACAGCGATTCTTTAGAGCTGCGGNACAGGACGCCCTCTGATG 120

QY 121 TGAAGAACTTCTCTGGCAACACGTGCGTGAATGAAGGCAAACTCGAAGCCCTCAG 180
Db 121 TGAAGAACTTCTCTGGCAACACGTGCGTGAATGAAGGCAAACTCGAAGCCCTCAG 180

QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACAACTCAAGTAGGCTCACCCTCAATCGCAA 240
Db 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACAACTCAAGTAGGCTCACCCTCAATCGCAA 240

QY 241 ACTTACCAAGTTAAACAACTTGAAGCTTGAACCTAAGCACTAACAGAGCTCAGTGG 300
Db 241 ACTTACCAAGTTAAACAACTTGAAGCTTGAACCTAAGCACTAACAGAGCTCAGTGG 300

QY 301 GCGTAGAAGTATTCACAGGCTGCTGATGAGAGGAGGATGAGGAGGAGTGGAGGAGT 420
Db 301 GCGTAGAAGTATTCACAGGCTGCTGATGAGAGGAGGATGAGGAGGAGTGGAGGAGT 420

QY 361 AAATTTAAAGAGCTTGAAGAGAGCTTGGTGAAGAGAGAGAGGCTCAGAGCGGAGGAGT 480
Db 361 AAATTTAAAGAGCTTGAAGAGAGCTTGGTGAAGAGAGAGAGGCTCAGAGCGGAGGAGT 480

QY 781 AAGAACTGAAGATGAGGAGAGAGAGCTGCTTAAAGTGAATTAATCTATTTTGAAGAAAT 840
Db 781 AAGAACTGAAGATGAGGAGAGAGAGCTGCTTAAAGTGAATTAATCTATTTTGAAGAAAT 840
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Db 781 GAGAACTGAAGATGAGGAGAGAGATGATGACTAACTGAATAACCTATTTTGAAGAAAT 840
QY 841 CTTTTGTGATTTTACTGTTTGTAGCGGTACCCCTCTCCCGCCACCTCTAATCTCTGCC 900
Db 841 CTTATTGTGATTTGACTGTTTACCCATATCCCTCTCCCGCCCTCTTAATCTCTGCC 900
QY 901 CCCTGAA 907
Db 901 CCCTGAA 907

RESULT 14
US-09-591-500-25
; Sequence 25, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkoi, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-591-500-25

Query Match      90.7%; Score 822.2; DB 22; Length 907;
Best Local Similarity 94.2%; Pred. No. 2.8e-152;
Matches 854; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 1 GGGTTCGGGGTTTATGATGTAATTCGGCTGCGCGGGAGGCTCTGCAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATGATGTAATTCGCGCGGGAGGCTCTGCAGAGAGAGAGCGC 60

QY 61 GAGAGATGAGATGGGACAGCGATTCTTTAGAGCTGCGGAACGGGACGCCCTCTGATG 120
Db 61 GAGAGATGAGATGGGACAGCGATTCTTTAGAGCTGCGGAACAGGACGCCCTCTGATG 120

QY 121 TGAAGAACTTCTCTGGCAACACGTGCGTGAATGAAGGCAAACTCGAAGCCCTCAG 180
Db 121 TGAAGAACTTCTCTGGCAACACGTGCGTGAATGAAGGCAAACTCGAAGCCCTCAG 180

QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACAACTCAATCAAGTAGGCTCACCCTCAATCGCAA 240
Db 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACAACTCAAGTAGGCTCACCCTCAATCGCAA 240

QY 241 ACTTACCAAGTTAAACAACTTGAAGAGCTTGAACCTAAGCACTAACAGAGCTCAGTGG 300
Db 241 ACTTACCAAGTTAAACAACTTGAAGAGCTTGAACCTAAGCACTAACAGAGCTCAGTGG 300

QY 301 GCGTAGAAGTATTCAGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 301 GCGTAGAAGTATTCAGCAGAAAGTGTCCGAACCTCAGCAGCTCAATTTAAGTGGCAACA 360

QY 361 AAATTTAAAGAGCTCAGCAGCAATAGAGCCCTCGAAAAGTTAGAAAAGTTAGAGAGCTTAG 420
Db 361 AAATTTAAAGAGCTCAGCAGCAATAGAGCCCTCGAAAAGTTAGAAAAGTTAGAGAGCTTAG 420

QY 421 ACCTTTTCACTTGGCGAGTAACCACTGGAACCTGGAACCTGGAACCTGGAACCTGGAACCTG 480
Db 421 ACCTTTTCACTTGGCGAGTAAACCACTGGAACCTGGAACCTGGAACCTGGAACCTGGAACCT 480

QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCCGATGACAAAGGAGGCGCCCTAATCGG 540
Db 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCCGATGACAAAGGAGGCGCCCTAATCGG 540
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Db 481 TCCGCAACTCACATATCTCGACGCTATGACCGGACGACAGAGGCCCTGACTCGG 540
Qy 541 ATGCTGAGGGCTTTGTGGAGTGCCTGGATGACACAGGAGGAGGATGAGGATGAGGAGGAGT 600
Db 541 ATGCTGAGGGCTACGTGGAGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 600
Qy 601 ATGATGAAGATGCTCAGTGAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Db 601 ATGATGAAGATGCTCAGTGAATGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Qy 661 AAGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
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Qy 721 TAGATGATGAGGAGATGAAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGT 780
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Qy 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Db 781 GAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Qy 841 CCTTTGTGATTTACTGTTTTTGTAGCGGTACCCCTCTCCCTCCCTCCCTCCCTCTCTATCTGCTGCC 900
Db 841 CCTATTGTGATTTGACTGTTTTTACCCTATATCCCTCTCCCTCCCTCCCTCTCTATCTGCTGCC 900
Qy 901 CCCTGAA 907
Db 901 CCCTGAA 907

RESULT 15
US-09-591-500-28
; Sequence 28, Application US/09591500
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/09/591,500
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-09-591-500-28

Query Match 90.7%; Score 822.2; DB 22; Length 907;
Best Local Similarity 94.2%; Pred. No. 2.8e-152;
Matches 854; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
Qy 1 GGGTTCGGGGTTTATTGATTGAATTCGGCTGGCGGGGAGCCCTCTCCAGAGAGAGAGCCG 60
Db 1 GGGTTCGGGGTTTATTGATTGAATTCGGCGGGGAGCCCTCTGAGAGAGAGAGCCG 60
Qy 61 GAGAGATGAGATGGGACGAGGATTCATTTAGAGCTGCGGAACGGGAGCCCTCTGTATG 120
Db 61 GAGAGATGAGATGGGACGAGGATTCATCTAGAGCTGCGGACAGGAGCCCTCTGTATG 120
Qy 121 TGAAGAAGCTTGTCTGGACACAGTCTGGTTCGAATGAAGGCAAACTCGAAGCGCTCACAG 180

Db 121 TGAAGAAGCTTGTCTGGTCAACAGTCTGGTCAATGAAGGCAAACTCGAAGCGCTCACAG 180
Qy 181 ATGAATTTGAAGAAGCTTGAATTTCTTAAGTACAACTAACCTAGGCTTCACCTCAATCGCAA 240
Db 181 ATGAATTTGAAGAAGCTTGAATTTCTTAAGTACAACTAACCTAGGCTTCACCTCAATCGCAA 240
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Db 241 ACTTACCAAGTTAAACAACCTTAAGAAGCTTGAAGTAAAGCAGTAAACAGAGCTTCAGTGG 300
Qy 301 GCTAGAACTTATGGCAGAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
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Qy 361 AAATTAAGACCTTCAGCACAATAGAGCCCTGAAAAGTTAGAAAACCTTCGAGAGCTAG 420
Db 361 AAATTAAGACCTTCAGCACAATAGAGCCCTGAAAAGTTAGAAAACCTTCAGAGCTAG 420
Qy 421 ACCTTTTCACTTTCGAGGTAAACCACTGAACTACTTGAGAGAGATGTTTCAAGCTCC 480
Db 421 ACCTTTTCACTTTCGAGGTAAACCACTGAACTACTTGAGAGAGATGTTTCAAGCTCC 480
Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGATCACAAAGAGGAGGAGGAGGAGGAGT 540
Db 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCGGATCACAAAGAGGAGGAGGAGGAGGAGT 540
Qy 541 ATGCTGAGGGCTTGTGGAGTGCCTGGATGACAAGGAGGAGGAGGATGAGGATGAGGAGGAGT 600
Db 541 ATGCTGAGGGCTTGTGGAGTGCCTGGATGACAAGGAGGAGGAGGATGAGGATGAGGAGGAGT 600
Qy 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Db 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGGAGGAGGATGAGGAGGAGGAGGAGT 660
Qy 661 AAGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
Db 661 AAGAGGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
Qy 721 TAGATGATGAGGAGATGAAGAGAGCTTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGT 780
Db 721 TAGATGAGGAGGAGATGAAGAGAGCTTGGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGT 780
Qy 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Db 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Qy 841 CCTTTTGTGATTTTACTGTTTTTGTAGCGGTACCCCTCTCCCTCCCTCTCTAACTCTGCTGCC 900
Db 841 CCTATTGTGATTTGACTGTTTTTACCCTATATCCCTCTCCCTCCCTCTCTAACTCTGCTGCC 900
Qy 901 CCCTGAA 907
Db 901 CCCTGAA 907

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Job time : 2187.68 secs

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 21:58:38 ; Search time 56,5612 Seconds
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Title: US-09-591-500-4

Perfect score: 907

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 361435 seqs, 346278564 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	907	100.0	907	6	US-10-273-334-4		Sequence 4, Appl
2	884.6	97.5	907	6	US-10-273-334-30		Sequence 30, Appl
3	857.8	94.6	905	6	US-10-273-334-19		Sequence 19, Appl
4	857.8	94.6	905	6	US-10-273-334-26		Sequence 26, Appl
5	856.2	94.4	905	6	US-10-273-334-7		Sequence 7, Appl
6	833.4	91.9	907	6	US-10-273-334-9		Sequence 9, Appl
7	827.8	91.3	906	6	US-10-273-334-33		Sequence 33, Appl
8	823.8	90.8	907	6	US-10-273-334-13		Sequence 13, Appl
9	822.2	90.7	907	6	US-10-273-334-25		Sequence 25, Appl
10	822.2	90.7	907	6	US-10-273-334-28		Sequence 28, Appl
11	817.8	90.2	905	6	US-10-273-334-17		Sequence 17, Appl
12	812.8	89.6	908	6	US-10-273-334-32		Sequence 32, Appl
13	801.8	88.4	905	6	US-10-273-334-11		Sequence 11, Appl
14	782.2	86.2	907	6	US-10-273-334-6		Sequence 6, Appl
15	751	82.8	895	6	US-10-273-334-23		Sequence 23, Appl
16	738.2	81.4	895	6	US-10-273-334-21		Sequence 21, Appl
17	736.6	81.2	895	6	US-10-273-334-15		Sequence 15, Appl
18	716	78.9	889	6	US-10-273-334-3		Sequence 3, Appl
19	716	78.9	716	6	US-10-273-334-1		Sequence 1, Appl
20	375.8	41.4	1937	5	US-09-724-676-18913		Sequence 18913, A
21	375.8	41.4	1937	5	US-09-724-676A-18913		Sequence 18913, A
22	129.4	14.3	147	5	US-09-513-999C-24429		Sequence 24429, A
23	109.2	12.0	3489	6	US-10-194-046-1		Sequence 1, Appl
24	105.2	11.6	616	6	US-10-266-131-2731		Sequence 2731, Ap
25	101	11.1	659158	5	US-09-771-208A-20		Sequence 20, Appl
26	100.4	11.1	648	6	US-10-152-319A-2106		Sequence 2106, Ap

27	99.4	11.0	318	5	US-09-513-999C-14277	Sequence 14277, A
28	95	10.5	2550	5	US-09-724-676-41735	Sequence 41735, A
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30	95	10.5	2709	5	US-09-724-676-41736	Sequence 41736, A
31	95	10.5	2709	5	US-09-724-676A-41736	Sequence 41736, A
32	95	10.5	2805	5	US-09-724-676-41728	Sequence 41728, A
33	95	10.5	2805	5	US-09-724-676A-41728	Sequence 41728, A
34	95	10.5	2964	5	US-09-724-676A-41729	Sequence 41729, A
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36	95	10.5	3382	5	US-09-724-676-41723	Sequence 41723, A
37	95	10.5	3382	5	US-09-724-676A-41723	Sequence 41723, A
38	95	10.5	3637	5	US-09-724-676-41717	Sequence 41717, A
39	95	10.5	3637	5	US-09-724-676A-41717	Sequence 41717, A
40	95	10.5	3817	5	US-09-724-676A-41745	Sequence 41745, A
41	95	10.5	3817	5	US-09-724-676A-41745	Sequence 41745, A
42	95	10.5	4072	5	US-09-724-676-41732	Sequence 41732, A
43	95	10.5	4072	5	US-09-724-676A-41732	Sequence 41732, A
44	92.2	10.2	2001	5	US-09-724-676-40546	Sequence 40546, A
45	92.2	10.2	2001	5	US-09-724-676A-40546	Sequence 40546, A

ALIGNMENTS

RESULT 1
US-10-273-334-4
; Sequence 4, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheaver, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodko, Shrinani S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-4

Query Match 100.0%; Score 907; DB 6; Length 907;
Best Local Similarity 100.0%; Pred. No. 3e-189;
Matches 907; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy	1	GGGTTCGGGGTTTATTGATTGCGCTGGCGCGGAGCCTCTGCAGAGAGAGCGC	60
Db	1	GGGTTCGGGGTTTATTGATTGCGCTGGCGCGGAGCCTCTGCAGAGAGAGCGC	60
Qy	61	GAGAGATGGAGATGGCGAGCGGATTATTAGAGCTGCGGAACGGGACGCCCTCTGATG	120
Db	61	GAGAGATGGAGATGGCGAGCGGATTATTAGAGCTGCGGAACGGGACGCCCTCTGATG	120
Qy	121	TGAAGAACTGTCTCGACACAGTCGGTCGATGAAGCAACTCGAGGCTCAGAC	180
Db	121	TGAAGAACTGTCTCGACACAGTCGGTCGATGAAGCAACTCGAGGCTCAGAC	180
Qy	181	ATGAATTTGAAGAACTGGAATTTCTTAAGTACAATCAACGTAGGCTCACCTCAATCGCA	240
Db	181	ATGAATTTGAAGAACTGGAATTTCTTAAGTACAATCAACGTAGGCTCACCTCAATCGCA	240
Qy	241	ACTTACCAGATTAAACAACTTAAGAGGTTGAAGCTTAAGCAGTAAACAGAGCCTCAGTGG	300
Db	241	ACTTACCAGATTAAACAACTTAAGAGGTTGAAGCTTAAGCAGTAAACAGAGCCTCAGTGG	300

US-10-273-334-19

; Sequence 19, Application US/10273334

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kochevar, Gerald J.

; APPLICANT: Brody, Jonathan R.

; APPLICANT: Kodkol, Shrihari S.

; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

; FILE REFERENCE: 031787.0076

; CURRENT APPLICATION NUMBER: US/10/273.334

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: US/09/591,500

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: PCT/US98/26433

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 905

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (64)..(453)

; OTHER INFORMATION:

US-10-273-334-19

Query Match

Best Local Similarity 94.6%; Score 857.8; DB 6; Length 905;

Matches 883; Conservative 0; Mismatches 22; Indels 2; Gaps 1;

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QY 1 GGGTTCGGGGTTTATTGATTAATTCGGCTGGCGGGAGCCCTCTGAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTAATTCGGCTGGCGGGAGCCCTCTGAGAGAGAGAGCGT 58
QY 61 GAGAGATGGAGATGGGAGAGCGGATTCATTTAGAGCTGCGGAGCGGAGCCCTCTGATG 120
Db 59 GAGAGATGGAGATGGGAGAGCGGATTCATTTAGAGCTGCGGAGCGGAGCCCTCTGATG 118
QY 121 TGAAGAACTTGCTCTGGAGCAACAGTCGATGAATGAAGCAAACTCGAAGCGCTCACAG 180
Db 119 TGAAGAACTTTCTCTGGAGCAACAGTCAGTCAATGAAGCAAACTTGAAGCGCTCACAG 178
QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACATGAGCCCTCACTCAATCGCAA 240
Db 179 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACATGAGCCCTCACTCAATCGCAA 238
QY 241 ACTTACCAAGTTAAACAACTTAAGAAGCTTGAAGCTTAAGCTAAGCAAGAGCGCTCAGTCG 300
Db 239 ACTTGCCAAAGTTAAACAACTTAAGAAGCTTGAAGCTTAAGCTAAGCAAGAGCGCTCAGTCG 298
QY 301 GCCTAGAAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 299 GCCTAGAAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 358
QY 361 AAATTAAAGACCTCAGCACAATAGAGCCCTGAAAAGTTAGAAACCTCGAGAGCTTAG 420
Db 359 AAATTAAAGACCTCAGCACAATAGAGCCCTGAAAAGTTAGAAACCTCGAGAGCTTAG 418
QY 421 ACCTTTTCACTTCGGAGGTAAACCAACTGAACAACTTACTGAGAGAGATGTTCAAGCTCC 480
Db 419 ACCTTTTCACTTCGGAGGTAAACCAACTGAAACAACTTACTGAGAGAGATGTTCAAGCTCC 478
QY 481 TCCTGCAACTCACAATCTCAACGGGTGTGACCCGGATGACAGAGAGCGCCCTTAATCTCGG 540
Db 479 TCCTGCAACTCACAATCTCAACGGGTGTGACCCGGATGACAGAGAGCGCCCTTAATCTCGG 538
QY 541 ATGGTGAGGCGCTTTGTGGAGTGGCTGGATGACAAGAGAGAGATGAGGATGAGGAGGAGT 600
Db 539 ATGGTGAGGCGCTTTGTGGAGTGGCTGGATGACAAGAGAGAGATGAGGATGAGGAGGAGT 598
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QY 601 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGACGAGGATGAGGAGGAGGAACTGTG 660
Db 599 ATGATGAAGATGCTCAGGTAAATGGAAGATGAGGAGACGAGGATGAGGAGGAGGAACTGTG 658
QY 661 AAGAGGAGGACGTGAGTGGAGAGCGAGGAGAGAGATGAAGGTTATACAAATGGAGAGG 720
Db 659 AAGAGGAGGACGTGAGTGGAGAGCGAGGAGAGAGATGAAGGTTATACAAATGGAGAGG 718
QY 721 TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAAGAGGGTCAAGAAGCGGAAAT 780
Db 719 TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAAGAGGGTCAAGAAGCGGAAAT 778
QY 781 AAGAACTGAAGATGAGGAGAGAGAGCGATGCCCTAAGTGAATAATCTATTTTGAATAAT 840
Db 779 AAGAACTGAAGATGAGGAGAGAGAGCGATGCCCTAAGTGAATAATCTATTTTGAATAAT 838
QY 841 CCTTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCGCCCTCACTCAATCTGCGC 900
Db 839 CCTTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCGCCCTCACTCAATCTGCGC 898
QY 901 CCTGTAA 907
Db 899 CCTGTAA 905
```

RESULT 4

US-10-273-334-26

; Sequence 26, Application US/10273334

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kochevar, Gerald J.

; APPLICANT: Brody, Jonathan R.

; APPLICANT: Kodkol, Shrihari S.

; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY

; FILE REFERENCE: 031787.0076

; CURRENT APPLICATION NUMBER: US/10/273.334

; CURRENT FILING DATE: 2002-10-18

; PRIOR APPLICATION NUMBER: US/09/591,500

; PRIOR FILING DATE: 2000-12-06

; PRIOR APPLICATION NUMBER: PCT/US98/26433

; PRIOR FILING DATE: 1998-12-11

; PRIOR APPLICATION NUMBER: US 60/069,677

; PRIOR FILING DATE: 1997-12-11

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 26

; LENGTH: 905

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (64)..(453)

; OTHER INFORMATION:

US-10-273-334-26

Query Match

Best Local Similarity 94.6%; Score 857.8; DB 6; Length 905;

Matches 883; Conservative 0; Mismatches 22; Indels 2; Gaps 1;

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QY 1 GGGTTCGGGGTTTATTGATTAATTCGGCTGGCGGGAGCCCTCTGAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTTATTGATTAATTCGGCTGGCGGGAGCCCTCTGAGAGAGAGAGCGT 58
QY 61 GAGAGATGGAGATGGGAGAGCGGATTCATTTAGAGCTGCGGAGCGGAGCCCTCTGATG 120
Db 59 GAGAGATGGAGATGGGAGAGCGGATTCATTTAGAGCTGCGGAGCGGAGCCCTCTGATG 118
QY 121 TGAAGAACTTTCTCTGGAGCAACAGTCGATGAATGAAGCAAACTCGAAGCGCTCACAG 180
Db 119 TGAAGAACTTTCTCTGGAGCAACAGTCAGTCAATGAAGCAAACTTGAAGCGCTCACAG 178
QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACATGAGCCCTCACTCAATCGCAA 240
Db 179 ATGAATTTGAAGAACTGGAATTTCTTAAGTACATCAACATGAGCCCTCACTCAATCGCAA 238
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Db 179 ATGAATTTGAAGAACTGGAATTTATTAATACAAATCAACATAGGCTCACCTCAATTCGAA 238
Qy 241 ACTTACCAAGTTAAACAACTTTAGAGCTTGAAGCTTAAGCAGTAACAGAGCCCTCAGTGG 300
Db 239 ACTTCCAAAGTTAAACAACTTTAGAGCTTGAAGCTTAAGCAGTAACAGAGCCCTCAGTGG 298
Qy 301 GCTAGAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 299 GCCTAGAAGTATTGGCAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 358
Qy 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAGTTAGAAAACCTCAGAGAGCTTAG 420
Db 359 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAGTTAGAAAACCTCAGAGAGCTTAG 418
Qy 421 ACCTTTTACCTTGCAGAGTAAACACCTGAACAACTACTGAGAGAAAGATGTTCAAGCTCC 480
Db 419 ACCTTTTACCTTGCAGAGTAAACACCTGAACAACTACTGAGAGAAAGATGTTCAAGCTCC 478
Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCGCCCTAACTCGG 540
Db 479 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCGCCCTAACTCGG 538
Qy 541 ATGGTGAGGGCTTTGTGAGTGCCTGGATGACAGAGGAGGAGATGAGGATGAGGAGGAGT 600
Db 539 ATGGTGAGGGCTTTGTGAGTGCCTGGATGACAGAGGAGGAGATGAGGATGAGGAGGAGT 598
Qy 601 ATGATGAAGATCCTCAGTAAAGTAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
Db 599 ATGATGAAGATCCTCAGTAAAGTAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 658
Qy 661 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 720
Db 659 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 718
Qy 721 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 780
Db 719 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 778
Qy 781 AAGAACTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Db 779 AAGAACTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 838
Qy 841 CCTTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCTCCCTCCCTCCCTCCCTCCCT 900
Db 839 CCTTTTGTGATTTTACTGTTTGTAGCCGTATCCCTCTCCCTCCCTCCCTCCCTCCCTCCCT 898
Qy 901 CCTGAA 907
Db 899 CCTGAA 905

RESULT 5

US-10-273-334-7
; Sequence 7, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 905

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(453)
; OTHER INFORMATION:
US-10-273-334-7

Query Match 94.4%; Score 856.2; DB 6; Length 905;

Best Local Similarity 97.2%; Pred. No. 3.7e-178;

Matches 882; Conservative 0; Mismatches 23; Indels 2; Gaps 1;

Qy 1 GGTTCCGGGTTTATGATTAATTCGGCTGGCGCGGGAGCCCTCTCCAGAGAGAGAGCCG 60
Db 1 GGTTCCGGGTTTATGATTAATTCGGCTGGCGCGGGAGCCCTCTCCAGAGAGAGAGCCG 58
Qy 61 GAGAGATGAGATGGCAGACGATTCATTTAGAGCTGGGAACGGAGCCCTCTGATG 120
Db 59 GAGAGATGAGATGGGCAAAATGATTCATTTAGAGCTGGGAACGGAGCCCTCTGATG 118
Qy 121 TGAAGAACTTGTCTTGGCAACAGTCGGTCGAATGAAGCAAACTCGAAGGCCCTCACAG 180
Db 119 TGAAGAACTTGTCTTGGCAACAGTCAGTCAAATGAAGCAAAATTTGAAGGCCCTCACAG 178
Qy 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTACAATCAACGTAGGCCCTCACCTCAATCGCAA 240
Db 179 ATGAATTTGAAGAACTGGAATTTAAATACAATCAACATAGGCCCTCACCTCAATTCGCAA 238
Qy 241 ACITACCAAGTTTAAACAACTTAAAGAGCTTGAAGCTTAAGCACTAAGCAGTAACAGAGCCCTCAGTGG 300
Db 239 ACITGCCCAAGTTTAAACAACTTAAAGAGCTTGAAGAGCTTGAACCTAAGCAGTAACAGAGCCCTCAGTGG 298
Qy 301 GCCTAGAAGTATTGGCAAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 299 GCCTAGAAGTATTGGCAAGAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 358
Qy 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAGTTAGAAAACCTCGAGAGCTTAG 420
Db 359 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAGTTAGAAAACCTCGAGAGCTTAG 418
Qy 421 ACCTTTTCACCTTGGAGGTAAACCACTGAACTACTGAGAGAGATGTTCAAGCTCC 480
Db 419 ACCTTTTCACCTTGGAGGTAAACCACTGAACTACTGAGAGAGATGTTCAAGCTCC 478
Qy 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAGAGGAGGCGCCCTAACTCGG 540
Db 479 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAGAGGAGGCGCCCTAACTCGG 538
Qy 541 ATGGTGAGGGCTTTGTGAGTGCCTGATGACAGAGGAGGAGGATGAGGATGAGGAGGAGT 600
Db 539 ATGGTGAGGGCTTTGTGAGTGCCTGATGACAGAGGAGGAGGATGAGGATGAGGAGGAGT 598
Qy 601 ATGATGAAGATCCTCAGTAAAGTAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 660
Db 599 ATGATGAAGATCCTCAGTAAAGTAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 658
Qy 661 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 720
Db 659 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 718
Qy 721 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 780
Db 719 TAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 778
Qy 781 AAGAACTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 840
Db 779 AAGAACTCAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 838
Qy 841 CCTTTTGTGATTTTACTGTTTGTAGCCGTACCCCTCTCCCTCCCTCCCTCCCTCCCTCCCT 900
Db 839 CCTTTTGTGATTTTACTGTTTGTAGCCGTATCCCTCTCCCTCCCTCCCTCCCTCCCTCCCT 898
Qy 901 CCTGAA 907

```
Db 899 CCCTGAA 905
|||||||
RESULT 6
US-10-273-334-9
; Sequence 9, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrinari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/10/273,334
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 907
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-10-273-334-9
Query Match 91.3%; Score 833.4; DB 6; Length 907;
Best Local Similarity 94.9%; Pred. No. 3.5e-173;
Matches 861; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY 1 GGGTTCGGGGTTATTGATTGAATTCGGCTGGCGCGGGAGCCCTCTCAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTATTGATTGAATTCGGCGCGGGAGCCCTCTCAGAGAGAGAGCGC 60
QY 61 GAGAGATGGAGATGGCGAGACGGATTCAATTAGAGCTGGCGGAACGGGAGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGCGAGACGGATTCAATTAGAGCTGGCGGAACGGGAGCCCTCTGATG 120
QY 121 TGAAGAACTTCCTCGGACAACTGCGTGGTGAATGAAGCAAACTCGAAGGCGCTCACAG 180
Db 121 TGAAGAACTTCCTCGGACAACTGCGTGGTGAATGAAGCAAACTCGAAGGCGCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTACAATCAACGTAGGCCCTCACTCAATCGCA 240
Db 181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTACAATCAACGTAGGCCCTCACTCAATCGCA 240
QY 241 ACTTACAAAGTTAAACAACTTAAGAAGCTTGAAGCTTGAAGCTTAAGCAAGTAAAGAGCCCTCAGTGG 300
Db 241 ACTTGCACAAAGTTAAACAACTTAAGAAGCTTGAAGCTTGAAGCTTAAGCAAGTAAAGAGCCCTCAGTGG 300
QY 301 GCCTAGAAGTATTGGCAGAAAGCTTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 301 GCCTAGAAGTATTGGCAGAAAGCTTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
QY 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACCTTCGAGAGCTTAG 420
Db 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACCTTCAGAGCTTAG 420
QY 421 ACCTTTTCACTTCGGAGGTAAACCAACTGAACACTTACTGAGAGAGATGTTTCAAGCTCC 480
Db 421 ACCTTTTCACTTCGGAGGTAAACCAACTGAACACTTACTGAGAGAGATGTTTCAAGCTCC 480
QY 481 TCCTGCAACTCACAATCTCAAGGGCTGTGACCCGGATGACAAAGAGGCGCCCTTAAGTGG 540
Db 481 TCCTGCAACTCACAATCTCAAGGGCTGTGACCCGGATGACAAAGAGGCGCCCTTAAGTGG 540
QY 541 ATGGTGAGGCGCTTTGTGGAGTGCCTGGATGACAAGAGAGAGGATGAGGATGAGGAGAGT 600
Db 541 ATGGTGAGGCGCTACGTGGAGGCGCTGGATGATCAGGAGGAGGATGAGGATGAGGAGAGT 600
QY 601 ATGATGAAGATGCTCAGGTAATGAGAGATGAGGAGGACGAGGATGAGGAGGAGGACGTG 660
Db 601 ATGATGAAGATGCTCAGGTAATGAGAGATGAGGAGGACGAGGATGAGGAGGAGGAGGTG 660
QY 661 AAGAGGAGGACGTGAGTGGAGACGAGGAGGAGGATGAAGGTATTATAACAATGGAGAG 720
Db 661 AAGAGGAGGACGTGAGTGGAGAGGAGGAGGATGAAGGTATTATAACAATGGAGAG 720
QY 721 TAGATGATGAGGAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCAAGACGAAAAT 780
Db 721 TAGATGACGAGGAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTCAAGACGAAAAT 780
QY 781 AAGAAACTCAAGATGAGGAGAGAGAGGATGCTTAAGTGAATTAATCTATTGTAATAATT 840
Db 781 GAGAACTCAAGATGAGGAGAGAGAGGATGCTTAAGTGAATTAATCTATTGTAATAATT 840
QY 841 CCTTTTGTGATTTACTGTTTATAGCCGTACCCCTCTCCCCCCCCCTCTTAATCCTGCC 900
Db 841 CCTATTGTGATTTGACTGTTTTTACCATATCCCTCTCCCCCCCCCTCTTAATCCTGCC 900
QY 901 CCCTGAA 907
Db 901 CCCTGAA 907
RESULT 7
US-10-273-334-33
; Sequence 33, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kocheavar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrinari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(812)
; OTHER INFORMATION:
US-10-273-334-33
Query Match 91.3%; Score 827.8; DB 6; Length 906;
Best Local Similarity 95.3%; Pred. No. 5.9e-172;
Matches 864; Conservative 0; Mismatches 42; Indels 1; Gaps 1;
QY 1 GGGTTCGGGGTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTGCAGAGAGAGAGCGC 60
Db 1 GGGTTCGGGGTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTGCAGAGAGAGAGCGC 60
QY 61 GAGAGATGGAGATGGCGAGAGCGGATTCAATTAGAGCTGGCGGAACGGGAGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGCGAGAGCGGATTCAATTAGAGCTGGCGGAACGGGAGCCCTCTGATG 120
QY 121 TGAAGAACTTCCTCGGACAACTGCGTGGTGAATGAAGCAAACTCGAAGGCGCTCACAG 180
Db 121 TGAAGAACTTCCTCGGACAACTGCGTGGTGAATGAAGCAAACTCGAAGGCGCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTACAATCAACGTAGGCCCTCACTCAATCGCA 240
Db 181 ATGAATTTGAAGAACTGGAAATTCCTTAAGTACAATCAACGTAGGCCCTCACTCAATCGCA 240
QY 241 ACTTACAAAGTTAAACAACTTAAGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 300
Db 241 ACTTGCACAAAGTTAAACAACTTAAGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAG 300
QY 301 GCCTAGAAGTATTGGCAGAAAGCTTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 301 GCCTAGAAGTATTGGCAGAAAGCTTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
QY 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACCTTCGAGAGCTTAG 420
Db 361 AAATTAAGACCTCAGCACAATAGAGCCCTGAAAAAGTTAGAAAACCTTCAGAGCTTAG 420
QY 421 ACCTTTTCACTTCGGAGGTAAACCAACTGAACACTTACTGAGAGAGATGTTTCAAGCTCC 480
Db 421 ACCTTTTCACTTCGGAGGTAAACCAACTGAACACTTACTGAGAGAGATGTTTCAAGCTCC 480
QY 481 TCCTGCAACTCACAATCTCAAGGGCTGTGACCCGGATGACAAAGAGGCGCCCTTAAGTGG 540
Db 481 TCCTGCAACTCACAATCTCAAGGGCTGTGACCCGGATGACAAAGAGGCGCCCTTAAGTGG 540
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QY	841	CCTTTTGATGATTTTAC	GTGTTTTT	TAGCGGTACCCCGCTCTCC	CCCCCCACACTCTAATCCTGCC	900
Db	841	CCTATTGTGATTTGACT	GTGTTTTT	ACCACATATCCCTCTCTCC	CCCCCCCCCTCTAATCCTGCC	900
QY	901	CCCTGAA	907			
Db	901	CCCTGAA	907			
RESULT 9						
US-10-273-334-25						
; Sequence 25, Application US/10273334						
; GENERAL INFORMATION:						
; APPLICANT: Pasternack, Gary R.						
; APPLICANT: Kocheavar, Gerald J.						
; APPLICANT: Brody, Jonathan R.						
; APPLICANT: Kodkol, Shrihari S.						
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY						
; FILE REFERENCE: 031787.0076						
; CURRENT APPLICATION NUMBER: US/10/273,334						
; CURRENT FILING DATE: 2002-10-18						
; PRIOR APPLICATION NUMBER: US/09/591,500						
; PRIOR FILING DATE: 2000-12-06						
; PRIOR APPLICATION NUMBER: PCT/US98/26433						
; PRIOR FILING DATE: 1998-12-11						
; PRIOR APPLICATION NUMBER: US 60/069,677						
; PRIOR FILING DATE: 1997-12-11						
; NUMBER OF SEQ ID NOS: 51						
; SOFTWARE: PatentIn version 3.1						
; SEQ ID NO 25						
; LENGTH: 907						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
US-10-273-334-25						

Db	481	TCGCCAACTCACATATCTCGACGGCTATGACCGGGACGACAAAGAGGCCCTGACTCGG	540
QY	541	ATGCGTGAGGGCTTTCTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATCAGGAGGAGT	600
Db	541	ATGCTGAGGGCTACCTGGAGGGCTTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	600
QY	601	ATGATGAAGATGCTCAGCTAATGGAAGATGAGGAGGACGAGGATGAGGAGGAGGAACCTG	660
Db	601	ATGATGAAGATGCTCAGCTAGTGAAGACGAGGAGGACGAGGATGAGGAGGAGGAGT	660
QY	661	AAGAGGAGGACCTGAGTGGACGACGAGGAGGAGAGGATGAAGTTTATAACAATGGAGAGG	720
Db	661	AAGAGGAGGACCTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGGTTATAACGATCGAGAG	720
QY	721	TAGATGATGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGAAAT	780
Db	721	TAGATGACGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTCAGAAGCGAAAC	780
QY	781	AGAACAATGAAGATGAGGAGGAGAACGATGCCTAAGTGGAAATATCTATTTTGAAGAAAT	840
Db	781	GAGAACCCTGAAGATGAGGAGGAGAACGATGATGACTAAGTGAATTAACCTATTTTGAAGAAAT	840
QY	841	CGTTTGTGATTTTACTCTTTTACCGTCGATCCCGCTCTCCCGCCCACTCTAATCTCTGCC	900
Db	841	CCTATTTGTGATTTGACTGTTTTTACCATATCCCGCTCTCCCGCCCGCTCTAATCTCTGCC	900
QY	901	CCCTGAA 907	
Db	901	CCCTGAA 907	
RESULT 10			
US-10-273-334-28			
; Sequence 28, Application US/10273334			
; GENERAL INFORMATION:			
; APPLICANT: Pasternack, Gary R.			
; APPLICANT: Kocheavar, Gerald J.			
; APPLICANT: Brody, Jonathan R.			
; APPLICANT: Kodkol, Shrihari S.			
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY			
; FILE REFERENCE: 031787.0076			
; CURRENT APPLICATION NUMBER: US/10/273,334			
; CURRENT FILING DATE: 2002-10-18			
; PRIOR APPLICATION NUMBER: US/09/591,500			
; PRIOR FILING DATE: 2000-12-06			
; PRIOR APPLICATION NUMBER: PCT/US98/26433			
; PRIOR FILING DATE: 1998-12-11			
; PRIOR APPLICATION NUMBER: US 60/069,677			
; PRIOR FILING DATE: 1997-12-11			
; NUMBER OF SEQ ID NOS: 51			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 28			
; LENGTH: 907			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (66)..(812)			
; OTHER INFORMATION:			
US-10-273-334-28			

[illegible]

QY 841 CTTTGTGATTTACTGTTTTAGCCGTACCCCTCTCCCGCCCACTCTAATCCTGCC 900
Db 839 CCTATTGGAATTGACITGTTTTAGCCGTATCCCTCTCCCGCCCACTCTAATCCTGCC 898
QY 901 CCCTGAA 907
Db 899 CCCTGAA 905
RESULT 12
US-10-273-334-32
; Sequence 32, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 32
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-273-334-32

Query Match 89.6%; Score 812.8; DB 6; Length 908;
Best Local Similarity 94.2%; Pred. No. 1.1e-168;
Matches 855; Conservative 0; Mismatches 52; Indels 1; Gaps 1;
QY 1 GGGTTCGGGTTTATTGATTGAATTCGGTGGCGGGAGCCCTCTCAGAGAGAGAGCGG 60
Db 1 GGGTTCGGGTTTATTGATTGAATTCGGTGGCGGGAGCCCTCTCAGAGAGAGAGCGG 60
QY 61 -GAGAGATGAGATGGGACGAGGATTCATTTAGAGCTGCGGAACGGGAGCGCCCTCTGAT 119
Db 61 GGAGAGATGAGATGGGACGAGGATTCATTTAGAGCTGCGGAACGGGAGCGCCCTCTGAT 120
QY 120 GTCAAGAACTTCTCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCACA 179
Db 121 GTCAAGAACTTCTCTGGACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTCACA 180
QY 180 GATGAATTTGAAGAACTTGAATTTAAGTACAACTCAAGCTAGGCTCACCCTCAATCGCA 239
Db 181 GATGAATTTGAAGAACTTGAATTTAAGTACAACTCAAGCTAGGCTCACCCTCAATCGCA 240
QY 240 AACTTACCAAGTTAACAACCTTAAGAAGCTTGAAGCTTAAGCAGTAACAGAGCTCAGTG 299
Db 241 AACTTACCAAGTTAACAACCTTAAGAAGCTTGAAGCTTAAGCAGTAACAGAGCTCAGGG 300
QY 300 GGCTAGAGATTGCGCAGAAAGTGTCCAAACCTCATACATCTAAATTAAGTGGCAAC 359
Db 301 GGCTAGAGATTGCGCAGAAAGTGTCCAAACCTCATACATCTAAATTAAGTGGCAAC 360
QY 360 AAAATTAAGAGCTCAGCACAATAGAGCCCTGAAAAGCTTGAAGAACTTCAGAGCTTA 419
Db 361 AAAATTAAGAGCTCAGCACAATAGAGCCCTGAAAAGCTTGAAGAACTTCAGAGCTTA 420
QY 420 GACCTTTTCACTTGGAGGTAACCAACCTGAACAACTACTGAGAGAAGATGTTCAAGCTC 479
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QY 480 CTCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGGAGGCCCTTAACTCG 539

Db 481 CTCCTGCAACTCACATATCTGACGGCTATGACCGGGAGCAAGGAGGCCCTGACTCG 540
QY 540 GATGGTGAGGCTTTGTGGAGTCCCTGGATGACAAGGAGGAGGATGAGATGAGGAGGAG 599
Db 541 GATGCTGAGGCTACGTGGAGGCCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 600
QY 600 TATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAG 659
Db 601 TATGATGAAGATGCTCAGGTAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAGGAG 660
QY 660 GAAGAGGAGGAGTGTGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 719
Db 661 GAAGAGGAGGAGTGTGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 720 GTAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 779
Db 721 GTAGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 780 TAAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 839
Db 781 CGAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 840 TCCTTTTGTGATTTACTGTTTTAGCCCTACCCCTCTCCCGCCCACTCTAATCCTGCC 899
Db 841 TCCTTTTGTGATTTACTGTTTTAGCCCTACCCCTCTCCCGCCCACTCTAATCCTGCC 900
QY 900 CCCCTGAA 907
Db 901 CCCCTGAA 908
RESULT 13
US-10-273-334-11
; Sequence 11, Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)..(810)
; OTHER INFORMATION:
US-10-273-334-11

Query Match 88.4%; Score 801.8; DB 6; Length 905;
Best Local Similarity 93.5%; Pred. No. 2.8e-166;
Matches 848; Conservative 0; Mismatches 57; Indels 2; Gaps 1;
QY 1 GGGTTCGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTCAGAGAGAGAGCGG 60
Db 1 GGGTTCGGGTTTATTGATTGAATTCGGCTGGCGGGAGCCCTCTCAGAGAGAGAGCGG 58
QY 61 GAGAGATGAGATGGGACGAGCGGATTCATTTAGAGCTGCGGAACGGGAGCGCCCTCTGATG 120
Db 59 GAGAGATGAGATGGGCAAAATGGATTCATTTAGAGCTGCGGAACGAGGAGGCCCTCCGATG 118

Db 841 CCTATTGTGATTTGACTGTTTTTACCACATATCCCTCTCCCTCCCTCTAATCTCTGCC 900
QY 901 CCCTGAA 907
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Db 901 CCCTGAA 907
RESULT 15
US-10-273-334-23
; Sequence 23. Application US/10273334
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kochevar, Gerald J.
; APPLICANT: Brody, Jonathan R.
; APPLICANT: Kodkol, Shrihari S.
; TITLE OF INVENTION: GENE FAMILY WITH TRANSFORMATION MODULATING ACTIVITY
; FILE REFERENCE: 031787.0076
; CURRENT APPLICATION NUMBER: US/10/273,334
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US/09/591,500
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: PCT/US98/26433
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: US 60/069,677
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(767)
; OTHER INFORMATION:
US-10-273-334-23

Query Match 82.8%; Score 751; DB 6; Length 895;
Best Local Similarity 91.0%; Pred. No. 3.5e-155;
Matches 825; Conservative 0; Mismatches 70; Indels 12; Gaps 2;
QY 1 GGGTTCCGGGGTTTATTGATTGAATTCGGCTGGCGGGGAGCCCTCTGCAGAGAGAGCGC 60
Db 1 GGGTTCCGGGGTTTATTGATTGAATTCGGCTGGCGGGGAGCCCTCTGCAGAGAGAGCGC 60
QY 61 GAGAGATGGAGATGGCGACAGGATTCATTAGAGCTGGGACCGGAGCGCCCTCTGATG 120
Db 61 GAGAGATGGAGATGGCGACAGGATTCATTAGAGCTGGGACCGGAGCGCCCTCTGATG 120
QY 121 TGAAGAAGCTTGTCTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCCCTCACAG 180
Db 121 TGAAGAAGCTTGTCTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGGCCCTCACAG 180
QY 181 ATGAATTTGAAGAACTGGAAATCTTAAAGTACAACTAACCTAGAGCTCAATCGCAA 240
Db 181 ATGAATTTGAAGAACTGGAAATCTTAAAGTACAACTAACCTAGAGCTCAATCGCAA 240
QY 241 ACTTACCAAGTTAAACAACTTAAAGAGCTTGAAGCTAGAGCTAACAGAGCTCAGTGG 300
Db 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT 288
QY 301 GCGTAGAAGTATGGCAGAAAAAGTGTCCAAACCTCATACATCTAAATTTAAGTGGCAACA 360
Db 289 GCGTAGAAGTATGGCAGAAAAAGTGTCCAAACCTCACGACCTATATTTAAGTGGCAACA 348
QY 361 AAATTAAGACCTCAGCAACATAGAGCCCTCGAAAAGTTAGAAAACCTCGAGAGCTTAG 420
Db 349 AAATTAAGACCTCAGCAACATAGAGCCCTCGAAAAGTTAGAAAACCTCGAGAGCTTAG 408
QY 421 ACCTTTTCACTTGGAGGTAACCAACCTGAACAACTACTGAGAGAGATGTTCAAGCTCC 480
Db 409 ACCTTTTCAATTTGGAGGTAACCAACCTGACGACTACGGAGAAAAACGTTTCAAGCTTC 468

QY 481 TCCTGCAACTCACATATCTCAACGGCTGTGACCCGGATGACAAGAGGCCCCCTAATCTCG 540
Db 469 TCCTGCAACTCACATATCTCGACAGCTGTACTGGGACCCACAAGGAGGCCCTTACTCAG 528
QY 541 ATGGTGAGGGCTTTGTGGAGTGCCTGGATGACAAGGAGGAGGATGAGGATGAGGAGGAT 600
Db 529 ATATTGAGGACCACTGGAGGCCCTGGATGACGAGGAGGAGGATGAGGATGAGGAGGAT 588
QY 601 ATGATGAAGATGCTCAGGTPAATGGAAGATGAGGAGGAGGATGAGGAGGAGGAGGATG 660
Db 589 ATGATGAAGATGCTCAGGTPAATGGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGATG 648
QY 661 AAGAGGAGGAGGATGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
Db 649 AAGAGGAGGAGGATGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 708
QY 721 TAGATGATGAGGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
Db 709 TAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 768
QY 781 AAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
Db 769 GAGAACTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 828
QY 841 CCTTTTGTGATTTTACTGTTTACCCCTACCCCTCTCCCTCCCTCTAATCTCTAATCTGCC 900
Db 829 CCTATTGTGATTTGACTGTTTACCCTATCCCTCTCTCCCTCCCTCTAATCTCTAATCTGCC 888
QY 901 CCCTGAA 907
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Db 889 CCCTGAA 895

Search completed: December 9, 2002, 00:34:21
Job time : 59.5612 secs

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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 19:17:03 ; Search time 1647.82 seconds
(without alignments)
15701.003 Million cell updates/sec

Title: US-09-591-500-3
Perfect score: 889
Sequence: 1 ggggtcgaggtttattgatt.....ctccaatctgccccctgaa 889

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl :

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_ov.*
- 5: gb_sy.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_br.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_mus.*
- 34: em_htg_pln.*
- 35: em_htg_rod.*
- 36: em_htg_mam.*
- 37: em_htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	889	100.0	5785	9	AF008216	AF008216 Homo sapi
2	889	100.0	70449	9	AC105250	AC105250 Homo sapi
3	764.2	86.0	1136	9	BC007200	BC007200 Homo sapi
4	761	85.6	1052	6	AR009985	AR009985 Sequence 1
5	761	85.6	1052	6	I91514	I91514 Sequence 1
6	761	85.6	1052	6	I96074	I96074 Sequence 1
7	761	85.6	1052	9	HSU73477	HSU73477 Human acidi
8	756.2	85.1	916	9	HSPHAP1	X75090 H.sapiens m
9	720.2	81.0	925	9	AF025684	AF025684 Homo sapi
10	686.4	77.2	164945	9	AC089987	AC089987 Homo sapi
11	671	75.5	162482	9	AC022740	AC022740 Homo sapi
12	669.4	75.3	149015	9	AC107992	AC107992 Homo sapi
13	669.4	75.3	186886	2	AC016297	AC016297 Homo sapi
14	659.2	74.2	904	9	HSU71084	U71084 Homo sapien
15	640.4	72.0	750	9	HSU60823	U60823 Human poten
16	602.4	67.8	1017	10	RATLANP	D32209 Rat mRNA fo
17	573.4	64.5	863	10	AF022957	AF022957 Mus muscu
18	570.8	64.2	980	6	AR009986	AR009986 Sequence
19	570.8	64.2	980	6	AX305936	AX305936 Sequence
20	570.8	64.2	980	6	I91515	I91515 Sequence 3
21	570.8	64.2	980	6	I96075	I96075 Sequence 3
22	570.8	64.2	980	10	MMU73478	U73478 Mus musculu
23	512.8	57.7	771	9	BC000608	BC000608 Homo sapi
24	483.8	54.4	1656	9	AY007110	AY007110 Homo sapi
25	438.2	49.3	101819	2	AC129809	AC129809 Rattus no
26	438.2	49.3	170170	2	AC106610	AC106610 Rattus no
27	429.2	48.3	759	6	AR009987	AR009987 Sequence
28	429.2	48.3	759	6	I91516	I91516 Sequence 4
29	429.2	48.3	759	6	I96075	I96075 Sequence 4
30	359	40.4	79457	2	AC098396	AC098396 Rattus no
31	297.8	33.5	1011	9	HSPHAP12A	Y07569 H.sapiens m
32	297.8	33.5	1035	9	BC013003	BC013003 Homo sapi
33	297.8	33.5	1371	9	BC019658	BC019658 Homo sapi
34	297.8	33.5	1371	9	HSAPRIL	Y07969 H.sapiens m
35	297.8	33.5	1475	9	HSU70439	U70439 Human silve
36	297.8	33.5	3980	9	BC000476	BC000476 Homo sapi
37	284.4	32.0	168182	2	AC068338	AC068338 Homo sapi
38	284.4	32.0	200445	2	AC105137	AC105137 Homo sapi
39	272.8	30.7	1225	10	AB025581	AB025581 Rattus no
40	264.6	29.8	1397	10	BC003489	BC003489 Mus muscu
41	264.6	29.8	1408	10	BC005628	BC005628 Mus muscu
42	263.6	29.7	1127	10	AB025582	AB025582 Mus muscu
43	260.8	29.3	238142	2	AL611930	AL611930 Mus muscu
44	258	29.0	198926	10	AL683843	AL683843 Mouse DNA
45	244	27.4	1293	9	HSPHAP12B	Y07570 H.sapiens m

ALIGNMENTS

RESULT 1	AF008216	5785 bp	DNA	linear	PRI 05-FEB-1999
LOCUS	AF008216				
DEFINITION	Homo sapiens candidate tumor suppressor pp32rl (PP32RL) gene,				
ACCESSION	AF008216				
VERSION	AF008216.1	GI:2738512			
KEYWORDS	complete cds.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 5785)				
	Kadkol,S.S., Brody,J.R., Pevsner,J., Bai,J. and Pasternack,G.R.				
	Modulation of oncogenic potential by alternative gene use in human				

prostate cancer
Nature Medicine (1999) In press
2 (bases 1 to 5785)
Kochevar,G.J., Brody,J.R. and Pasternack,G.R.
The Structure of a Gene Encoding pp32r1, a New Member of the pp32
Family
Unpublished
3 (bases 1 to 5785)
Kochevar,G.J., Brody,J.R. and Pasternack,G.R.
Direct Submission
Submitted (13-JUN-1997) Pathology, Johns Hopkins University School
of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA
Location/Qualifiers
1. 5785
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
4453. 5157
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4453. 5157
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/function="candidate tumor suppressor"
/note="in contrast to pp32, pp32r1 augments
oncogene-mediated transformation of rat embryo fibroblasts
(Mol. Biol. Cell 8(Suppl.): 137A, 1997.); similar to other
members of the human pp32 family including pp32, encoded
by GenBank Accession Number U73477, SSP29, encoded by
GenBank Accession Number U70439, PHAPI2a, encoded by
GenBank Accession Number Y07569, PHAPI2b, encoded by
GenBank Accession Number Y07570, and APRIL protein,
encoded by GenBank Accession Number Y07969; expressed in
prostate cancer"
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/product="pp32r1"
/protein_id="AADI2746.1"
/db_xref="GI:2738513"
/translation="MEMGRIHSELNRAPDVKEALDNSRNEKLEALIDFEEL
EFLSKINGLTSIDSLPKLRLKLEUVSGGLEVLAEKPCNLTHLYSGNKIKDLSTI
EPLKLNLSLDFNCEVTLNDYENFVKLLQLTLDSCYWDHKEAPYSIEDIH
EGLDEEGEHEBEYDQAVEDEGEEREEEDVDVSGDEEEDVNGDEVDGE
EDEELGEERQKRK"
BASE COUNT 1755 a 1087 c 1162 g 1781 t
ORIGIN
Query Match 100.0%; Score 889; DB 9; Length 5785;
Best Local Similarity 100.0%; Pred. No. 4.8e-149;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGTTGCGAGGTTATTGATTGAATTCGGCTGGCAGGAGGCTCTGCAGACAGAGAGCGC 60
DB 4388 GGGTTGCGAGGTTATTGATTGAATTCGGCTGGCAGGAGGCTCTGCAGACAGAGAGCGC 4447
QY 61 GAGAGATGAGATGGCAGAGGATTTCATTAGAGCTCGGGAACAGGGCGCCCTCTGATG 120
DB 4448 GAGAGATGAGATGGCAGAGGATTTCATTAGAGCTCGGGAACAGGGCGCCCTCTGATG 4507
QY 121 TGAAGAACTTGCCTGGACACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTTCACAG 180
DB 4508 TGAAGAACTTGCCTGGACACACAGTCGGTCAATGAAGGCAAACTCGAAGCCCTTCACAG 4567
QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240
DB 4568 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 4627
QY 241 ACTTACCAGGTTAAGTTGAGAACTTGAAGTCTCAGGGGGCCCTGGAAGTAT 300
DB 4628 ACTTACCAGGTTAAGTTGAGAACTTGAAGTCTCAGGGGGCCCTGGAAGTAT 4687
QY 301 TGGCGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAAATTAAGACC 360
DB 4688 TGGCGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAAATTAAGACC 4747
QY 361 TCAGCACATAGAGCCACTGAAACAGTAGTAGAANAACCTCAAGAGCTTAGACCTTTTCATTT 420

Db 4748 TCAGCACATAGAGCCACTGAAACAGTAGTAGAANAACCTCAAGAGCTTAGACCTTTTCATTT 4807
QY 421 GCAGGTAACCAACCTGAAACGACTACGAGAGAAACAGTGTTCAGGCTTTCCTCCCACTCA 480
Db 4808 GCAGGTAACCAACCTGAAACGACTACGAGAGAAACAGTGTTCAGGCTTTCCTCCCACTCA 4867
QY 481 CATATCTCGACAGCTTACTTGGGACCAACAGAGAGCCCTTACTCAGATATTGAGGACC 540
Db 4868 CATATCTCGACAGCTTACTTGGGACCAACAGAGAGCCCTTACTCAGATATTGAGGACC 4927
QY 541 ACCTGAGGGCCCTGGATGACGAGGAGGAGGTTCAGCATGAGGAGGATGATGAGAGTG 600
Db 4928 ACCTGAGGGCCCTGGATGACGAGGAGGAGGTTCAGCATGAGGAGGATGATGAGAGTG 4987
QY 601 CTCAGGTAGTGGAAAGATGAGGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 4988 CTCAGGTAGTGGAAAGATGAGGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
QY 661 TGAGTGGAGGGACGAGGAGGAGGATGAAGAGGTTATTAACGATGGAGAGGTAGATGGCGAGG 720
Db 5048 TGAGTGGAGGGACGAGGAGGAGGATGAAGAGGTTATTAACGATGGAGAGGTAGATGGCGAGG 5107
QY 721 AAGATGAAGAGAGCTTGTGAGAGAAAGGGGTTCAGAGCGAAATGAGAACCTGGAAG 780
Db 5108 AAGATGAAGAGAGCTTGTGAGAGAAAGGGGTTCAGAGCGAAATGAGAACCTGGAAG 5167
QY 781 ATGAGGGAAGAAGATGATGACTAGTAGAATAACCTATTTTGAANAATTCCTATTGTGATT 840
Db 5168 ATGAGGGAAGAAGATGATGACTAGTAGAATAACCTATTTTGAANAATTCCTATTGTGATT 5227
QY 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 889
Db 5228 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 5276

RESULT 2
AC105250/c
LOCUS AC105250 70449 bp DNA linear PRI 09-MAR-2002
DEFINITION Homo sapiens BAC clone RP11-39C10 from 4, complete sequence.
ACCESSION AC105250 AC011026
VERSION AC105250.3 GI:19310326
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 70449)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 70449)
AUTHORS Desai,A., Creason,K. and Kozlowski,A.
TITLE The sequence of Homo sapiens BAC clone RP11-39C10
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 70449)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (26-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 70449)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Mar 9, 2002 this sequence version replaced gi:18376931.

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc

EGYVEGLDDEEDEDREYDEDAQVVEDEDEDEDEEEDVSGEEDERDGYNDGE
VDDDEEDELGEERQKRPEDGEDDD"
BASE COUNT 369 a 207 c 337 g 223 t
ORIGIN

Query Match	86.0%;	Score 764.2;	DB 9;	Length 1136;
Best Local Similarity	93.0%;	Pred. No. 9e-127;		
Matches 823;	Conservative 0;	Mismatches 50;	Indels 12;	Gaps 2;
QY	1	GGGTTTCAGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTGTCACACAGAGAGCGC	60	
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QY	61	GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTGCGGAACAGGCGCCCTCTGATG	120	
Db	129	GAGAGATGGAGATGGCAGACGGATTTCATTTAGAGCTGCGACAGGAGCGCCCTCTGATG	188	
QY	121	TGAAGAAGACTTCCCTGGACACACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG	180	
Db	189	TGAAGAAGACTTGTCTGGACAACAGTCGGTCGAATGAAGGCAAACTCGAAGGCTCACAG	248	
QY	181	ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGAGCCCTCACCTCAATCTCAG	240	
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QY	241	ACTTACCAAAAGTTA---AAGTTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG	288	
Db	309	ACTTACCAAAAGTTAAACAAACTTAAGAGGCTTGAACCTAAGCGATAACAGAGTCTCAGGGG	368	
QY	289	GCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA	348	
Db	369	GCCTGGAAGTATTGGCAGAAAGTGTCCGAAACCTCAGCATCTAAATTTAAGTGGCAACA	428	
QY	349	AAATTAAGAGCTTCAGCACAAATGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG	408	
Db	429	AAATTAAGAGCTTCAGCACAAATGAGCCACTGAAAAGTTAGAAAACCTCAAGAGCTTAG	488	
QY	409	ACCTTTTCAATTTGGAGGTAAACCAACTGAACGACTACGGAGGAAAACGTTGTTCAAGCTTC	468	
Db	489	ACCTTTTCAATTTGGAGGTAAACCAACTGAACGACTACCGAGAAAATGTGTTCAAGCTCC	548	
QY	469	TCCTGCAACTCACATATCTCGACAGCTGTTACTTGGGACACACAGGAGGCCCTTACTCAG	528	
Db	549	TCCCGCAACTCACATATCTCGAGGGCTATGACCGGACGACAGGAGGCGCCCTGACTCGG	608	
QY	529	ATATTGAGGACCACTGCGAGGGCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGT	588	
Db	609	ATGCTGAGGGCTACGTGGAGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	668	
QY	589	ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGGCGGAGGAGGAGGAGGAAGGTG	648	
Db	669	ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGACGAGGATGAGGAGGAGGAGGTG	728	
QY	649	AAGAGGAGGACGTGAGTGGAGGGACGAGGAGGATGAAGAAGTTTATACGATGGAGAGG	708	
Db	729	AAGAGGAGGACGTGAGTGGAGGGAGGAGGAGGATGAAGAAGTTTATACGATGGAGAGG	788	
QY	709	TAGATGCGGAGGAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTTCAGAGCGCAAAAT	768	
Db	789	TAGATGACGAGGAGATGAAGAAGCTTGGTGAAGAAGAAAGGGTTCAGAGCGCAAAAC	848	
QY	769	GAGAACCTGAAGATGAGGGAGAAAGATGACTTAAGTGAATAAACCCTATTTTGAATAAT	828	
Db	849	GAGAACCTGAAGATGAGGGAGAAAGATGACTTAAGTGAATAAACCCTATTTTGAATAAT	908	
QY	829	CCTATTGTGATTGACTGTTTTTACCATAATCCCTCCCGCCCTCC	873	
Db	909	CCTATTGTGATTGACTGTTTTTACCATAATCCCTCTCCCGCCCTCC	953	

RESULT 4
AR009985
LOCUS AR009985 1052 bp DNA linear PAT 04-DEC-1998

DEFINITION Sequence 1 from patent US 5756676.
ACCESSION AR009985
VERSION AR009985.1 GI:3968790
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack, G.R.
TITLE Mammalian protein associated with uncontrolled cell division
JOURNAL Patent: US 5756676-A 1 26-MAY-1998;
FEATURES Location/Qualifiers
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 /organism="unknown"
BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN

Query Match 85.6%; Score 761; DB 6; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.3e-126;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

Qy	1	GGGTTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAGAGAGCGC	60		
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Qy	61	GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTCGGGAACAGGCGCCCTCTGATG	120		
Db	92	GAGAGATGGAGATGGCAGACGGATTTCATTTAGAGCTCGGGAACAGGAGCGCCCTCTGATG	151		
Qy	121	TGAAAGAACTTCCCTGGACAAACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG	180		
Db	152	TGAAAGAACTTCTCTCGACACACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG	211		
Qy	181	ATGAATTTGAAGAACTGGAAATCTTAAAGTAAATCAAGGAGGCGCTCACCTCAATCTCAG	240		
Db	212	ATGAATTTGAAGAACTGGAAATCTTAAAGTAAATCAACGTAGGCGCTCACCTCAATCGCAA	271		
Qy	241	ACCTTACCAAAAGTTA---AAGTTGAGAAAAGCTTGAACCTA-----AGAGTCTCAGGGG	288		
Db	272	ACCTTACCAAAAGTTAAACAAACTTAAGAAGCTTGAACCTAAGCGATAACAGAGTCTCAGGGG	331		
Qy	289	GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACA	348		
Db	332	GCCTAGAAGTATTGGCAGAAAAGTGTCCGAACCTCACGCATCTAAATTTAAGTGGCAACA	391		
Qy	349	AAATTAAGACCTTCAGCAACATAGAGCCACCTGAACAGTTAGAAAACCTCAAGAGCTTAG	408		
Db	392	AAATTAAGACCTTCAGCAACATAGAGCCACCTGAAAAAAGTTAGAAAACCTCAAGAGCTTAG	451		
Qy	409	ACCTTTTTCAAATTCGAGGTTAAACCAACCTGAAGGACTACGGAGAAAACCGTGTTCAGGCTTC	468		
Db	452	ACCTTTTTCAAATTCGAGGTTAAACCAACCTGAAGGACTACCGAGAAAATGTGTTCAAGCTTCC	511		
Qy	469	TCCTGCAACTCACATATCTCGACAGCTGTCTACTGGGACCAACAGGAGGCCCTTACTCAG	528		
Db	512	TCCCGCAACTCACATATCTCGACGGCTATGACCGGAGCAGACAAGGAGGCCCTGACTCGG	571		
Qy	529	ATATTGAGGACCACTGGAGGGCCCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGT	588		
Db	572	ATGCTGAGGGGCTACCTGGAGGGCCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	631		
Qy	589	ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGGAGGGCGGAGGAGGAGGAGGAAGGTG	648		
Db	632	ATGATGAAGATGCTCAGGTAGTGGAAAGACGAGGAGGAGGACGAGGATGAGGAGGAAGGTG	691		
Qy	649	AAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGTTTATACCATGGAGAGG	708		
Db	692	AAGAGGAGGACGTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGTTTATACCATGGAGAGG	751		
Qy	709	TAGATGGCGGAGGAAGATGAAGAAGAGCTTGGTGAAGAGAAAGGGGTGAGAAAGCCAAAAT	768		
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QY 829 CCTATTGTGATTTGACTGTTTTTACCATATCCCT-----CCCCCTCCAATCCTGCC 882
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QY 883 CCCTGAA 889
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Db 932 CCCTGAA 938

RESULT 5
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LOCUS I91514 1052 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 1 from patent US 5726018.
ACCESSION I91514
VERSION I91514.1 GI:3935984
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack,G.R.
TITLE Nucleic acid based assays to detect a novel mammalian protein
associated with uncontrolled cell division
JOURNAL Patent: US 5726018-A 1 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..1052
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BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN

Query Match 85.6%; Score 761; DB 6; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.3e-126;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
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Db 32 GGGTTCGGGTTTATTGATTGAATTCGCCGGCGGGAGCCTCTGCAGAGAGAGAGCGC 91
QY 61 GAGAGATGAGATGGCAGAGCGGATTCATTTCAGAGCTGCGGAACAGGCGCCCTCTGATG 120
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Db 92 GAGAGATGAGATGGCAGAGCGGATTCATTTCAGAGCTGCGGAACAGAGAGCGCCCTCTGATG 151
QY 121 TGAAGAAGACTTCCCTTGACACACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCAG 180
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Db 152 TGAAGAAGACTTGTCTTGACACACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCAG 211
QY 181 ATGAATTTGAAGACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
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Db 212 ATGAATTTGAAGACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 271
QY 241 ACTTACCAAGTTA---AGTTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
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Db 272 ACTTACCAAGTTAACAACACTTTAGAAGCTTGAACCTAAGCGATAACAGAGTCTCAGGG 331
QY 289 GCCTGGAAGTATTGCAGAAAGTGTCCAAACCTCAGCATCTATATTAAAGTGCACAA 348
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QY 349 AAATTTAAAGACTCAGCACAATAGAGCCACTGAACAGATTAGAAAACCTCAAGAGCTTAG 408
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Db 392 AAATTTAAAGACTCAGCACAATAGAGCCACTGAAGAGTTAGAAAACCTCAAGAGCTTAG 451
QY 409 ACCTTTTCAATTGCGAGGTACCAACCTGAACGACTACGGAGAAAACCTGTTTCAAGCTTC 468
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Db 452 ACCTTTTCAATTGCGAGGTACCAACCTGAACGACTACCGAGAAAATGTGTTTCAAGCTTC 511
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Db 572 ATCCTGAGGCTACGTCGGAGGCCCTGGATGATGAGGAGGAGGATGAGGAGGAT 631
QY 589 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGCGCAGGAGGAGGAGGAGGTG 648
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Db 632 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGACGAGGATGAGGAGGAGGAGGTG 691
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QY 709 TAGATGCGGAGGAAGATGAAGAAGAGCTTTGGTGAAGAAAGGGGTCAAGAGCGAAAT 768
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Db 752 TAGATGACGAGGAAGATGAAGAAGAGCTTTGGTGAAGAAAGGGGTCAAGAGCGAAAC 811
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QY 829 CCTATTGTGATTGACTGTTTTTACCATATCCCT-----CCCCCTCCAATCCTGCC 882
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Db 872 CCTATTGTGATTGACTGTTTTTACCATATCCCTCTCCCCCCCCCTCTAATCCTGCC 931
QY 883 CCCTGAA 889
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Db 932 CCCTGAA 938

RESULT 6
196074
LOCUS I96074 1052 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 1 from patent US 5734022.
ACCESSION I96074
VERSION I96074.1 GI:3940544
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1052)
AUTHORS Pasternack,G.R.
TITLE Antibodies to a novel mammalian protein associated with
uncontrolled cell division
JOURNAL Patent: US 5734022-A 1 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..1052
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BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN

Query Match 85.6%; Score 761; DB 6; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.3e-126;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGAGCGC 60
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Db 32 GGGTTCGGGTTTATTGATTGAATTCGCCGGCGGGAGCCTCTGCAGAGAGAGAGCGC 91
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Db 152 TGAAGAAGACTTGTCTTGACACACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCAG 211
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Db 212 ATGAATTTGAAGACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 271
QY 241 ACTTACCAAGTTA---AGTTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
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Db 452 ACCTTTTCAATTGCGAGGTACCAACCTGAACGACTACCGAGAAAATGTGTTTCAAGCTTC 511
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QY 709 TAGATGGCCAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAAT 768
Db 752 TAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAAC 811
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RESULT 7
HSU73477 1052 bp mRNA linear PRI 02-JAN-1997
LOCUS Human acidic nuclear phosphoprotein pp32 mRNA, complete cds.
DEFINITION U73477
ACCESSION U73477
VERSION U73477.1 GI:1763272
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1052)
Chen,T.-H., Brody,J.R., Romantsev,F.E., Yu,J.-G., Kayler,A.E.,
Voneiff,E., Kuhajda,F.P. and Pasternack,G.R.
Structure of pp32, an Acidic Nuclear Protein Which Inhibits
Oncogene-Induced Formation of Transformed Foci
Mol. Biol. Cell (1996) In press
2 (bases 1 to 1052)
Chen,T.-H., Brody,J.R., Romantsev,F.E., Yu,J.-G., Kayler,A.E.,
Voneiff,E., Kuhajda,F.P. and Pasternack,G.R.
Direct Submission
Submitted (04-OCT-1996) Pathology, The Johns Hopkins University
School of Medicine, 720 Rutland Avenue, Baltimore, MD 21205, USA
Location/Qualifiers
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BASE COUNT 326 a 196 c 316 g 214 t
ORIGIN
Query Match 85.6%; Score 761; DB 9; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.3e-126;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;
QY 1 GGGTTCGAGGTTATTGATTGGCTGGCAGCAGAGCCCTCTGCAGACAGAGAGCGC 60
Db 32 GGGTTCGGGGTTATTGATTGAATTCGGCCGGCGGGAGCCTCTGCAGAGAGAGCGC 91
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Db 752 TAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAAC 811
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Db	624	ATGCTGAGGGCTAGTGGAGGGCCCTGGATGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT	683
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QY	649	AAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATTAACGATGGAGG	708
Db	744	AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGGTTATTAACGATGGAGG	803
QY	709	TAGATGCGGAGGAGATGAAGAAGACGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAAT	768
Db	804	TAGATGCGGAGGAGATGAAGAAGACGCTTGGTGAAGAAGAAAGGGGTGAGAAGCGAAAC	863
QY	769	GAGAACTGAAGATGAGGGGAGAAAGATGACTAAGTAGAATAACCTATTTTGAAGAAAT	828
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LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			

Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R.,
 Washington,C., Watlington,S., Williams,G., Williamson,A.,
 Wleceyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J.,
 Zorrilla,S., Kucherlapati,R., Weinstock,G. and Gibbs,R.
 Direct Submission
 Unpublished
 2 (bases 1 to 164945)
 Worley,K.C.
 Direct Submission
 Submitted (07-FEB-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 164945)
 Worley,K.C.
 Direct Submission
 Submitted (01-JUN-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 164945)
 Worley,K.C.
 Direct Submission
 Submitted (05-JUN-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 164945)
 Worley,K.C.
 Direct Submission
 Submitted (29-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 6 (bases 1 to 164945)
 Worley,K.C.
 Direct Submission
 Submitted (07-MAR-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 7 (bases 1 to 164945)
 Worley,K.C.
 Direct Submission
 Submitted (07-MAY-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Jun 1, 2001 this sequence version replaced gi:14150337.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
 entire insert of this clone. Overlapping regions of clones are only
 sequenced and submitted once, so the sequence for the remainder of
 the insert may be found in the record for the adjacent clones.
 Overlapping clones are noted at the beginning and end of the
 Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches
 of a local database that includes entries from dbSTS, GDB, and
 local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
 unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
 (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
 EST and cDNA sequences. Genes demonstrate at least two exons
 flanked by consensus splice sites that maintained sequence
 continuity across the splice junctions. Sequences that are not
 identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
 standard of double strand coverage with a minimum of 2 clones and 2
 reads with no ambiguities or 2 chemistries with a minimum of 2
 clones and 3 reads with no ambiguities. If the sequence quality for
 a region does not meet this standard, it will be indicated in the
 annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
 standards - estimated error rate less than 1 per 10,000 bases.
 Reports of lowest quality individual bases and measures of base
 quality are listed below. Description of the metrics can be found
 at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

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repeat_region	/rpt_family="(CAA)n" 1759..2636
repeat_region	/rpt_family="L1PA11" 2662..3133
repeat_region	/rpt_family="L1M4" 3133..3390
repeat_region	/rpt_family="L1M4" 3391..3687
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QY 61 GAGACATGAGATGGGACAGGATTCATTGACAGCTCGGAAACAGAGCGCCCTCTGATG 120
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Db 138925 GAGATGGAGATGGGCAAAATGGATTCATTATAGAGCTCGGAAACAGAGCGCCCTCCGATG 138866
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QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
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QY 241 ACTTACCAAAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
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QY 888 AA 889
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AC022740
VERSION AC022740.4 GI:13786480
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 15, clone RP11-617D22
JOURNAL Unpublished
REFERENCE
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Bada,F., Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Hearford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lands,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Oliviar,T.M., Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D., Roy,A., Santos,R., Severi,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,J., Vassiliev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

TITLE
JOURNAL

REFERENCE
AUTHORS

Submitted (06-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 162482)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barna,N., Bastien,L., Boguslavskiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Hearford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Karatas,A., LaRocque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL

COMMENT

Submitted (25-APR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 25, 2001 this sequence version replaced gi:13184169.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu

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AUTHORS	Li, M., Makkinje, A. and Damuni, Z.		
TITLE	Molecular identification of Ilpp2A, a novel potent heat-stable inhibitor protein of protein phosphatase 2A		

JOURNAL	Biochemistry	35	(22),	6998-7002	(1996)
MEDLINE	96240314				
PUBMED	8679524				
REFERENCE	2	(bases 1 to 750)			
AUTHORS	Li, M., Makkinje, A. and Damuni, Z.				
TITLE	Submitted (13-JUN-1996)				
JOURNAL	Pennsylvania State University College of Medicine, 500 University Drive, Hershey, PA 17033, USA				
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QY 774 CCTGAAGATGAGGGGAGAGATGACTAA 803
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Search completed: December 8, 2002, 22:38:39
Job time : 1957.82 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 19:14:43 ; Search time 167.801 Seconds
(without alignments)
11930.941 Million cell updates/sec

Title: US-09-591-500-3

Perfect score: 889

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Scoring table: IDENTITY_NUC

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	761	85.6	1052	21	AAA88238
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10	760.2	85.5	906	21	AAA88240	Human prostatic ad
11	756.2	85.1	916	20	AAV71743	Human V3 loop HIV
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14	570.8	64.2	980	17	AAT27713	Mouse pp32 cDNA cl
15	570.8	64.2	980	24	AB199657	Mouse ischaemic co
16	429.2	48.3	762	13	AAQ21630	pp35-related cDNA
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18	297.8	33.5	1371	24	ABK84741	Human cDNA differe
19	296.4	33.3	966	20	AAH81537	DNA encoding a hum
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21	215.2	24.2	3453	23	ABV21871	Human prostate exp
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25	214	24.1	701	23	AAH81537	DNA encoding novel
26	193.4	21.8	1863	22	AAH81537	Statmin protein 8
27	173	19.5	628	24	ABQ59657	Human colon cancer
28	154.2	17.3	186	15	AAQ57449	U2snRNP A like pro
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30	127.6	14.4	560	24	ABL38556	Human colon tumour
31	121	13.6	333	21	AAA43216	Xenopus secreted e
32	110	12.4	3489	21	AAA30290	Kaposi's sarcoma-a
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35	110	12.4	32207	20	AAH81537	KSHV LUR DNA (nucl
36	110	12.4	137507	19	AAH81537	KSHV long unique c
37	109.6	12.3	390	23	AAH81537	DNA encoding novel
38	107.6	12.1	16442	18	AAH81537	Partial mouse WRN
39	105.6	11.9	49999	20	AAH81537	Murine LOBO genom
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44	103.2	11.6	1050	22	AAH81537	Mutational hot spo
45	103.2	11.6	2849	22	AAH81537	Human retinitis pi

ALIGNMENTS

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XX	AAH81537	
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DE	Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;	
KW	prostatic adenocarcinoma; antineoplastic activity;	
KW	transformation suppression; malignant potential; neuroendocrine;	
KW	neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.	
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XX	XX	
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PA	(UYJO) UNIV JOHNS HOPKINS.	
XX	XX	
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XX	XX	
DR	WPI; 1999-385626/32.	
XX	XX	
PT	Phosphoprotein 32 (pp32) related genomic sequences	

XX PS Claim 1; Fig 5; 65pp; English.

CC The present sequence represents the genomic sequence of phosphoprotein 32 (pp32) variant pp32r2. The pp32r1 and pp32r2 sequences are associated with cancer in prostate, especially prostatic adenocarcinomas. Normal pp32 exerts antineoplastic activity through suppression of transformation. Cancer-associated pp32 variants augment, rather than inhibit, transformation. Determining the presence of a gene encoding residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a diagnostic method for predicting malignant potential of neuroendocrine, neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.

XX SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 100.0%; Score 889; DB 20; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.1e-198;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
DB 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60

QY 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 120
DB 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 120

QY 121 TGAAGAAGACTTCCCTGGACAACTGCGTGCATGAAGGCAAACTCGAAGCCCTCAGAC 180
DB 121 TGAAGAAGACTTCCCTGGACAACTGCGTGCATGAAGGCAAACTCGAAGCCCTCAGAC 180

QY 181 ATGAATTTGAAGAACTGGAAATTTCTTAAGTAAATCAACGGAGGCTCACTCAATCTCAG 240
DB 181 ATGAATTTGAAGAACTGGAAATTTCTTAAGTAAATCAACGGAGGCTCACTCAATCTCAG 240

QY 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGCGCTGGAAGTAT 300
DB 241 ACTTACCAAGTTAAAGTTGAGAAAGCTTGAACCTAAGAGTCTCAGGGGCGCTGGAAGTAT 300

QY 301 TGGCAGAAAGTGTCCAACTCAGGCATCTATATTTAAGTGGCAACAAATTTAAAGACC 360
DB 301 TGGCAGAAAGTGTCCAACTCAGGCATCTATATTTAAGTGGCAACAAATTTAAAGACC 360

QY 361 TCAGCACAATAGAGCACTGAAACAGTTAGAAACCTCAAGAGCTTAGACCTTTTCAATT 420
DB 361 TCAGCACAATAGAGCACTGAAACAGTTAGAAACCTCAAGAGCTTAGACCTTTTCAATT 420

QY 421 GCGAGGTAAACCACTGAACGACTACGGAGAAACGTTTCAAGCTTCTCTGCAACTCA 480
DB 421 GCGAGGTAAACCACTGAACGACTACGGAGAAACGTTTCAAGCTTCTCTGCAACTCA 480

QY 481 CATATCTCAGAGCTGTTACTGGGACCACAGAGGCCCCCTTACTCAGATATTGAGGACC 540
DB 481 CATATCTCAGAGCTGTTACTGGGACCACAGAGGCCCCCTTACTCAGATATTGAGGACC 540

QY 541 ACCTGAGGCGCTGGATGACGAGGAGGGGTGACATGAGGAGGATGATGATGAAGATG 600
DB 541 ACCTGAGGCGCTGGATGACGAGGAGGGGTGACATGAGGAGGATGATGATGAAGATG 600

QY 601 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 601 CTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660

QY 661 TGAGTGGAGGGACAGGAGGATGAAGAGGTTTAAACATGGAGAGTATGATGCGGAGG 720
DB 661 TGAGTGGAGGGACAGGAGGATGAAGAGGTTTAAACATGGAGAGTATGATGCGGAGG 720

QY 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAATTCAGAACCTGAAG 780
DB 721 AAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGAAATTCAGAACCTGAAG 780

QY 781 ATGAGGGAAGAGATGATGACTAAGTAGAATAACCTATTTTTGAATAATTTCTATTGTGATT 840
DB 781 ATGAGGGAAGAGATGATGACTAAGTAGAATAACCTATTTTTGAATAATTTCTATTGTGATT 840

DB 781 ATGAGGGAAGAGATGATGACTAAGTAGAATAACCTATTTTGAAAAATTCCTATTGTGATT 840

QY 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 889
DB 841 TGACTGTTTTTACCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 889

RESULT 2
AAA88239
ID AAA88239 standard; DNA; 889 BP.
XX AC AAA88239;
XX DT 15-DEC-2000 (first entry)
XX DE Human variant pp32r2 genomic DNA sequence.
XX KW Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.
XX OS Homo sapiens.
XX PN W0200045852-A1.
XX PD 10-AUG-2000.
XX PF 03-FEB-2000; 2000WO-US02656.
XX PR 03-FEB-1999; 99US-0118667.
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX PI Pasternack GR, Bai J;
XX PT Treatment of cancer comprising restoration of pp32 function in malignant cells -
XX PS Example 5; Fig 5; 90pp; English.
XX CC The present invention describes a method (M1) for treating malignant cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an inducer of pp32 expression comprising measuring pp32 expression by cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an inducer of pp32 function comprising measuring protein phosphatase activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents which may be used to treat cancer. Human pp32 is a phosphoprotein which has been mapped to chromosome 15q22.3-q23. The present sequence represents the human variant pp32r2 genomic DNA sequence from an example of the present invention.

XX SQ Sequence 889 BP; 286 A; 167 C; 260 G; 176 T; 0 other;

Query Match 100.0%; Score 889; DB 21; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.1e-198;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60
DB 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60

QY 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 120
DB 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTGCGGAACAGAGCGCCCTCTGATG 120

QY 121 TGAAGAAGACTTCCCTGGACAACTGCGTGCATGAAGGCAAACTCGAAGCCCTCAGAC 180
DB 121 TGAAGAAGACTTCCCTGGACAACTGCGTGCATGAAGGCAAACTCGAAGCCCTCAGAC 180

Qy	181	ATGAATTTGAAGAACTTGGAAATCTTTAAGTAAAAATCAACGGAGGCTTCACCTCAATCTCAG	240
Db	181	ATGAATTTGAAGAACTTGGAAATCTTTAAGTAAAAATCAACGGAGGCTTCACCTCAATCTCAG	240
Qy	241	ACTTACCAAAAGTTAAAGTTGAGAAAAGCTTGAACCTAAGAGTCTCAGGGGCGCTTGGAAAT	300
Db	241	ACTTACCAAAAGTTAAAGTTGAGAAAAGCTTGAACCTAAGAGTCTCAGGGGCGCTTGGAAAT	300
Qy	301	TGGCAGAAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAAATTAAGAGCC	360
Db	301	TGGCAGAAAAAGTGTCCAAACCTCACGCATCTATATTTAAGTGGCAACAAAAATTAAGAGCC	360
Qy	361	TCAGCACAAATAGAGCCCACTGAAACAGTGTAGAAAACCTCAAGAGCTTAGACCTTTTCAAT	420
Db	361	TCAGCACAAATAGAGCCCACTGAAACAGTGTAGAAAACCTCAAGAGCTTAGACCTTTTCAAT	420
Qy	421	GCAGGTTAACCAACCTGAAAGACTACGGAGAAAACGTGTTCAAGCTTCTCCTGCAACTCA	480
Db	421	GCAGGTTAACCAACCTGAAAGACTACGGAGAAAACGTGTTCAAGCTTCTCCTGCAACTCA	480
Qy	481	CATATCTCGACAGCTGTTACTTGGGCCACCAAGGAGGCGCCCTTACTCAGATATTGAGGACC	540
Db	481	CATATCTCGACAGCTGTTACTTGGGCCACCAAGGAGGCGCCCTTACTCAGATATTGAGGACC	540
Qy	541	ACCTTGGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATG	600
Db	541	ACGTGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATG	600
Qy	601	CTCAGGTAGTGGAAAGTATGAGGAGGGCGAGGAGGAGGAGGAGTGAAGAGGAGGAGC	660
Db	601	CTCAGGTAGTGGAAAGTATGAGGAGGGCGAGGAGGAGGAGGAGTGAAGAGGAGGAGC	660
Qy	661	TGAGTGGAGGGGACGAGGAGGATGAAGAAGTTTATAACGATGAGAGGTAGATGGCGAG	720
Db	661	TGAGTGGAGGGGACGAGGAGGATGAAGAAGTTTATAACGATGAGAGGTAGATGGCGAG	720
Qy	721	AAGATGAAGAAGAGCTTTGGTGAAGAAAGAGGGGTGAGAAGCGAAATGAGAACTTGAAG	780
Db	721	AAGATGAAGAAGAGCTTTGGTGAAGAAAGAGGGGTGAGAAGCGAAATGAGAACTTGAAG	780
Qy	781	ATGAGGCAGAGAGTATGATCACTAAGTAGAATAACCTATTTTGAAGAAATTCCTATTGTGATT	840
Db	781	ATGAGGCAGAGAGTATGATCACTAAGTAGAATAACCTATTTTGAAGAAATTCCTATTGTGATT	840
Qy	841	TGACTGTTTTTACCCATATCCCCCTCCCCCTCCAACTCCTGCCCCCTGAA	889
Db	841	TGACTGTTTTTACCCATATCCCCCTCCCCCTCCAACTCCTGCCCCCTGAA	889

RESULT 3	
AAA88237	
ID	AAA88237 standard; DNA; 1035 BP.
XX	
XX	
AC	AAA88237;
XX	
DT	15-DEC-2000 (first entry)
XX	
DE	Human variant pp32r1 nucleotide sequence.
XX	
KW	Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW	acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW	malignant; cytostatic; gene therapy; ds.
XX	
XX	
OS	Homo sapiens.
XX	
PN	WO200045852-A1.
XX	
PD	10-AUG-2000.
XX	
PF	03-FEB-2000; 2000WO-US02656.
XX	
PR	03-FEB-1999; 99US-0118667.

XX	(UYJO) UNIV JOHNS HOPKINS.
PA	
XX	
XX	Pasternack GR, Bai J;
XX	
XX	WPI; 2000-514896/46.
DR	P-ESDB; AAB20655.
XX	
XX	Treatment of cancer comprising restoration of pp32 function in
PT	malignant cells -
XX	
XX	Example 3; Fig 3; 90pp; English.
PS	
XX	
CC	The present invention describes a method (M1) for treating malignant
CC	cells comprising restoration of pp32 function. Also described are:
CC	(1) a method (M2) of screening to determine whether a compound is an
CC	inducer of pp32 expression comprising measuring pp32 expression by
CC	cells cultured in the presence and absence of the compound; and
CC	(2) a method (M3) of screening to determine whether a compound is an
CC	inducer of pp32 function comprising measuring protein phosphatase
CC	activity in cells cultured in the presence and absence of the compound.
CC	The methods are useful for treating cancer and for identifying agents
CC	which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC	has been mapped to chromosome 15q22.3-q23. The present sequence
CC	represents the human variant pp32r1 nucleotide sequence from
CC	an example of the present invention.
XX	
XX	Sequence 1035 BP; 322 A; 189 C; 308 G; 216 T; 0 other;
SQ	

Query Match	100.0%	Score 889;	DB 21;	Length 1035;
Best Local Similarity	100.0%;	Prod. No. 1.1e-198;		
Matches 889;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GGGTCGAGGTTTATTGATTGAATTCGGCTGCGACGAGAGCCTCTGCAGACAGAGAGCGC	60	
Db	32	GGGTCGAGGTTTATTGATTGNAATTCGGCTGGCAGCAGAGCCTCTGCAGACAGAGAGCGC	91	
Qy	61	GAGAGATGGAGATGGCGACAGCGGATTCATTCAGAGCTCGGAACAGGCGGCCCTCTGTATG	120	
Db	92	GAGAGATGGAGATGGCGACAGCGGATTCATTCAGAGCTCGGAACAGGCGGCCCTCTGTATG	151	
Qy	121	TCAAGAACTTCGCTCGACACACAGTCGGTCCGAATGAAGGCAAACTCCAAGCCCTCACAG	180	
Db	152	TGAAGAAGCTTCGCTCGACACACAGTCGGTCCGAATGAAGGCAAACTCCAAGCCCTCACAG	211	
Qy	181	ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCCTCACCTCAATCTCAG	240	
Db	212	ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGGAGGCCTCACCTCAATCTCAG	271	
Qy	241	ACTTACCAAAGTTAAAGTTGAAAGCCTTGAACTAAGAGTCTCAGGGGGCCTGGAAGTAT	300	
Db	272	ACTTACCAAAGTTAAAGTTGAAAGCCTTGAACTAAGAGTCTCAGGGGGCCTGGAAGTAT	331	
Qy	301	TGGCAGAAAAGTGTCCAAACCTTCACGCATCTATATTAAAGTGGCAACAAAATTAAGACCC	360	
Db	332	TGGCAGAAAAGTGTCCAAACCTTCACGCATCTATATTAAAGTGGCAACAAAATTAAGACCC	391	
Qy	361	TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT	420	
Db	392	TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGACCTTTTCAATT	451	
Qy	421	GGAGGTAAACCAACCTGAAACGACTACGGAGAAAAGTGTTCAAGCTTCTCTGCAACTCA	480	
Db	452	GGAGGTAAACCAACCTGAAACGACTACGGAGAAAAGTGTTCAAGCTTCTCTGCAACTCA	511	
Qy	481	CATATCTCGACAGCTGTTACTGGGACCACAAAGAGGGCCCTTACTCAGATATTGAGGACC	540	
Db	512	CATATCTCGACAGCTGTTACTGGGACCACAAAGAGGGCCCTTACTCAGATATTGAGGACC	571	
Qy	541	ACGTGGAGGGCCTGGATGACGAGGAGGAGGGTGACGATGAGGAGAGTATGATGAAGATG	600	
Db	572	ACGTGGAGGGCCTGGATGACGAGGAGGAGGGTGACGATGAGGAGAGTATGATGAAGATG	631	

malignant; cytostatic; gene therapy; ds.

Query Match 100.0%; Score 889; DB 21; Length 5785;
Best Local Similarity 100.0%; Pred. No. 2e-198;
Matches 889; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGACAGCCTCTGCAGACAGAGAGCGC 60
Db 4388 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGACAGCCTCTGCAGACAGAGAGCGC 4447
Qy 61 GAGAGATGGAGATGGCGACAGCGGATTCATTTCAGAGCTGCGGAACAGAGCGCCCTCTGTATG 120
Db 4448 GAGAGATGGAGATGGCGACAGCGGATTCATTTCAGAGCTGCGGAACAGAGCGCCCTCTGTATG 4507
Qy 121 TGAAGAACTTGCCTGGACACAGTCGGTTCGATGAGGCAAACTCGAAGCCCTCACAG 180
Db 4508 TGAAGAACTTGCCTGGACACAGTCGGTTCGATGAGGCAAACTCGAAGCCCTCACAG 4567
Qy 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGCGCTCACCTCAATCTCAG 240
Db 4568 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGCGCTCACCTCAATCTCAG 4627
Qy 241 ACTTACCAAGTTAAAGTTGAGAAGCTTGAAGTCTCAGGAGGCTGGAAGTAT 300
Db 4628 ACTTACCAAGTTAAAGTTGAGAAGCTTGAAGTCTCAGGAGGCTGGAAGTAT 4687
Qy 301 TGGCAGAAAAGTGCCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGAGACC 360
Db 4688 TGGCAGAAAAGTGCCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTAAGAGACC 4747
Qy 361 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTAGAGCTTTTCAATT 420
Db 4748 TCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAGAGCTTTTCAATT 4807
Qy 421 GCGAGGTAACCAACCTGAAGAGCTTACGGAGAAAACGTTTCAAGCTTCTCCTGCAACTCA 480

Db 4808 GCGAGCTAACCAACCTGAAGAGCTACGGAGAAAAGCGTTTCAAGCTTCTCCTGCAACTCA 4867
Qy 481 CATATCTCGACAGCTGTTTACTGGGACCAACAAGSAGSCCCTTACTCAGATATTGAGGACC 540
Db 4868 CATATCTCGACAGCTGTTTACTGGGACCAACAAGSAGSCCCTTACTCAGATATTGAGGACC 4927
Qy 541 ACCTGAGGGCCTGGATGACGAGGAGGGTGAGCATGAGGAGGATGATGATGAAGATG 600
Db 4928 ACCTGAGGGCCTGGATGACGAGGAGGGTGAGCATGAGGAGGATGATGATGAAGATG 4987
Qy 601 CTCAGGTAGTGAAGATGAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
Db 4988 CTCAGGTAGTGAAGATGAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5047
Qy 661 TGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATAACATGAGAGGATGATGATGCGGAGG 720
Db 5048 TGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATAACATGAGAGGATGATGATGCGGAGG 5107
Qy 721 AAGATGAAGAAGAGCTTGGTGAAGAAAGGGGTGAGAAGCGAAAATGAGAACCTGAAG 780
Db 5108 AAGATGAAGAAGAGCTTGGTGAAGAAAGGGGTGAGAAGCGAAAATGAGAACCTGAAG 5167
Qy 781 ATGAGGAGAAAGATGATGACTAAGTAGATAACCTATTTTGAAAAATTCCTATTGTGATT 840
Db 5168 ATGAGGAGAAAGATGATGACTAAGTAGATAACCTATTTTGAAAAATTCCTATTGTGATT 5227
Qy 841 TGACTGTTTTTACCCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 889
Db 5228 TGACTGTTTTTACCCATATCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTGAA 5276

RESULT 6
AAT27712
ID AAT27712 standard; cDNA; 1052 BP.
XX
AC AAT27712;
XX
DT 30-JUL-1996 (first entry)
XX
DE Human pp32 cDNA.
XX
KW pp32; cancer; diagnosis; therapy; antisense; cell proliferation;
KW lymphoid tumour; epithelial tumour; colon carcinoma;
KW prostate carcinoma; non-Hodgkin lymphoma; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 97..846
FT /*tag= a
XX
PN WO9610092-A1.
XX
PD 04-APR-1996.
XX
PF 28-SEP-1995; 95WO-US12414.
XX
PR 28-SEP-1994; 94US-0314503.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Kuhajda FP, Pasternack GR;
XX
DR WPI; 1996-200930/20.
DR P-PSDB; AAR95900.
XX
PT New method of diagnosing cancer using pp32 cDNA - by detecting the
PT level of mRNA hybridising to pp32 cDNA; also for inhibiting cell
XX proliferation and screening anti-cancer drugs.
PS Claim 1; Fig 10a; 129pp; English.
XX
CC Human cDNA (AAT27712) cloned from HL-60 cells codes for a 32 kDa

CC protein, pp32 (AAR95900). The level of expression of pp32 correlates
CC with the malignant potential of lymphoid and epithelial tumours. The
CC cDNA clone was identified using a partial murine pp32 clone. The
CC human sequence may be used for specific diagnostic assays of tumour
CC tissue or in the creation of antisense expression vectors to inhibit
CC expression of pp32 by tumour cells as a means of cancer therapy.
CC It can also be used to transfect mammalian cells that are then
CC used to screen for anti-cancer drugs.
XX
SQ

Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;

Query Match 85.6%; Score 761; DB 17; Length 1052;
Best Local Similarity 92.5%; Pred. No. 1.1e-168;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATGATTCGAATTCGGCTGCGCAGAGCCTCTGCAGACAGAGCGC 60
DB 32 GGGTTCGGGGTTTATGATTCGAATTCGGCGCGGAGCCTCTGCAGAGAGAGCGC 91
QY 61 GAGAGATGAGATGGCAGCGGATTCATTTCAGAGCTCGCGAAGAGCGGCCCTCTGATG 120
DB 92 GAGAGATGAGATGGCAGCGGATTCATTTCAGAGCTCGCGAAGAGCGGCCCTCTGATG 151
QY 121 TGAAGAAGATTCGCCCTGCGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCTTCACAG 180
DB 152 TGAAGAAGATTCGCCCTGCGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCTTCACAG 211
QY 181 ATGAATTTGAGAAGCTGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 240
DB 212 ATGAATTTGAGAAGCTGAATTCCTTAAGTAAATCAACGGAGGCTCACCTCAATCTCAG 271
QY 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
DB 272 ACTTACCAAGTTAAGAACTTAAGAGCTTGAACCTAAGCGATTAACAGAGTCTCAGGGG 331
QY 289 GCCTGGAAGTATTCGCGAAGAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACA 348
DB 332 GCCTGGAAGTATTCGCGAAGAGTGTCCGAAACCTCAGCATCTAAATTTAAGTGGCAACA 391
QY 349 AAATTTAAAGACCTCAGCACATAGAGCCACTGAACAGTGTAGAAACCTCAAGAGCTTAG 408
DB 392 AAATTTAAAGACCTCAGCACATAGAGCCACTGAAGAGTGTAGAAACCTCAAGAGCTTAG 451
QY 409 ACCTTTCAATTCGAGGTAAACCACTGAACGACTACGGAGAAAGCTGTTCAGGCTTC 468
DB 452 ACCTTTCAATTCGAGGTAAACCACTGAACGACTACGGAGAAAGTGTTCAGGCTTC 511
QY 469 TCCTGCAACTCACATATCTGACAGCTGTTACTGGGACCAAGAGGCGCCCTTACTCAG 528
DB 512 TCCTGCAACTCACATATCTGACAGCTGTTACTGGGACCAAGAGGCGCCCTTACTCAG 571
QY 529 ATATTGAGGACACCTGAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGT 588
DB 572 ATGCTGAGGCTTACCTGGAGGCGCTGGATGATGAGGAGGAGGTGAGGATGAGGAGGT 631
QY 589 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGTG 648
DB 632 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGTG 691
QY 649 AAGAGGAGGAGCTGAGTGGAGGCGGACGAGGAGGTGAAGAAGGTTATAACGATGGAGG 708
DB 692 AAGAGGAGGAGCTGAGTGGAGGCGGAGGAGGAGGTGAAGAAGGTTATAACGATGGAGG 751
QY 709 TAGATGGCGAGGAGGAGTGAAGAAGCTTGGTGAAGAAGAGGGGTGAGAGGCGAAAT 768
DB 752 TAGATGACGAGGAGGAGTGAAGAAGCTTGGTGAAGAAGAGGGGTGAGAGGCGAAAC 811
QY 769 GAGAACCCTGAAGATGAGGAGGAGTGAAGTAACTAAGTAACTATTTTGAAGAAAT 828
DB 812 GAGAACCCTGAAGATGAGGAGGAGTGAAGTAACTAAGTAACTATTTTGAAGAAAT 871
QY 829 CCTATTGTGATTTGACTGTTTTTACCCTATTCCTT-----CCGCCCTCAATCTCAG 882
DB 882 CCTATTGTGATTTGACTGTTTTTACCCTATTCCTT-----CCGCCCTCAATCTCAG 931

DB 872 CCTATTGTGATTTGACTGTTTTTACCCTATTCCTTCCCCCCCCCTCTTAATCTGCTGCC 931
QY 883 CCCTGAA 889
DB 932 CCCTGAA 938

RESULT 7

AAX81536
ID AAX81536 standard; DNA; 1052 BP.
XX
AC AAX81536;
XX
DT 26-AUG-1999 (first entry)
XX
DE Nucleotide sequence of normal human phosphoprotein 32 (pp32).
XX
KW Phosphoprotein 32; pp32; variant; pp32r1; pp32r2; cancer; prostate;
KW prostatic adenocarcinoma; antineoplastic activity;
KW transformation suppression; malignant potential; neuroendocrine;
KW neural; mesenchymal; lymphoid; epithelial; germ cell; tumour; ss.
XX
OS Homo sapiens.
XX
PN W09929906-A2.
XX
PD 17-JUN-1999.
XX
PF 11-DEC-1998; 98WO-US26433.
XX
PR 12-DEC-1997; 97US-0069677.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Brody JR, Kadkol SS, Kochevar GJ, Pasternack GR;
XX
DR WPI; 1999-385626/32.
XX
PT Phosphoprotein 32 (pp32) related genomic sequences
XX
PS Example 2; Fig 3; 65pp; English.
XX
CC The present sequence represents a human phosphoprotein 32 (pp32)
CC nucleotide sequence. The specification describes pp32 variants,
CC designated pp32r1 and pp32r2. The pp32r1 and pp32r2 sequences are
CC associated with cancer in prostate, especially prostatic adenocarcinomas.
CC Normal pp32 exerts antineoplastic activity through suppression of
CC transformation. Cancer-associated pp32 variants augment, rather than
CC inhibit, transformation. Determining the presence of a gene encoding
CC residues 146-163 of pp32r1 or pp32r2 in a sample is useful for a
CC diagnostic method for predicting malignant potential of neuroendocrine,
CC neural, mesenchymal, lymphoid, epithelial or germ cell-derived tumours.
XX
SQ Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;

Query Match 85.6%; Score 761; DB 20; Length 1052;
Best Local Similarity 92.5%; Pred. No. 1.1e-168;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATGATTCGAATTCGGCTGCGCAGAGCCTCTGCAGACAGAGCGC 60
DB 32 GGGTTCGGGGTTTATGATTCGAATTCGGCGCGGAGCCTCTGCAGAGAGAGCGC 91
QY 61 GAGAGATGAGATGGCAGCGGATTCATTTCAGAGCTCGCGAAGAGCGGCCCTCTGATG 120
DB 92 GAGAGATGAGATGGCAGCGGATTCATTTCAGAGCTCGCGAAGAGCGGCCCTCTGATG 151
QY 121 TGAAGAAGCTTCGCCCTGCGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCTTCACAG 180
DB 152 TGAAGAAGCTTCGCCCTGCGACACAGTCGGTGAATGAAGGCAAACTCGAAGCCTTCACAG 211
QY 181 ATGAATTTGAGAAGCTGGAATTCCTTAAGTAAATCAACGGAGGCGCTCACCTCAATCTCAG 240
DB 181 ATGAATTTGAGAAGCTGGAATTCCTTAAGTAAATCAACGGAGGCGCTCACCTCAATCTCAG 240

Db 212 ATGAATTTGAAGAAGTGAATTTCTTAAGTACAATCAACGTAGGCGCTCACCTCAATCGCAA 271
Qy 241 ACTTACCAAGCTTA---AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGG 288
Db 272 ACTTACCAAGCTTAACCAAACTTAAGAGCTTGAACCTAAGCGATAACAGAGTCTCAGGG 331
Qy 289 GCCTGGAAGTATTGGCGAAGAGTGTCCAAACCTCAGGCATCTATATTAAAGTGGCAACA 348
Db 332 GCCTAGAAGTATTGGCGAAGAGTGTCCGAACCTCAGGCATCTAAATTTAAGTGGCAACA 391
Qy 349 AAATTAAGACCTCAGCACAATAGAGCCACTGAACAGTTAGAAAACCTCAAGAGCTTAG 408
Db 392 AAATTAAGACCTCAGCACAATAGAGCCACTGAAAAGTTAGAAAACCTCAAGAGCTTAG 451
Qy 409 ACCTTTTCAATTTGGAGTAGTACCAACCTGAACGACTACGGAGAAACGTTCTCAAGCTTC 468
Db 452 ACCTTTTCAATTTGGAGTAGTACCAACCTGAACGACTACCGAGAAAATGTGTTCAAGCTTC 511
Qy 469 TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCACAAGGAGGCCCTTACTCAG 528
Db 512 TCCCGCAACTCACATATCTCGACGCTATGACCGGAGCAGACAGGAGGCCCTGACTCGG 571
Qy 529 ATATTGAGGACCACTGGAGGCCCTGTGATGACGAGGAGGAGGTTGACATGAGGAGGAGT 588
Db 572 ATGCTGAGGGCTACGTGGAGGCCCTGTGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631
Qy 589 ATGATGAGATGCTCAGGTAGTGAAGATGAGGAGGCCGAGGAGGAGGAGGAGGAGGAGT 648
Db 632 ATGATGAGATGCTCAGGTAGTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 691
Qy 649 AAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAGG 708
Db 692 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGGTTATAACGATGGAGAGG 751
Qy 709 TAGATGGCGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGCAAAAT 768
Db 752 TAGATGACGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGTTCAGAAGCGCAAAAC 811
Qy 769 GAGAACCTGAGATGAGGAGGAGATGATGACTAAGTGAATAACCTATTTTGAAGAAAT 828
Db 812 GAGAACCTGAGATGAGGAGGAGATGATGACTAAGTGAATAACCTATTTTGAAGAAAT 871
Qy 829 CCTATTGTGATTTGACTGTGTTTTACCATATCCCT-----CCCCCTCCATCCTGCC 882
Db 872 CCTATTGTGATTTGACTGTGTTTTACCATATCCCTCTCCCTCCCTCCCTCTATCCTGCC 931
Qy 883 CCCTGAA 889
Db 932 CCCTGAA 938

RESULT 8
AAA88238

ID AAA88238 standard; DNA; 1052 BP.

AC AC

AAA88238;

DT 15-DEC-2000 (first entry)

XX Human pp32 nucleotide sequence.

XX Human; pp32; chromosome 15q22.3-q23; cancer; phosphoprotein; APRIL;
KW acidic protein rich in leucine; chromosome 15q25; tumour suppressor;
KW malignant; cytostatic; gene therapy; ds.

XX Homo sapiens.

OS

XX WO200045852-A1.

XX 10-AUG-2000.

XX 03-FEB-2000; 2000WO-US02656.

PR 03-FEB-1999; 99US-0118667.
XX (UYJO) UNIV JOHNS HOPKINS.
PA Pasternack GR, Bai J;
PI WPI; 2000-514896/46.
XX P-PSDB; AAB20656.
DR Treatment of cancer comprising restoration of pp32 function in
DR malignant cells -
XX
XX Example 3; Fig 3; 90pp; English.
XX The present invention describes a method (M1) for treating malignant
CC cells comprising restoration of pp32 function. Also described are:
CC (1) a method (M2) of screening to determine whether a compound is an
CC inducer of pp32 expression comprising measuring pp32 expression by
CC cells cultured in the presence and absence of the compound; and
CC (2) a method (M3) of screening to determine whether a compound is an
CC inducer of pp32 function comprising measuring protein phosphatase
CC activity in cells cultured in the presence and absence of the compound.
CC The methods are useful for treating cancer and for identifying agents
CC which may be used to treat cancer. Human pp32 is a phosphoprotein which
CC has been mapped to chromosome 15q22.3-q23. The present sequence
CC represents the human pp32r1 nucleotide sequence from an example of
CC the present invention.
XX
SQ Sequence 1052 BP; 326 A; 196 C; 316 G; 214 T; 0 other;

Query Match 85.6%; Score 761; DB 21; Length 1052;

Best Local Similarity 92.5%; Pred. No. 1.1e-168;

Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

Qy 1 GGGTTCCAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGACAGAGAGCGC 60

Db 32 GGGTTCCGGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCTCTGCAGAGAGAGAGCGC 91

Qy 61 GAGAGATGAGATGGCGACACGGATTCAATCAGAGTCGGAAACAGGGCGCCCTCTGATG 120

Db 92 GAGAGATGAGATGGCGACACGGATTCAATCAGAGTCGGAAACAGGGCGCCCTCTGATG 151

Qy 121 TGAAGAACTTCGCCCTGGACAAACAGTCGCTCGAATGAAGCAAACTCGAAGCCCTCAGAC 180

Db 152 TGAAGAACTTCGCCCTGGACAAACAGTCGCTCGAATGAAGCAAACTCGAAGCCCTCAGAC 211

Qy 181 ATGAATTTGAAGAACTGGAAATTTTAAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAG 240

Db 212 ATGAATTTGAAGAACTGGAAATTTTAAAGTAAATCAACGGAGGCCCTCACCTCAATCTCAG 271

Qy 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288

Db 272 ACTTACCAAGTTAACAACAACTTAAGAAGCTTGAACCTAAGCGATACACAGAGTCTCAGGGG 331

Qy 289 GCCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCAGGCATCTATATTTAAGTGGCAACA 348

Db 332 GCCTAGAAGTATTGGCAGAAAAAGTGTCCGAACCTCAGGCATCTAAATTTAAGTGGCAACA 391

Qy 349 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408

Db 392 AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 451

Qy 409 ACCTTTTCAATTTGCGAGGTAAACCAACCTGAACGACTACGGAGAAACAGTGTTCAGAGCTTC 468

Db 452 ACCTTTTCAATTTGCGAGGTAAACCAACCTGAACGACTACGGAGAAACAGTGTTCAGAGCTTC 511

Qy 469 TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACACAGGAGGCCCTTACTCAG 528

Db 512 TCCCGCAACTCACATATCTCGACGCGCTATGACCGGAGCAGCAAGAGGCCCTTGACTGG 571

Qy 529 ATATTGAGGACCACTGGAGGGCGCTGGATGACGAGGAGGGGTGAGCATGAGGAGGAGT 588

Db 572 ATGCTGAGGGCTACGTGGAGGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631

XX WO200175067-A2.
PN 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
PA Drmanac RT, Liu C, Tang YT;
XX WPI: 2001-639362/73.
PI P-PSDB; ABG12202.
XX
DR New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 1; SEQ ID No 12193; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS4197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1155 BP; 340 A; 219 C; 347 G; 249 T; 0 other;

Query Match 83.5%; Score 742; DB 23; Length 1155;
Best Local Similarity 91.9%; Pred. No. 3.3e-164;
Matches 834; Conservative 0; Mismatches 55; Indels 19; Gaps 4;

Qy 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCCACGACGAGCCCTCTCGACGACAGAGCGC 60
Dy 57 GGGTTCGGGGTTTATTGATTGAATTCGGCGCGCGGGAGCCCTCTCGACGACGAGAGCGC 116
Qy 61 GAGAGATGGAGATGGGACGAGCGGATTTCATTCAGAGCTCGCGAACAGCGGCCCTCTGATG 120
Dy 117 GAGAGATGGAGATGGGACGAGCGGATTTCATTCAGAGCTCGCGAACAGCGGCCCTCTGATG 176
Qy 121 TGAAGAACTTGCCTCGACAACTCGGTGCGATGAAGGCAAACTCGAAGCCCTCACAG 180
Dy 177 TGAAGAACTTGTCTTGGACAACTCGGTGCGATGAAGGCAAACTCGAAGCCCTCACAG 236
Qy 181 ATGAATTTGAAGAAGCTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Dy 237 ATGAATTTGAAGAAGCTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCGCAA 296
Qy 241 ACTTACCAAGCTTA--AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGG 288
Dy 297 ACTTACCAAGCTTAACAAAGCTTGAAGAGCTTGAACCTAAGCGATGAACGAGAGTCTCAGGG 356
Qy 289 GCCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCAGG-CATCTATATTAAAGTGGCAAC 347

Db 357 GCCTGGAAGTATTGGCAGAAAAAGTGTCCGAACCTTCGCCCATCTAATTTAAGGTGCAAC 416
Qy 348 AAAATTAAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACTCAAGAGCTTA 407
Dy 417 AAAATTAAAGACCTCAGCACAAATAGAGCCACTTGA AAAAGTTAGAAAACTCAAGAGCTTA 476
Qy 408 GACCTTTTCAATTTGCCAGGTAAACCACTGAACGACTACGGAGAAAAACCTGTTCAAGCTT 467
Dy 477 GACCTTTTCAATTTGCCAGGTAAACCACTGAACGACTACGGAGAAAAATGTTTCAAGCTC 536
Qy 468 CTCTCTCAACTCACATATCTCGACAGCTGTACTGGGACCAACAAGGAGGCCCTTACTCA 527
Dy 537 CTCTCTCAACTCACATATCTCGACGCTATGACCGGAGCAGCAAGGAGGCCCTTACTCG 596
Qy 528 GATATTGAGGACCACTGAGGAGCCCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAG 587
Dy 597 GATGCTGAGGGCTACCTGGAGGCGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 656
Qy 588 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 647
Dy 657 TATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGATGAGGAGGAGGAGT 716
Qy 648 GAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAGGTTATACCATGAGAG 707
Dy 717 GAAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAGGTTATACCATGAGAG 776
Qy 708 GTAGATGGGAGGAGGAGGATGAAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGG 767
Dy 777 GTAGATGACGAGGAGGAGGATGAAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGG 836
Qy 768 TGGAACCTTGAAGATGAGGAGGAGGAGGATGATGACTAAGTGAATTAACCTATTTTGA 827
Dy 837 CGAAGACCTTGAAGATGAGGAGGAGGAGGATGATGACTAAGTGAATTAACCTATTTTGA 896
Qy 828 TCCTATTGTGATTGACTGTTTACCCATATCCCT-----CCCCCTCCAATCCTGC 881
Dy 897 TCCTATTGTGATTGACTGTTTACCCATATCCCTCTCCCCCCCCCTCCCAATCCTGC 956
Qy 882 CCCCTGAA 889
Dy 957 CCCCTGAA 964

RESULT 13
ID AAA15294 standard; cDNA; 750 BP.
XX
AC AAA15294;
XX
DT 04-SEP-2000 (first entry)
XX
DE cDNA encoding a protein phosphatase 2A inhibitor.
XX
KW Syndecan-4; angiogenesis; proteoglycan; protein kinase C;
KW delta-isoenzyme; alpha isoenzyme; protein phosphatase; infarction;
KW endothelial cell proliferation; endothelial cell migration; anoxia;
KW myocardial infarction; chronic myocardial ischemia; heart tissue; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..750
FT /*tag= a
XX
XX WO200027416-A1.
XX
XX 18-MAY-2000.
XX
XX 10-NOV-1999; 99WO-US26647.
XX
XX 12-NOV-1998; 98US-0190976.
XX

PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.	
XX	Simons M, Horowitz A;	
XX	WPI: 2000-376307/32.	
DR	P-PSDB; AAY93262.	
XX	Stimulating angiogenesis, useful particularly for treating cardiac	
PT	anoxia and infarction, by preventing phosphorylation of specific	
PT	residue in syndecan-4, present in endothelial cells -	
XX	Disclosure; Page 35; 73pp; English.	
XX	The present sequence encodes a protein phosphatase 2A inhibitor. The	
CC	protein phosphatase 1 is used in the method of the invention. The	
CC	specification describes a method for stimulating angiogenesis within	
CC	variable cells, tissues, or organs in situ. The method comprises	
CC	treating target endothelial cells such that Ser183, in the	
CC	intracellular cytoplasmic domain of syndecan-4 proteoglycan, is	
CC	present in non-phosphorylated form in at least some syndecan-4 molecules.	
CC	The cells are treated with an inhibitor of syndecan-4 protein kinase C	
CC	(PKC) delta-isoenzyme, an agent that increases intracellular activity of	
CC	the PKC alpha-isoenzyme, or an agent that activates at least one of	
CC	protein phosphatases 1 or 2A. Keeping Ser183 in the non-phosphorylated	
CC	form results in activation of protein kinase C alpha isoenzyme, which is	
CC	essential for endothelial cell proliferation and migration in situ.	
CC	Syndecan-4 participates in intracellular signalling through	
CC	oligomerisation of its cytoplasmic tail and this process does not	
CC	occur if Ser183 is phosphorylated. The method can be used in vivo or	
CC	in vitro, to stimulate angiogenesis in cells or tissues which are	
CC	defective or have suffered anoxia or infarction, particularly myocardial	
CC	infarction, or chronic myocardial ischemia of heart tissue, and to	
CC	study mechanisms involved in control of angiogenesis.	
XX		
SQ	Sequence 750 BP; 260 A; 130 C; 229 G; 131 T; 0 other;	
Query Match 72.0%; Score 640.4; DB 21; Length 750;		
Best Local Similarity 92.9%; Pred. No. 1.8e-140;		
Matches 697; Conservative 0; Mismatches 41; Indels 12; Gaps 2;		
QY	66 ATGGAGATGGGACAGGGATTTCATTCAGAGTCGCGAAGCGGCGCCCTCATGTGAAA 125	
DB	1 ATGGAGATGGGACAGGGATTTCATTCAGAGTCGCGAAGCGGCGCCCTCATGTGAAA 60	
QY	126 GAACCTTGCCCTGGACAACAGTGGTGGATGAAGGCAAACTCGAAGCCCTCACAGATGAA 185	
DB	61 GAACCTTGCTTGACACACAGTCGGTGGATGAAGCAAACTCGAAGCCCTCACAGATGAA 120	
QY	186 TTTGAAGAAGTGGAAATCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAGACTTA 245	
DB	121 TTTGAAGAAGTGGAAATCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAGACTTA 180	
QY	246 CCAAAGCTTA---AAGTTGAGAAAGCTTGAACTA-----AGAGTCTCAGGGGCGCTG 293	
DB	181 CCAAAGTTAAACAACCTTAAGAAGCTTGAACCTAAGCGGATAACAGAGTCTCAGGGGCGCTG 240	
QY	294 GAAGTATTGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGCAACAAAATT 353	
DB	241 GAAGTATTGGCAGAAAAGTGTCCGAACCTCAGCATCTAATTTAAGTGGCAACAAAATT 300	
QY	354 AAGAGCTCAGACAAATAGAGGCACTGAACAGTTAGAAAACCTCAAGAGCTTAGACCTT 413	
DB	301 AAGAGCTCAGACAAATAGAGGCACTGAAAAAGTTAGAAAACCTCAAGAGCTTAGACCTT 360	
QY	414 TTCAATTGCGAGGTAAACCAACCTGAAAGTACGAGAAAGCTGTTCAAGCTTCTCCCTG 473	
DB	361 TTCAATTGCGAGGTAAACCAACCTGAAAGTACGAGAAAGTGTGTTCAAGCTTCTCCCG 420	
QY	474 CAACTCACATATCTCGACAGCTGTTACTGGGACCACAGAGGCGCCCTTACTTCAGATATT 533	
DB	421 CAACTCACATATCTCGACAGCTGTTACTGGGACCACAGAGGCGCCCTTACTTCAGATATT 480	
QY	534 GAGGACCACTGGAGGGCCCTGGATGACGAGGAGGGGTGACATGAGGAGGATGATGAT 593	
DB	481 GAGGGCTACCTGGAGGGCCCTGGATGATGAGGAGGAGGATGAGGAGGAGTATGAT 540	
QY	594 GAAGATGCTCAGCTAGTGGAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 653	
DB	541 GAAGATGCTCAGCTAGTGGAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600	
QY	654 GAGGACCTGAGTGGAGGGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 713	
DB	601 GAGGACCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660	
QY	714 GCGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGAGGGGTCAGAAGCGAATAATCAGAA 773	
DB	661 GAGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGAGGGGTCAGAAGCGAATAATCAGAA 720	
QY	774 CCTGAAGATCAGGAGGAGAGATGATGACTAA 803	
DB	721 CCYGAAGATCAGGAGGAGAGATGATGACTAA 750	
RESULT 14		
AAT27713		
ID	AAT27713 standard; cDNA; 980 BP.	
XX	AC AAT27713;	
DT	30-JUL-1996 (first entry)	
XX	Mouse pp32 cDNA clone A202.	
XX	pp32; cancer; diagnosis; therapy; antisense; cell proliferation;	
KW	lymphoid tumour; epithelial tumour; colon carcinoma;	
KW	prostate carcinoma; non-Hodgkin lymphoma; ds.	
OS	Mus sp.	
XX	WO9610092-A1.	
XX	04-APR-1996.	
XX	28-SEP-1995; 95WO-US12414.	
XX	28-SEP-1994; 94US-0314503.	
XX	(UYJO) UNIV JOHNS HOPKINS.	
XX	Kuhajda FP, Pasternack GR;	
XX	WPI; 1996-200930/20.	
XX	New method of diagnosing cancer using pp32 cDNA - by detecting the	
PT	level of mRNA hybridising to pp32 cDNA; also for inhibiting cell	
PT	proliferation and screening anti-cancer drugs.	
XX	Claim 1; Fig 10c; 129pp; English.	
XX	A mouse cDNA clone (AAT27713), designated A202, codes for a 32 kDa	
CC	protein, pp32, associated with the malignant potential of lymphoid	
CC	and epithelial tumours. It was obtd. from a murine A20 cDNA	
CC	library by screening with a probe based on murine pp35 peptide,	
CC	and use of a human pp32 cDNA clone (see also AAT27712) fragment	
CC	to re-screen the A20 cDNA library. A partial cDNA clone (see	
CC	also AAT27715 and AAR95902) was also isolated. The cDNA may be used	
CC	to design probes and primers useful in diagnostic assays of tumour	
CC	tissue.	
XX	Sequence 980 BP; 312 A; 169 C; 302 G; 197 T; 0 other;	
SQ	Query Match 64.2%; Score 570.8; DB 17; Length 980;	
Best Local Similarity 82.9%; Pred. No. 4e-124;		
Matches 706; Conservative 0; Mismatches 127; Indels 19; Gaps 4;		
QY	50 ACAGAGAGCGGAGAGATGGAGATGGGACAGCGGATTCATTCAGAGCTGCGGACAGGGC 109	

Db 10 AGAGAGAGCGGAGAGATGGAGATGGACAAACGGAATTTATTTAGAGCTGCGGAACAGGAC 69
QY 110 GCCCTCTGATGTGAAGAACTTGCCTTGGACACACAGTCGTCGATCAAGGCAAACTCGA 169
Db 70 GCCCTCTGATGTGAAGAGCTGGTCCCTGGATAGTCTGTAAGTCAATTTGAAGGCAAAATCGA 129
QY 170 AGCCCTCACAGATGAATTTGAAGAACTTGAATTTCTTAAAGTAAATCAACGAGGCGCTCAC 229
Db 130 AGGCTCACGATGAGTTTGAAGAACTTGAATTTCTTAAAGTAAATCAACGATAGGCTCAC 189
QY 230 CTCATCTCAGACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AG 277
Db 190 CTCATTTTCCAACTTACCAAGTTTAAACAACTCAAGAAAGCTTGAATTAAGCGGAAACAG 249
QY 278 AGTCTCAGGGGCTGGAAGTATTTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTT 337
Db 250 AATCTCAGGGGACTGGAAGTATTTGGCAGAAAGTGTCCAAACCTTAAAGCATCTAATTT 309
QY 338 AAGTGGCAACAAATTAAGAACTTCAAGCAATAGAGCCACTGAAACAGTTAGAAAACCT 397
Db 310 AAGTGGCAACAAATTAAGATCTCAGCAATAGAGCCGCTGAAGAACTTGAAGATCT 369
QY 398 CAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCACTGAACGACTACGAGAAACCT 457
Db 370 CAAGAGCTTAGACCTTTTCAATTCGAGGTAAACCACTGAACGACTTACGAGAAACCT 429
QY 458 GTTCAAGCTTCTCTGCAATCTACATATCTCGACAGCTGTACTGGGACCAAGAGGC 517
Db 430 GTTCAAGCTTCTCTGCAATCTACATATCTCGACAGCTGTACTGGGACCAAGAGGC 489
QY 518 CCCTTACTCAGATATTGAGGACCACTGAGGAGGCGCTTGGATCAGGAGGAGGTTGAGCA 577
Db 490 CCCGACTCCGATGTTGAGGCTACGTGGA-----GGATGACGACGAGGAATGAGGA 543
QY 578 TGAGGAGGATGATGATGAAGATCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGA 637
Db 544 TGAGGAGGATGATGATGAATATGCCAGCTAGTGGAAAGATGAAGAGGTTGAGGA 603
QY 638 GGAGGAAGGTGAAGAGGAGGAGCTGAGTGGAGGCGGAGGAGGATCAAGAGGTTATRA 697
Db 604 GGAAGAAGGGGAGGAGGAGGATGAGTGGAGGAGGAGGAGGATGAGGAGGTTATCAA 663
QY 698 CGATGGAGAGGTAGATGGCGAGGAAGATGAAGAGCTTGGTGAAGAAAGGCGTCA 757
Db 664 TGACGGGGAAGTGTGATCAGGAGGAGGAGGAGGAGCTGGTGAAGAAAGGAGTCA 723
QY 758 GAAGCGAAATGAACCTGAAGATGAGGAGGAGGAGGATGACTAAGTGAATTAACCTAT 817
Db 724 GAAGCGAAACGAGAACCGGACGATGAGGCGGAAGAGGATGACTAAGGA-ATCAACCTGT 782
QY 818 TTTCAAAATTCCTATTGTGATTTGACTGTTTTTACCCTATCCCTCCCTCCCTCAATC 877
Db 783 TTGGGAAATTCCTATTGTGATTTGACTGTTTTTACCCTATCCCTCCCTCCCTTATTC 842
QY 878 CTGCCCCCTGAA 889
Db 843 CTGCCCCCGAA 854

RESULT 15
ABI99657
ID ABI99657 standard; cDNA; 980 BP.
XX
AC ABI99657;
XX
DT 07-MAR-2002 (first entry)
XX
DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:687.
XX
KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX

OS Mus musculus.
XX
PN WO200188188-A2.
XX
PD 22-NOV-2001.
XX
PF 18-MAY-2001; 2001WO-JP04192.
XX
PR 18-MAY-2000; 2000JP-0145977.
XX
PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX
PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX
DR WPI: 2002-034733/04.
DR P-PSDB; ABB57251.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or
PT by determining the expression profile of a gene group comprising these
PT genes -
XX
PS Claim 2; Page 1714-1716; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC the expression levels of particular genes (ABI99202 to ABI99912, encoding
CC the protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The
CC expression levels or expression profiles produced by these genes are
CC used as an indicator when screening for ischaemic condition-improving
CC drugs or therapeutics for ischaemic diseases. ABI99913 and ABI99914
CC represent PCR primers for a mouse ischaemic condition related sequence,
CC which are used in the exemplification of the present invention.
XX
SQ Sequence 980 BP; 312 A; 169 C; 302 G; 197 T; 0 other;
Query Match 64.2%; Score 570.8; DB 24; Length 980;
Best Local Similarity 82.9%; Pred. No. 4e-124;
Matches 706; Conservative 0; Mismatches 127; Indels 19; Gaps 4;
QY 50 ACAGAGAGCGGAGAGATGGAGATGGCGACAGCGATTCATTTCAGAGCTGCGGAACAGGCG 109
Db 10 AGAGAGAGCGGAGAGATGGAGATGGCAACAGGATTTATTTAGAGCTGCGGAACAGGAC 69
QY 110 GCCCTCTGATGTGAAGAACTTGCCTTGGACACACAGTCGTCGATGAAGGCAAACTCGA 169
Db 70 GCCCTCTGATGTGAAGAGCTGCTCTGGATAACTGTAACTCAATTTGAAGGCAAAATCGA 129
QY 170 AGCCCTCACAGATGAATTTGAAGAACTTGAATTTCTTAAAGTAAATCAACGAGGCGCTCAC 229
Db 130 AGGCTCACGATGAGTTTGAAGAACTGGAATTCCTTAACTAATCAACGATAGGCTCAC 189
QY 230 CTCATCTCAGACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AG 277
Db 190 CTCATTTTCCAACTTACCAAGTTTAAACAACTCAAGAAAGCTTGAATTAAGCGGAAACAG 249
QY 278 AGTCTCAGGGGCTGGAAGTATTTGGCAGAAAGTGTCCAAACCTCAGCATCTATATTT 337
Db 250 AATCTCAGGGGACTGGAAGTATTTGGCAGAAAGTGTCCAAACCTTAAAGCATCTAATTT 309
QY 338 AAGTGGCAACAAATTAAGAACTTCAAGCAATAGAGCCACTGAAACAGTTAGAAAACCT 397
Db 310 AAGTGGCAACAAATTAAGATCTCAGCAATAGAGCCGCTGAAGAACTTGAAGATCT 369
QY 398 CAAGAGCTTAGACCTTTTCAATTTGCGAGGTAAACCACTTGAACGACTACGGAAGAAACCT 457
Db 370 CAAGAGCTTAGACCTTTTCAATTTGCGAGGTAAACCACTTGAACGACTACGGAAGAAACCT 429

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-591-500-3

Perfect score: 889

Sequence: 1 gggttcgaggtttattgatt.....ctccaatctgccccctgaa 889

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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 - 2: /cgn2.6/ptodata/1/ina/5B_COMB.seq:*
 - 3: /cgn2.6/ptodata/1/ina/6A_COMB.seq:*
 - 4: /cgn2.6/ptodata/1/ina/6B_COMB.seq:*
 - 5: /cgn2.6/ptodata/1/ina/PTUS_COMB.seq:*
 - 6: /cgn2.6/ptodata/1/ina/backfiles1.seq:*

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	761	85.6	1052	1 US-08-466-603-1	Sequence 1, Appli
2	761	85.6	1052	1 US-08-314-503A-1	Sequence 1, Appli
3	761	85.6	1052	1 US-08-468-066-1	Sequence 1, Appli
4	761	85.6	1052	2 US-08-466-717-1	Sequence 1, Appli
5	761	85.6	1052	3 US-08-466-743-1	Sequence 1, Appli
6	761	85.6	1052	5 PCT-US95-12414-1	Sequence 1, Appli
7	570.8	64.2	980	1 US-08-466-603-3	Sequence 3, Appli
8	570.8	64.2	980	1 US-08-314-503A-3	Sequence 3, Appli
9	570.8	64.2	980	1 US-08-468-066-3	Sequence 3, Appli
10	570.8	64.2	980	2 US-08-466-717-3	Sequence 3, Appli
11	570.8	64.2	980	3 US-08-466-743-3	Sequence 3, Appli
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16	429.2	48.3	759	2 US-08-466-717-4	Sequence 4, Appli
17	429.2	48.3	759	3 US-08-466-743-4	Sequence 4, Appli
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20	296.4	33.3	966	4 US-09-262-610-2	Sequence 2, Appli
21	110	12.4	3489	2 US-08-728-323A-1	Sequence 2, Appli
22	110	12.4	3489	4 US-09-298-568-1	Sequence 1, Appli
C 23	110	12.4	32207	2 US-08-770-379-20	Sequence 20, Appl
C 24	110	12.4	32207	4 US-08-757-669A-20	Sequence 20, Appl
C 25	110	12.4	32207	4 US-09-230-371A-20	Sequence 20, Appl
C 26	107.6	12.1	16442	3 US-08-781-891-208	Sequence 208, App
C 27	105.2	11.8	7218	1 US-08-232-463-14	Sequence 14, Appl

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C 29	102.4	11.5	1931	2 US-09-130-114-2	Sequence 2, Appli
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32	94.6	10.6	3901	2 US-08-574-959A-6	Sequence 6, Appli
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45	78	8.8	10596	1 US-07-884-811-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1

US-08-466-603-1
; Sequence 1, Application US/08466603
; Patent No. 5726018
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,603
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
US-08-466-603-1

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Query Match      85.6%; Score 761; DB 1; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.le-172;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

Qy 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCGACGAGCCCTCTGCAGACAGAGCGC 60
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Qy 289 GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGGATCTATATTTAAGTGGCAACA 348
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Qy 589 ATGATGAAGATCTCAGCTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGTG 648
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Db 872 CCTATTGATTTGACTGTTTTTACCATATCCCT-----CCCCCTCCAAATCCTGCC 931
Qy 883 CCTGAA 889
Db 932 CCTGAA 938
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RESULT 2
US-08-314-503A-1
; Sequence 1, Application US/08314503A
; Patent No. 5734022

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; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhnajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-314-503A-1
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Query Match      85.6%; Score 761; DB 1; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.le-172;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

Qy 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCGACGAGCCCTCTGCAGACAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTGAATTCGGCGCGCGGAGCCTCTGCAGAGAGAGCGC 91
Qy 61 GAGAGATGGAGATGGCGAGCGGATTTCATTAGAGCTGCGGAACAGAGCGCCCTCTGATG 120
Db 92 GAGAGATGGAGATGGCGAGCGGATTTCATTAGAGCTGCGGAACAGAGCGCCCTCTGATG 151
Qy 121 TGAAGAACTTGGCCCTGGACACAGTCGGTTCGAATGAAGCAAACTCGAAGCCCTCACAG 180
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Qy 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
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Qy 241 ACTTACCAGTGA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 288
Db 272 ACTTACCAGTGA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGG 331
Qy 289 GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGGATCTATATTTAAGTGGCAACA 348
Db 332 GCCTAGAAGTATTGGCAGAAAAGTGTCCGAACCTCAGGATCTATAATTTAAGTGGCAACA 391
Qy 349 AAATTAAGACCTCAGCACAATAGAGCCACTGAACAGCTTAGAAAACCTCAAGAGCTTAG 408
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Db 392 AAATTAAAGACCTCAGCACAAATAGAGCCACTGAAAAAGTTAGAAAACTCAAGAGCTTAG 451
QY 409 ACCTTTCAATTGGAGGTACCAACCTGACGACTGACGAGAACTGTTCAAGCTTC 468
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QY 469 TCCTGCAACTCACATATCTGCACAGCTGTACTGGGACCAAGGAGGCCCTTACTCAG 528
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QY 529 ATATTGAGGACCACTGGAGGCTTGATGACGAGGAGGAGGCTGATGAGGAGGAGT 588
Db 572 ATGCTGAGGCTACGTGGAGGCCCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAGT 631
QY 589 ATGATGAAGATGCTCAGSTAGTGAAGATGAGGAGGCCGAGGAGGAGGAGGAGGAGT 648
Db 632 ATGATGAAGATGCTCAGGTAGTGAAGACGAGGAGGAGGAGGAGGATGAGGAGGAGGAGT 691
QY 649 AAGAGGAGGAGCTGAGTGGAGGACGAGGAGGAGGATGAAGAGGTTATAACGATGGAGAGG 708
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QY 769 GAGAACTGAAGATGAGGAGGAGGAGGATGACTAAGTAGAATAACCTATTGAAAGAAAT 828
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QY 829 CCTATTGTGATTGACTGTTTTACCCTATATCCCT-----CCCCCTCCATCCCTGCC 882
Db 872 CCTATTGTGATTGACTGTTTTACCCTATATCCCTCTCTCCCCCTCTATCCCTGCC 931
QY 883 CCCTGAA 889
Db 932 CCCTGAA 938

RESULT 3

US-08-468-066-1
; Sequence 1, Application US/08468066
; Patent No. 5756676
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kubaide, Francis P.
; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patencin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,066
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-468-066-1

Query Match 85.6%; Score 761; DB 1; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.le-172;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

QY 1 GGGTTCAGGTTTATTGATTGGAATTCGGCTGGCAGCAGAGCCCTCTGCAGACAGAGCGC 60
Db 32 GGGTTCGGGGTTTATTGATTGGAATTCGCCCGCGGGAGCCCTCTGCAGAGAGAGCGC 91
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QY 529 ATATTGAGGACCACTGAGGAGGCCCTGGATGACGAGGAGGAGGCTGAGATGAGGAGGAGT 588
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Db 872 CCTATTGTGATTGACTGTTTTTACCCATATCCCTCTCCCCCCCCTCTAATCCTGCC 931
QY 883 CCCTGAA 889
Db 932 CCCTGAA 938
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US-08-466-717-1
; Sequence 1, Application US/08466717
; Patent No. 5874234
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5874234el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 06-JUN-1995
; APPLICATION NUMBER: US/08/466,717
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
US-08-466-717-1
Query Match 85.6%; Score 761; DB 2; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.le-172;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;
QY 1 GGTTTCGAGGTTTATGATTGAATTCGGTGGCAGCAGAGCCTCTGCACAGAGAGCGC 60
Db 32 GGTTTCGAGGTTTATGATTGAATTCGGTGGCAGCAGAGCCTCTGCACAGAGAGCGC 91
QY 61 GAGAGATGAGATGGCAGCAGGATTCATTCAGAGCTGGGAACAGGGCGCCTCTGATG 120
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QY 121 TGAAGAACCTTGCCCTGGACAAACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTACAG 180
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QY 181 ATGAATTTGAAGAACCTGGAATTCCTTAAGTAAATCAACAGGAGCCCTCAGCTCAATCTCAG 240
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RESULT 5
US-08-466-743-1
; Sequence 1, Application US/08466743
; Patent No. 6040173
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia

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; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,743
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 97..843
; US-08-466-743-1

Query Match 85.6%; Score 761; DB 3; Length 1052;
Best Local Similarity 92.5%; Pred. No. 3.1e-172;
Matches 839; Conservative 0; Mismatches 50; Indels 18; Gaps 3;

QY 1 GGGTTCGAGGTTTATTGATTGAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGCGC 60
DB 1 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 32 GGGTTCGGGGTTTATTGATTGAATTCGGCGCGCGCGGAGCCCTCTGCAGAGAGAGCGC 91
DB 3 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTGCGGAACAGAGCGGCCCTCTGATG 120
DB 6 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 92 GAGAGATGGAGATGGCAGACGGATTTCATTCAGAGCTGCGGAACAGAGCGGCCCTCTGATG 151
DB 9 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TGAAGAACTTGCCTGGACAACAGTCGGTGCATGAAGCAACAACTCGAAGCCCTCACAG 180
DB 12 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 152 TGAAGAACTTGCCTGGACAACAGTCGGTGCATGAAGCAACAACTCGAAGCCCTCACAG 211
DB 15 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 ATGAATTGAGAACTGGAATTCCTTAAGTAAATCAACGAGCGCCCTCAATCTCAG 240
DB 18 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 212 ATGAATTGAGAACTGGAATTCCTTAAGTAAATCAACGAGCGCCCTCAATCTCAG 271
DB 21 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 241 ACTTACCAAAAGTTA---AAGTTGAGAAAGCTTGAACTA-----AGAGTCTCAGGG 288
DB 24 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 272 ACTTACCAAAAGTTA---AAGTTGAGAAAGCTTGAACTA-----AGAGTCTCAGGG 331
DB 27 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 289 GCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGGCATCTATATTTAAGTGGCAACA 348
DB 29 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 332 GCCTGGAAGTATTGGCAGAAAGTGTCCAAACCTCAGGCATCTATATTTAAGTGGCAACA 391
DB 32 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 349 AAATTAAGACCTCAGCACATAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAG 408
DB 34 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 392 AAATTAAGACCTCAGCACATAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAG 451
DB 39 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 409 ACCTTTTCAATTGGAGGTAAACCACTGAACGACTACGGAGAAAGCTGTTCAAGCTTC 468
DB 40 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 452 ACCTTTTCAATTGGAGGTAAACCACTGAACGACTACGGAGAAAGCTGTTCAAGCTTC 511
DB 45 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 469 TCCTGCAACTCACATATCTCGACAGCTGTTTACTGGGACCAACAGAGGCGCCCTTACTCAG 528
DB 46 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 512 TCCGCAACTCACATATCTCGAGGGCTATGACCGGACGACAAAGAGGCCCTGACTCGG 571
QY 529 ATATTGAGGACACGCTGGAGGGCTTGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGT 588
DB 572 ATCTGAGGGCTACGTGGAGGGCTTGATGATGAGGAGGAGGAGGATGAGGAGGAGT 631
QY 589 ATGATGAAGATCTCAGGTAGTGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 648
DB 632 ATGATGAAGATCTCAGGTAGTGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 691
QY 649 AAGAGGAGGACGCTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATAACGATGGAGAG 708
DB 692 AAGAGGAGGACGCTGAGTGGAGGAGGAGGAGGAGGATGAAGAAGGTTATAACGATGGAGAG 751
QY 709 TAGATGCGGAGGAGATGAAGAAGACGCTTGGTGAAGAAGGAGGAGGAGGAGGAGGAGGAG 768
DB 752 TAGATGCGGAGGAGATGAAGAAGACGCTTGGTGAAGAAGGAGGAGGAGGAGGAGGAGGAG 811
QY 769 GAGAACCTGAAGATGAGGAGGAGGAGGATGATGACTTAAGTGAAGAAGGAGGAGGAGGAGGAG 828
DB 812 GAGAACCTGAAGATGAGGAGGAGGAGGATGATGACTTAAGTGAAGAAGGAGGAGGAGGAGGAG 871
QY 829 CCTATTGTGATTGACTGTTTACCCATATCCCTCT-----CCCCCTCCCAATCCTGCC 882
DB 872 CCTATTGTGATTGACTGTTTACCCATATCCCTCTCTCCCTCTCTCTCTCTCTCTCTCTCT 931
QY 883 CCCTGAA 889
DB 932 CCCTGAA 938

RESULT 6
PCT-US95-12414-1
; Sequence 1, Application PC/TUS9512414
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhlaida, Francis P.
; TITLE OF INVENTION: Novel Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Banner & Allegretti, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12414
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE: 22-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoscheit Esq., Dale H.
; REGISTRATION NUMBER: 19,090
; REFERENCE/DOCKET NUMBER: 1107.51507
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1052 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

```


QY 878 CTGCCCCCTGAA 889
Db 843 CTGCCCCCGAA 854

RESULT 9

US-08-468-066-3

; Sequence 3, Application US/08468066

; Patent No. 5756676

; GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kuhajda, Francis P.

; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With

; TITLE OF INVENTION: Uncontrolled Cell Division

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner, Birch, McKie & Beckett

; STREET: 1001 G Street, N.W.

; CITY: Washington, D.C.

; STATE: District of Columbia

; COUNTRY: U.S.A.

; ZIP: 20001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,066

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/314,503

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Posorske Esq., Laurence H.

; REGISTRATION NUMBER: 34,698

; REFERENCE/DOCKET NUMBER: 1107.47218

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 508-9153

; TELEFAX: 202 508-9299

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 980 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: mus sp

US-08-468-066-3

Query Match 64.2%; Score 570.8; DB 1; Length 980;
Best Local Similarity 82.9%; Pred. No. 5.4e-127;
Matches 706; Conservative 0; Mismatches 127; Indels 19; Gaps 4;

QY 50 ACAGAGAGCGGAGAGATGGAGATGGGAGACGAGGATTCATTTCAGAGCTGCGGAACAGGGC 109

Db 10 AGAGAGAGCGGAGAGATGGAGATGGGAGACGAGGATTCATTTCAGAGCTGCGGAACAGGAC 69

QY 110 GCCCTCTGATGTAAGAACTTGCCTGGACACAGTCGGTCTGTAATGAAGCAAACTCGA 169

Db 70 GCCCTCTGATGTAAGAACTTGCCTGGACACAGTCGGTCTGTAATGAAGCAAACTCGA 129

QY 170 AGCCCTCAGATGAATTTGAAGAACTGGAATCTTAAAGTAAATCAACGAGGCGCTCAC 229

Db 130 AGCCCTCAGGATGAGTTGAAGAACTGGAATCTTAAAGTAAATCAACGAGGCGCTCAC 189

QY 230 CTCATCTCAGACTTACCAAAAGTTA--AAGTTGAGAAAGCTTGAACCTA-----AG 277

Db 190 CTCATCTCAGACTTACCAAAAGTTA--AAGTTGAGAAAGCTTGAACCTA-----AG 249

QY 278 AGTCTCAGGGGCGCTGGGAAGTATTGGGAGAAAAGTGTCCAAAACCTCAGCATCTATATT 337

Db 250 AATCTCAGGGGACCTGGAGTATTGGCAGAGAAATGTCCGAACTTTAAGCATCTAAATTT 309
QY 338 AAGTGGCAACAAAATTAAAGACCTCAGCAACATAGAGCCACTGAAACAGTTAGAAAACCT 397
Db 310 AAGTGGCAACAAAATTAAAGATCTCAGCAACATAGAGCCCTGAAAGAGTTAGAAATCT 369
QY 398 CAAGAGCTTAGACCTTTTCAATTGCGAGGTAAACCACTGAACGACTACGGAGAAAACGT 457
Db 370 CAAGAGCTTAGACCTGTTTAACTGTGAGGTGACCACTGAATCCCTACCGAGAAAACGT 429
QY 458 GTTCAAGCTTCTCCTGCAACTCACATATCTCGACACTGTTTACTGGGACCAAGAGGCG 517
Db 430 GTTCAAGCTTCTCCTGCAAGCTCATGTACCTCGATGCTATGACAGGAGCAACAAGAGGCG 489
QY 518 CCCTTACTCAGATATTGAGGACCACTGGAGGCGCTGGATGAGGAGGAGGAGGTTGAGCA 577
Db 490 CCCGACTCCGATGTTGAGGGCTACGTGGA-----GGATGAGCGAGGAGAGATGAGGA 543
QY 578 TGAGGAGGAGTATGATGAGATGCTCAGGTAGTGGAGAGATGAGGAGGCGAGGAGGAGGA 637
Db 544 TGAGGAGGAGTATGATGATGATATCCCGAGCTAGTGGAGAGATGAGGAGGAGGTTGAGGA 603
QY 638 GGAGGAAGGTGAAGAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAGGTTATTA 697
Db 604 GGAAGAAGGGGAGGAGAGGATGTGAGTGGAGAGGAGGAGGAGGATGAGGAAGGTTTACAA 663
QY 698 CGATGGAGAGTATGATGGCGAGCAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTCA 757
Db 664 TGACGGGGAAGTGGATGACGAGGAAGCAAGAAAGCTGGTGAAGAAGAAGGGGAGTCA 723
QY 758 GAAGCGAAAATGAGAACTGAGATGAGGAGGAGAGATGATGACTAAGTAGAATAACCTAT 817
Db 724 GAAGCGAAAACGAGAACCGGACGATGAGGCGAAGAGGATGACTAAGGA-ATGAACCTGT 782
QY 818 TTTGAAAATTCCTATTGTGATTTGACTGTTTACCCTATATCCCTATCCCTCCCTCCCAATC 877
Db 783 TTGGGAAAATTCCTATTGTGATTTGACTGTTTACCCTATATCCCTCCCTCCCTTATTC 842
QY 878 CTGCCCCCTGAA 889
Db 843 CTGCCCCCGAA 854

RESULT 10
US-08-466-717-3
; Sequence 3, Application US/08466717
; Patent No. 5874234
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5874234el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,717
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:

QY	818	TTTGAAGAAATTCCTATTGTGATTGTTGACTGTTTTTACCCATATCCCTCCCTCCCTCCAATC	877
Db	783	TTGGGGAATTCCTATTGTGATTGTTGACTGTTTTTACCCATATCCCTCCCTCCCTCCAATC	842
QY	878	CTGCCCCCTGAA 889	
Db	843	CTGCCCCCGAA 854	
<p>RESULT 11</p> <p>US-08-466-743-3</p> <p>Sequence 3, Application US/08466743</p> <p>Patent No. 6040173</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Pasternack, Gary R.</p> <p>APPLICANT: Kuhnajda, Francis P.</p> <p>TITLE OF INVENTION: No. 6040173el Mammalian Protein Associated With</p> <p>TITLE OF INVENTION: Uncontrolled Cell Division</p> <p>NUMBER OF SEQUENCES: 9</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Banner, Birch, McKie & Beckett</p> <p>STREET: 1001 G Street, N.W.</p> <p>CITY: Washington, D.C.</p> <p>STATE: District of Columbia</p> <p>COUNTRY: U.S.A.</p> <p>ZIP: 20001</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.25</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/466,743</p> <p>FILING DATE:</p> <p>CLASSIFICATION:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/08/314,503</p> <p>FILING DATE:</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Posorske Esq., Laurence H.</p> <p>REGISTRATION NUMBER: 34,698</p> <p>REFERENCE/DOCKET NUMBER: 1107.47218</p> <p>TELECOMMUNICATION INFORMATION:</p> <p>TELEPHONE: 202 508-9153</p> <p>TELEFAX: 202 508-9299</p> <p>INFORMATION FOR SEQ ID NO: 3:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 980 base pairs</p> <p>TYPE: nucleic acid</p> <p>STRANDEDNESS: double</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: cDNA</p> <p>ORIGINAL SOURCE:</p> <p>ORGANISM: mus sp</p> <p>US-08-466-717-3</p>			
<p>Query Match 64.2%; Score 570.8; DB 3; Length 980;</p> <p>Best Local Similarity 82.9%; Pred. No. 5.4e-127;</p> <p>Matches 706; Conservative 0; Mismatches 127; Indels 19; Gaps 4;</p>			
QY	50	ACAGAGAGCGGAGATGAGATGGCGACACGATTCATTCAGAGCTGCGGAACAGGCG	109
Db	10	AGAGAGCGCGAGATGAGATGGCGACAAACGATTTATTTAGAGCTGCGGAACAGGAC	69
QY	110	GCCTCTGATGTGAAGAACTTCCCTGGACACAGTCGTCGAATGAAGGCAAACTCGA	169
Db	70	GCCTCTGATGTGAAGAGCTGCTCGTGNATCTTAAGTCAATTAAGGCAAAATCGA	129
QY	170	AGCCCTCAGAGTGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCTCAC	229
Db	130	AGGCCTCAGAGTGAATTTGAAGAACTGGAATTTCTTAAGTAAATCAACGGAGGCTCAC	189
QY	230	CTCAATCTCAGACTTACCAAGTTA--AGTTGAGAAAGCTTGACTA-----AG	277
Db	190	CTCAATTTCAACTTACCAAGTTAACAACCTCAGAAAGCTTGAATTAAGCGAAACAG	249
QY	278	AGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAGTCTCCAAACCTCACGCATCTATATT	337
Db	250	AATCTCAGGGGACCTGGAAGTATTGGCAGAGAAATGTCGAACCTTAAGCACTAAATTT	309
QY	338	AAGTGGCAACAAATTAAGACCTCAGCACATAGAGCCACTGAAACAGACTTAGAAAACT	397
Db	310	AAGTGGCAACAAATTAAGACCTCAGCACATAGAGCCACTGAAACAGACTTAGAGAACT	369
QY	398	CAAGAGCTTAGACCTTTCAATTCGAGGTACCAACCTGAACGACTACGGAGAAAAGCT	457
Db	370	CAAGAGCTTAGACCTTTCAATTCGAGGTACCAACCTGAACGACTACGGAGAAAAGCT	429
QY	458	GTTCAAGCTTCTCCTCAACTACATATCTCGACACTGTTACTGGGACCAACAGGAGGC	517
Db	430	GTTCAAGCTTCTCCTCAACTACATATCTCGACACTGTTACTGGGACCAACAGGAGGC	489
QY	518	CCCTTACTCAGATATTGAGACACACCTGGAGGCGCTGGATGACGAGGAGGGGTGAGCA	577
Db	490	CCCGACTCCGATGTTGAGGGCTACCTGGA-----GGATGACGAGGAGAGATGAGGA	543
QY	578	TGAGGAGGAGTATGATCAAGATCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGA	637
Db	544	TGAGGAGGAGTATGATCAAGATCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGA	603
QY	638	GGAGGAGGTGAAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATAA	697
Db	604	GGAGGAGGTGAAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATAA	663
QY	698	CGATGAGGAGGTAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTCA	757
Db	664	TGACGGGGAAGTGGATGACGAGGAGCAACGAGGAAGAGCTGCTGGAAGAAGAGGAGTCA	723
QY	758	GAAGCCAAATGAGAACCTTGAGATGAGGAGCAAGATGATGACTAAGTGAATAACCTAT	817
Db	724	GAAGCCAAATGAGAACCTTGAGATGAGGAGCAAGATGATGACTAAGTGAATAACCTAT	782

QY 758 GAAGCGAAATGAGAACTGAAGATGAGGAGAGAGATGACTAAGTAACTAGATAACCTAT 817
|||||
Db 724 GAAGCGAAACGAGAACCGGACGATGAGGCGAAGAGATGACTAAGGA-ATGAACCTGT 782
QY 818 TTTGAAAAATTCCTATTGTGATTGACTGTGTTTACCCATATCCCTCCCTCCCTCCCAATC 877
|||
Db 783 TTGGGAAATTCCTATTGTGATTGACTGTGTTTACCCATATCCCTCCCTCCCTCCCTATTTC 842
QY 878 CTGCCCCCTGAA 889
|||||
Db 843 CTGCCCCCGGAA 854

RESULT 13

US-08-466-603-4

; Sequence 4, Application US/08466603
; Patent No. 5726018

GENERAL INFORMATION:

; APPLICANT: Pasternack, Gary R.

; APPLICANT: Kuhajda, Francis P.

; TITLE OF INVENTION: No. 5726018el Mammalian Protein Associated With

; TITLE OF INVENTION: Uncontrolled Cell Division

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Banner, Birch, McKie & Beckett

; STREET: 1001 G Street, N.W.

; CITY: Washington, D.C.

; STATE: District of Columbia

; COUNTRY: U.S.A.

; ZIP: 20001

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,603

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/314,503

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Posorske Esq., Laurence H.

; REGISTRATION NUMBER: 34,698

; REFERENCE/DOCKET NUMBER: 1107.47218

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202 508-9153

; TELEFAX: 202 508-9299

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 759 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; ORIGINAL SOURCE:

; ORGANISM: Mus sp

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 3..548

; US-08-466-603-4

Query Match 48.3%; Score 429.2; DB 1; Length 759;
Best Local Similarity 83.1%; Pred. No. 2.4e-93;
Matches 515; Conservative 0; Mismatches 98; Indels 7; Gaps 2;

QY 270 GAACCTAAGAGTCTCAGGGCGCTGGAGTATTGGCAGAGAAAGTCCCAACCTCAGCGAT 329
|||
Db 24 GAAACAGATCTCAGGGACCTGGAGTATTGGCAGAGAAAGTCCCGAACCTTAAGCAT 83
QY 330 CTATATTTAAGTGGCAACAAATTAAGACCTCAGCACATAGAGCCACTGAAACAGTTA 389

Db 84 CTRAAATTTAGTGGCAACAAATAAAGATCTCAGCACAAATAGAGCCGTGAAGAAGTTA 143
QY 390 GAAACCTCAAGAGCTTAGACCTTTTCAATTTGCGAGGTAAACCAACCTGAACGACTACGGA 449
Db 144 GAGAAATCTCAAGAGCCTAGACCTGTTTAACTGTGAGGTGACCAACCTGAATGCCTACCGA 203
QY 450 GAAACGCTTCAAGCTTCTCTGCAACTTCACATATCTCGACAGCTGTGTACTGGGACCA 509
Db 204 GAAACGCTGTTCAAGCTCTCTGCCCCAGGTCATGTACCTCGATGGCTATGACAGGGACAAC 263
QY 510 AAGGAGGCCCTTACTCAGATATTGAGGAGCACCGTGGAGGGCCTGATCAGCAGGAGGAG 569
Db 264 AAGGAGGCCCTGACTCCGATGTTGAGGGCTACGTGGA-----GGATCAGCAGGAGGAA 317
QY 570 GGTGACATGAGGAGGATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGCGAG 629
Db 318 GATGAGGATGAGGAGGATGATGAATATGCCAGCTAGTGAAGATGAAGAGGAGAG 377
QY 630 GAGGAGGAGGAGGAGTGAAGAGGAGGAGCTGAGTGGAGGGGACGAGGAGGATGAAGAA 689
Db 378 GTTGAGGAGGAGGAGGAGGAGGAGGATGTGAGTGGAGAGGAGGAGGAGGAGGATGAGGAA 437
QY 690 GGTATACGATGCGAGGATGATGCGGAGGAGGATGAAGAGAGCTTGTGTGAAGAAGAA 749
Db 438 GGTACAATGACGGGGAAGTGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497
QY 750 AGGGGTCAGAGCGAAATGAGAACTGAAAGATGAGGAGGAGGAGGAGGAGGATGAAGTAGAA 809
Db 498 GGGAGTCAGAGCGAAACGAGAACCGGACGATGAGGGCGAAGAGGATGACTAAGGA-AT 556
QY 810 TRACCTATTTTGAATAATTCCTATTGTTGATTTGACTGTTTTTACCCATATCCCTCCCTCC 869
Db 557 GAACCTGTTTGGGGAATTCCTATTGTTGATTTGACTGTTTTTACCCATATCCCTCCCTCC 616
QY 870 CTCCTAATCTGCCCTGCTGAA 889
Db 617 TCCTATTCTGCCCCCGGAA 636

RESULT 14
US-08-314-503A-4
; Sequence 4, Application US/08314503A
; Patent No. 5734022
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5734022el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/314,503A
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299

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; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Mus sp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..548
US-08-314-503A-4

Query Match 48.3%; Score 429.2; DB 1; Length 759;
Best Local Similarity 83.1%; Pred. No. 2.4e-93;
Matches 515; Conservative 0; Mismatches 98; Indels 7; Gaps 2;

QY 270 GAACCTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCAT 329
DB 24 GAAACAGAAATCTCAGGGACCTGGAAGTATTGGCAGAGAAATGTCCGAACCTTAAGCAT 83
QY 330 CTATATTTAAGTGGCAACAATAATTAAGACCTCAGCACATAGAGCCACTGAAACAGTTA 389
DB 84 CTAATTTAAGTGGCAACAATAATTAAGATCTCAGCACATAGAGCCGCTGAAGAAGTTA 143
QY 390 GAAACCTCAGAGCTTAGACCTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGGA 449
DB 144 GAGATCTCAGAGCCCTAGACCTGTTAACTGTGAGTGACCAACCTGAATGCTTACCGA 203
QY 450 GAAACCTGTTCAAGCTTCTCCTGCACTCACAATATCGACAGCTGTTACTGGGACCAC 509
DB 204 GAAACCTGTTCAAGCTCCTGCCCGAGTCTACCTCGATGCTATGACAGGCAAC 263
QY 510 AAGGAGCCCTTACTCAGATATTGAGGACCACGTGGAGGCGCTGGATGACGAGGAGGAG 569
DB 264 AAGGAGCCCTCCGATCCGATGTTGGGGCTACGTGGA-----GGATGACGAGGAA 317
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DB 318 GATGAGGATGAGGAGGAGTATGATGAATATGCCAGCTAGTCCAGCTAGTGAAGATGAGGAGGAG 377
QY 630 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
DB 378 GTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
QY 690 GGTATACCATGAGAGGTAGATGCCAGGAGATGAAGAGAGCTTGGTGAAGAGAA 749
DB 438 GGTACAATGACGGGAAAGTGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497
QY 750 AGGGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 809
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QY 810 TAACCTATTTTGAATAATTCCTATTGTGATTTGATGCTGTTTACCATATCCCTCCCTCC 869
DB 557 GAACCTGTTTGGGAAATTCCTATTGTGATTTGATGCTGTTTACCATATCCCTCCCTCC 616
QY 870 CTCCTATCTGCCCCCTGAA 889
DB 617 TCCTATTCTGCCCCCGAA 636

RESULT 15
US-08-468-066-4
; Sequence 4, Application US/08468066
; Patent No. 5756676
; GENERAL INFORMATION:
; APPLICANT: Pasternack, Gary R.
; APPLICANT: Kuhajda, Francis P.
; TITLE OF INVENTION: No. 5756676el Mammalian Protein Associated With
; TITLE OF INVENTION: Uncontrolled Cell Division
; NUMBER OF SEQUENCES: 9
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.A.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,066
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/314,503
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske Esq., Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.47218
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9153
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 759 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Mus sp
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..548
US-08-468-066-4

Query Match 48.3%; Score 429.2; DB 1; Length 759;
Best Local Similarity 83.1%; Pred. No. 2.4e-93;
Matches 515; Conservative 0; Mismatches 98; Indels 7; Gaps 2;

QY 270 GAACCTAAGAGTCTCAGGGGCGCTGGAAGTATTGGCAGAAAAAGTGTCCAAACCTCACGCAT 329
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QY 330 CTATATTTAAGTGGCAACAATAATTAAGACCTCAGCACATAGAGCCACTGAAACAGTTA 389
DB 84 CTAATTTAAGTGGCAACAATAATTAAGATCTCAGCACATAGAGCCGCTGAAGAAGTTA 143
QY 390 GAAACCTCAGAGCTTAGACCTTTCAATTGCGAGGTAAACCAACCTGAACGACTACGGA 449
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QY 450 GAAACCTGTTCAAGCTTCTCCTGCACTCACAATATCGACAGCTGTTACTGGGACCAC 509
DB 204 GAAACCTGTTCAAGCTCCTGCCCGAGTCTACCTCGATGCTATGACAGGCAAC 263
QY 510 AAGGAGCCCTTACTCAGATATTGAGGACCACGTGGAGGCGCTGGATGACGAGGAGGAG 569
DB 264 AAGGAGCCCTCCGATCCGATGTTGGGGCTACGTGGA-----GGATGACGAGGAA 317
QY 570 GGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGTGTGGAAGATGAGGAGGCGGAG 629
DB 318 GATGAGGATGAGGAGGAGTATGATGAATATGCCAGCTAGTCCAGCTAGTGAAGATGAGGAGGAG 377
QY 630 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 689
DB 378 GTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 437
QY 690 GGTATACCATGAGAGGTAGATGCCAGGAGATGAAGAGAGCTTGGTGAAGAGAA 749
DB 438 GGTACAATGACGGGAAAGTGGATGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 497
QY 750 AGGGGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 809
DB 498 GGGAGTCAAGACGAAACGAGACCGACGATGAGGCGGAGGAGGAGGAGGAGGAGGAGGAG 556
QY 810 TAACCTATTTTGAATAATTCCTATTGTGATTTGATGCTGTTTACCATATCCCTCCCTCC 869
DB 557 GAACCTGTTTGGGAAATTCCTATTGTGATTTGATGCTGTTTACCATATCCCTCCCTCC 616
QY 870 CTCCTATCTGCCCCCTGAA 889
DB 617 TCCTATTCTGCCCCCGAA 636
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Qy	810	TAAGCTATTTGAAAAATTCCTATTGTGATTGACTGTTTTACCCCATATCCCTCCCC	869
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Qy	870	CTCCAATCCTGCCCTCGAA	889
Db	617	TCCTATTCTGCCCTCGAA	636

Search completed: December 8, 2002, 23:19:34
Job time : 43.6192 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 22:43:58 : Search time 40.5891 Seconds
(without alignments)
8540.478 Million cell updates/sec

Title: US-09-591-500-3

Perfect score: 889

Sequence: 1 ggggtcagggtttattgatt.....ctccaatcctgccccctgaa 889

Scoring table: IDENTRY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 350425 seqs, 194966369 residues

Total number of hits satisfying chosen parameters: 700850

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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- 11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175.4	19.7	718	10	US-09-910-943-76
2	171.8	19.3	771	10	US-09-910-943-166
3	171.6	19.3	748	10	US-09-910-943-132
4	146	16.4	763	10	US-09-910-943-622
5	127.6	14.4	557	9	US-10-046-935-2145
6	127.6	14.4	557	9	US-09-878-178-2145
7	121.2	13.6	720	9	US-10-101-487-74
8	121.2	13.6	720	9	US-10-101-487-76
9	118.6	13.3	522	9	US-10-101-487-71
10	118.6	13.3	530	9	US-10-101-487-73
11	118.6	13.3	554	9	US-10-101-487-69
12	118.6	13.3	554	9	US-10-101-487-106
13	102.8	11.6	575	10	US-09-864-761-20733
14	102.8	11.6	1369	10	US-09-864-761-3972
15	101	11.4	659158	9	US-09-771-208-20
16	94.4	10.6	423	10	US-09-864-761-18355
17	94.4	10.6	487	10	US-09-864-761-1597
18	92.6	10.4	344	10	US-09-864-761-19694
19	89.4	10.1	5387	9	US-10-001-873-22

c 20	89.2	10.0	53226	10	US-09-818-264-3	Sequence 3, Appl1
c 21	88.4	9.9	267	10	US-09-864-761-27984	Sequence 27984, A
c 22	88.4	9.9	474	10	US-09-864-761-11284	Sequence 11284, A
c 23	88.4	9.9	1944	10	US-09-864-761-2825	Sequence 2825, Ap
24	87.8	9.9	700	10	US-09-864-761-17529	Sequence 17529, A
25	87.6	9.9	3809	12	US-10-001-870-68	Sequence 68, Appl
c 26	84.2	9.5	399	10	US-09-864-761-2913	Sequence 2913, Ap
c 27	83.8	9.4	381	10	US-09-777-564-700	Sequence 700, App
28	83.6	9.4	390	10	US-09-790-399-7	Sequence 7, Appl1
29	83.4	9.4	299	10	US-09-864-761-21553	Sequence 21553, A
c 30	81.4	9.2	766	10	US-09-864-761-19608	Sequence 19608, A
c 31	80.8	9.1	438	10	US-09-864-761-4988	Sequence 4988, Ap
c 32	80.8	9.1	1282	9	US-10-002-344A-89	Sequence 89, Appl
c 33	80.6	9.1	305	10	US-09-864-761-19262	Sequence 19262, A
c 34	80.6	9.1	496	10	US-09-864-761-2534	Sequence 2534, Ap
35	80.2	9.0	4316	10	US-09-880-107-3713	Sequence 3713, Ap
36	80	9.0	350	10	US-09-822-263-19	Sequence 19, Appl
37	78.4	8.8	251	10	US-09-864-761-19674	Sequence 19674, A
38	78.4	8.8	345	10	US-09-822-263-17	Sequence 17, Appl
39	78.4	8.8	490	10	US-09-880-107-2261	Sequence 2261, Ap
40	78.4	8.8	497	10	US-09-822-263-33	Sequence 33, Appl
41	78.4	8.8	583	10	US-09-864-761-20772	Sequence 20772, A
42	78.4	8.8	1147	10	US-09-880-107-2311	Sequence 2311, Ap
43	78.4	8.8	1959	10	US-09-864-761-4012	Sequence 4012, Ap
c 44	77.4	8.7	276	10	US-09-864-761-20595	Sequence 20595, A
c 45	77.2	8.7	559	10	US-09-864-761-7684	Sequence 7684, Ap

ALIGNMENTS

RESULT 1

US-09-910-943-76
; Sequence 76, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/IG148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 718
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(718)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-76

Query Match	19.7%	Score 175.4;	DB 10;	Length 718;
Best Local Similarity	59.9%;	Pred. No. 1.8e-32;		
Matches 353;	Conservative 0;	Mismatches 221;	Indels 15;	Gaps 3;
Qy	64	AGATGGAGATGGCAGACGGATTTCATTTCAGAGCTCGGGAACAGGGCCCTCTGTATGTGA	123	
Db	132	ACATGGACATGAAAAGAGATTGATGCTGGAGCTCAGGAATCGGNAAGCGGCTGACGCTA	191	
Qy	124	AAGAATTTCCTTGGCAACACAGTCGGTCCGAATGAAGGCAAACTCGAACCCCTCACAGATG	183	
Db	192	AAGAATTGGTTCTAGATAACTGCCGTTTCAGACGATGGCAAAATTTATTGGACTGACCTCAG	251	
Qy	184	ATTTCGAGAAGCTGCAATTCCTTAAGTAAATCAACGGAGGCGCTCACCTCAATCTCAGACT	243	
Db	252	AGTTTGAAGCGTGGAGTTTCTCAGCATGTATAAATGTCAACTTATTTCTGTAGCTAACT	311	
Qy	244	TACCAAAAGTTT---AAAGTTGAGAAAGCTTGAACTAA-----GAGTCTCAGGGGGCC	291	
Db	312	TCCCAAGCTCCCAAGTTGAAAAAGCTGGAACTCAGTCACAATCGAATCTCTGGAGGAT	371	

Qy	292	TGGAAGTATTGGCAGAAAAAGTGTC	CAAAACCTC	ACGATCTATATTTAAAGTGGCAACAAA	351
Db	372	TAGAGGTACTGGCAGACGGACCCAAATTT	TGACACACCTTGA	ACCTCAGTGGGAACAAGA	431
Qy	352	TTAAAGACCTCAGCACACAATAGAGCCACT	GAAACAGTTT	AGAAAACTTCAGAGCTT	411
Db	432	TAAAGAGATAAATACCTTAGAGCCACTT	TAAGAACTACCTCATCTCAT	GAGTCTGGAAC	491
Qy	412	TTTTCAATTCGGAGGTAAACCACTG	AACCACTG	ACGACATACGGAGAAACGTGTTCAAGCTTCTCC	471
Db	492	TCTTTTAACTGTGAGGTGACCATGCT	TAAACAACTAC	ACGGGAGAGTGTTTTTGAACCTTCTCC	551
Qy	472	TGCAACTCACATATCTCGACAGCTGTT	TACTGGGACAC	ACAGGAGGCCCTTACTCAGATA	531
Db	552	CTAGCTTACCTTTTATAGTGGTTTTGAT	CCAGATGACC	ACGAGGCTCCAGATTTCTGATC	611
Qy	532	TTGAGGACCACTGGAGGGCGCTG	ATCAGCAGGAGGAGGCTG	AGCATGAGGAGGAGTATG	591
Db	612	CAGAGG--CTGAAGATTTAGAGG	AAATCGAGGATGCTG	GAGGAGGATGAAGAAGATG	668
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RESULT 2
US-09-910-943-166
; Sequence 166, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/1G148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 771
; TYPE: DNA
; ORGANISM: xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(771)
; OTHER INFORMATION: n may be a o r c o r t/u
US-09-910-943-166

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RESULT 3
US-09-910-943-132
; Sequence 132, Application US/09910943
; Patent No. US20020081610A1
; GENERAL INFORMATION:
; APPLICANT: Hemmati-Brivanlou, Ali
; APPLICANT: Altman, Curtis
; TITLE OF INVENTION: Assays and Materials for Embryonic Gene Expression
; FILE REFERENCE: 7529/1G148US1
; CURRENT APPLICATION NUMBER: US/09/910,943
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 742
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 132
; LENGTH: 748
; TYPE: DNA
; ORGANISM: Xenopus laevis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(748)
; OTHER INFORMATION: n may be a or g or c or t/u
US-09-910-943-132

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Qy	472	TG	CAACTCACATATCTCGACAGCTGTTTACTGGGACCA	CACAGGAGGCCCTT	ACTCTCAGATA		531
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Qy	532	TT	GAGGACCACTGTGGAGGGCGCTGGATCAGCAGGAGGAGGT	TGAGCATGAGGAGGAGTATG			591
Db	613	CAGANG	---	CTGAAGAATT	TNAGGAAAATGGACAGGATGCTGAGGAGGAT	GAANAATG	669
Qy	592	AT	GAGATGCTCAGGTAGT	GGAAGATGA	619		
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RESULT 5

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US-10-046-935-2145
; Sequence 2145, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Scolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INFLAMMATORY BOWEL DISEASE
; FILE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121-527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2145
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-2145

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Query Match	14.4%;	Score 127.6;	DB 9;	Length 557;
Best Local Similarity	56.0%;	Pred. No. 3.2e-21;		
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QY	366	ACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTTAGACCTTTTCAATTGCGAG	425	
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QY	426	GTAACCAACCTGACGAGCTACGGAGAAACGTTGTCAGGTTCTCTGCAACCTACACATAT	485	
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QY	61	ATCAACAACCTGGAAGATTATAGAGAAAGTATTTTGAAGTACTGCGAGAAATACATATC	120	
DB				
QY	486	CTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTACATATTGAGGACCACGTG	545	
DB				
	121	TTAGATGGAATTTGATCAGGAGGATATGAAGCCCGGACTCTGAAGAGGAGGATGATGAG	180	
QY	546	GAGGCGCTGGATGACGAGGAGGAGGTGACATGAGGAGGAGTATGATGAAGATGCTCAG	605	
DB				
	181	GATGCCATGAAGATGATGAAGAGGAGAGGAAATGAAGCTGGTCCACCGGAAGGATAT	240	
QY	606	GTAGTGAAGATGAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT	665	
DB				
	241	GAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA	300	
QY	666	GGAGGGGACGAGGAGGATGAAGAAGGTTATTAACGATGGAGAGGTAGATGGCGGAGGAGAT	725	
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	301	GCAGGTTTCAGAGTTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	360	
QY	726	GAAGAGAGCTTGGTGAAGAGAAACGGGTCAGAACCGGAAATGAGAACCTGGAAGATGAG	785	
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	361	GAATTCAGGATGAAGAGATGATGACTATGTTGAAGAGGGGAGGAGGAGGAGGAGGAGGAA	420	
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DB				
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RESULT 6
US-09-878-178-2145
; Sequence 2145, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiaog, Yudi
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secret, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2145
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-2145

Query Match      14.4%; Score 127.6; DB 9; Length 557;
Best Local Similarity 56.0%; Pred. No. 3.2e-21;
Matches 241; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

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QY 426 GTAACCAACCTGAACGACTACGGAGAAAACGTGTTCAAGCTTCTCCCTCAACTCACATAT 485
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ATCACAACCTGGAGATATATAGAAAAGTATTTTGAACCTACTGCAGCAATCACATAC 120

QY 486 CTCGACAGCTGTACTGGGACCAACAGGAGGCCCTTACTCAGATATTTAGGACCCACGTG 545
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Db 121 TTAGATGGATTTCAGGAGGATATCAAGCGCGGACTCTGAAGAGGAGGATGATGAG 180

QY 546 GAGGCGCTGGATGACGAGGAGGAGGCTGAGCATGAGGAGGAGTATGATGAAGATGCTCAG 605
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Db 181 GATGCGATGAAGATGATGAAGAGGAGGAGGAAAATGAAGCTGTCCACCGGAAGGATAT 240

QY 606 GTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGTCACT 665
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Db 241 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300

QY 666 GGAGGGGACGAGGAGGAGGATGAAGAAGTTTATAACGATGAGGAGGATGATGCGGAGGAAG 725
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Db 301 GCAGGTTACAGATTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360

QY 726 GAAGAGAGCTTGGTGAAGAAGAAGGGGTCAGAGCGGAAAATGAGACCTTGAAGATGAG 785
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Db 361 GAAATTCAGATGAAGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

QY 786 GGAGAAGATG 795
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Db 421 GAGGAAGAAG 430

RESULT 7
US-10-101-487-74
; Sequence 74, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
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FILE REFERENCE: 077319/0329
CURRENT APPLICATION NUMBER: US/10/101,487
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/277,705
PRIOR FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 74
LENGTH: 720
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligonucleotide
NAME/KEY: CDS
LOCATION: (2)..(718)
US-10-101-487-74

Query Match      13.6%; Score 121.2; DB 9; Length 720;
Best Local Similarity 61.9%; Pred. No. 1.1e-19;
Matches 192; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 503 GGACCACAAGAGGAGGCCCTTACTACATATTGAGGACCACTGGAGGCGCTGGATGACGA 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 414

QY 563 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 622
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 415 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 474

QY 623 GCGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 682
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 475 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 534

QY 683 TGAAGAAGGTTTAAACGATGAGAGGATGATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 742
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 594

QY 743 AGAAGAAGGGGTCAGAACGAAAATGAGAACCTTGAAGATGAGGAGGAGGAGGAGGAGGAG 802
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 654

QY 803 AGTAGAATAA 812
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 655 AGAGGAGGAA 664

RESULT 8
US-10-101-487-76/c
; Sequence 76, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-101-487-76

Query Match      13.6%; Score 121.2; DB 9; Length 720;
Best Local Similarity 61.9%; Pred. No. 1.1e-19;
Matches 192; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 503 GGACCACAGGAGGCCCTTACTCAGATATTGAGGACCACTGTCAGGCGCTGGATGACGA 562
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 370 GGAAGAGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 311

QY 563 GGAGGAGGTTATACGATCAGGAGGAGTATGATGAAGATCCTCAGGTAGTGAAGATGAGGA 622
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 310 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 251

QY 623 GGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 682
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 250 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 191

QY 683 TGAAGAAGGTTATACGATCAGGAGGAGTATGATGAAGATCCTCAGGTAGTGAAGATGAGGA 742
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 190 AGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 131

QY 743 AGAAGAAGGGGTGAGAGGCGAAATGAGAACCTGAGATCAGGAGGAGGAGGAGGAGGAGGAGGA 802
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 130 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 71

QY 803 AGTAGAATAA 812
    || | || |
Db 70 AGAGGAGGAA 61

RESULT 9
US-10-101-487-71
; Sequence 71, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 71
; LENGTH: 522
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: CDS
; LOCATION: (1)..(522)
US-10-101-487-71

Query Match      13.3%; Score 118.6; DB 9; Length 522;
Best Local Similarity 61.5%; Pred. No. 4.1e-19;
Matches 190; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 503 GGACCACAGGAGGCCCTTACTCAGATATTGAGGACCACTGTCAGGCGCTGGATGACGA 562
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 132 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 191
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QY 563 GGAGGAGGTTGACATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGACGA 622
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 192 GGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 251

QY 623 GGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 682
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 252 GGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 311

QY 683 TGAAGAAGGTTATACGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGA 742
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 312 GGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 371

QY 743 AGAAGAAGGGGTGACAGCGGAAATGAGAACCTGAGATGAGGAGGAGGAGGAGGAGGAGGA 802
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 372 GGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 431

QY 803 AGTAGAATA 811
    ||| | ||| |
Db 432 GGAAGAAGA 440

RESULT 10
US-10-101-487-73/c
; Sequence 73, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/101,487
; PRIOR FILING DATE: 2002-03-20
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-101-487-73

Query Match      13.3%; Score 118.6; DB 9; Length 530;
Best Local Similarity 61.5%; Pred. No. 4.1e-19;
Matches 190; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 503 GGACCACAGGAGGCCCTTACTCAGATATTGAGGACCACTGTCAGGCGCTGGATGACGA 562
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 399 GGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 340

QY 563 GGAGGAGGTTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGA 622
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 339 GGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 280

QY 623 GGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 682
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 279 GGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 220

QY 683 TGAAGAAGGTTATACGATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGA 742
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 219 GGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 160

QY 743 AGAAGAAGGGGTGACAGCGGAAATGAGAACCTGAGATGAGGAGGAGGAGGAGGAGGAGGA 802
    ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | |||
Db 159 GGAAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 100
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QY 803 AGTAGAATA 811
| | | | |
Db 99 GGAAGAAGA 91

RESULT 11

US-10-101-487-69
; Sequence 69, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/101,487
; PRIORITY FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: CDS
; LOCATION: (1)..(528)
US-10-101-487-69

Query Match 13.3%; Score 118.6; DB 9; Length 554;
Best Local Similarity 61.5%; Pred. No. 4.2e-19;
Matches 190; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 503 GGACCAAGAGGAGGCCCTTACTCAGATATTGAGACACCGTGGAGGCCCTGGATGACGA 562
| | | | |
Db 174 GGAAGAAGAGGAGGAGGAAGAAGAGAGAGGAGGAGGAAGAAGAAGAGGAAGA 233
| | | | |
QY 563 GGAGGAGGTGAGCATGAGGAGGAGTATGATCAAGATGCTCAGGTAGTGAAGATGAGGA 622
| | | | |
Db 234 GGAAGAAGAGGAGGAGGAAGAAGAGAGGAGGAGGAAGAAGAAGAGGAAGA 293
| | | | |
QY 623 GGGCGAGGAGGAGGAGGAGGAAGGTGAAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGA 682
| | | | |
Db 294 GGAAGAAGAGGAGGAGGAAGAAGAGAGGAGGAGGAAGAAGAAGAGGAAGA 353
| | | | |
QY 683 TGAAGAAGCTTTAAGCATGGAGAGGTAGATGCCGAGGAAGATGAAGAAGACCTTGGTGA 742
| | | | |
Db 354 GGAAGAAGAGGAGGAGGAAGAAGAGAGGAGGAAGAAGAGGAGGAAGAAGAGGAAGA 413
| | | | |
QY 743 AGAAGAAGAGGGGTTCAGAACCGAAATGAGAACCTGAAAGATGAGGAGGAAGATGATGACTA 802
| | | | |
Db 414 GGAAGAAGAGGAGGAGGAAGAAGAGAGGAGGAAGAAGAGGAGGAAGAAGAGGAAGA 473
| | | | |
QY 803 AGTAGAATA 811
| | | | |
Db 474 GGAAGAAGA 482

RESULT 12

US-10-101-487-106
; Sequence 106, Application US/10101487
; Patent No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIORITY FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26

; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/101,487
; PRIORITY FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: CDS
; LOCATION: (1)..(537)
US-10-101-487-106

Query Match 13.3%; Score 118.6; DB 9; Length 554;
Best Local Similarity 61.5%; Pred. No. 4.2e-19;
Matches 190; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

QY 503 GGACCAAGAGGAGGCCCTTACTCAGATATTGAGACACCGTGGAGGCCCTGGATGACGA 562
| | | | |
Db 174 GGAAGAAGAGGAGGAGGAAGAAGAGAGGAGGAGGAAGAAGAAGAGGAAGA 233
| | | | |
QY 563 GGAGGAGGTGAGCATGAGGAGGAGTATGATGAAGATGCTCAGGTAGTGAAGATGAGGA 622
| | | | |
Db 234 GGAAGAAGAGGAGGAGGAAGAAGAGAGGAGGAGGAAGAAGAAGAGGAAGA 293
| | | | |
QY 623 GGGCGAGGAGGAGGAGGAGGAAGGTGAAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGA 682
| | | | |
Db 294 GGAAGAAGAGGAGGAGGAAGAAGAGAGGAGGAGGAAGAAGAAGAGGAAGA 353
| | | | |
QY 683 TGAAGAAGCTTTAAGCATGGAGAGGTAGATGCCGAGGAAGATGAAGAAGACCTTGGTGA 742
| | | | |
Db 354 GGAAGAAGAGGAGGAGGAAGAAGAGAGGAGGAAGAAGAGGAGGAAGAAGAGGAAGA 413
| | | | |
QY 743 AGAAGAAGAGGGGTTCAGAACCGAAATGAGAACCTGAAAGATGAGGAGGAAGATGATGACTA 802
| | | | |
Db 414 GGAAGAAGAGGAGGAGGAAGAAGAGAGGAGGAAGAAGAGGAGGAAGAAGAGGAAGA 473
| | | | |
QY 803 AGTAGAATA 811
| | | | |
Db 474 GGAAGAAGA 482

RESULT 13

US-09-864-761-20733
; Sequence 20733, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIORITY FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26


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; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 12
US-09-864-761-3972

Query Match      11.6%; Score 102.8; DB 10; Length 1969;
Best Local Similarity 61.7%; Pred. No. 3.8e-15;
Matches 164; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 534 GAGGACCACTGGAGGCGCTCGATCACGAGGAGGAGGGTGGATGAGGAGGAGTATGAT 593
DB 600 GAGAAGAGGAAGAGATCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 659
QY 594 GAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 653
DB 660 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 719
QY 654 GAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGTTTATACGATGGAGAGGTAGAT 713
DB 720 GAAGAGAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 779
QY 714 GCGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGCTCAGAAGCGAAATGAGAA 773
DB 780 GAGGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 839
QY 774 COTGAAGATGAGGAGGAGAGATGATGA 799
DB 840 GAGGAGGAAGAGGAGGAGGAGGA 865

RESULT 15
US-09-771-208-20/c
; Sequence 20, Application us/09771208
; Patent No. US20020155564A1
; GENERAL INFORMATION:
; APPLICANT: MEDRANO, JUAN
; APPLICANT: BRADFORD, ERIC
; APPLICANT: HORVAT, SIMON
; TITLE OF INVENTION: CLONING OF A HIGH-GROWTH GENE
; FILE REFERENCE: 407T-923710US
; CURRENT APPLICATION NUMBER: US/09/771,208
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 08/999,477
; PRIOR FILING DATE: 1997-12-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 659158
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (123459)..(123478)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (602466)..(602485)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (546998)..(547017)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (494715)..(494814)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (390986)..(391005)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (346860)..(346823)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (317174)..(317193)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (280353)..(280373)
; OTHER INFORMATION: n is unidentified a, c, g, or t
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; NAME/KEY: misc_feature
; LOCATION: (271829)..(271848)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (183872)..(183891)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (170625)..(170645)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; LOCATION: (132700)..(132700)
; OTHER INFORMATION: n is unidentified a, c, g, or t
; NAME/KEY: misc_feature
; OTHER INFORMATION: n is a, c, g, or t
US-09-771-208-20

Query Match      11.4%; Score 101; DB 9; Length 659158;
Best Local Similarity 65.1%; Pred. No. 1.1e-13;
Matches 149; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 534 GAGGACCACTGGAGGCGCTTGGATGACGAGGAGGAGGGTGAGCATGAGGAGGAGTATGAT 593
DB 251090 GAGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGAA 251031
QY 594 GAAGATGCTCAGGTAGTGGAAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 653
DB 251030 GAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 250971
QY 654 GAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGTTTATACCATGAGGAGGTAGAT 713
DB 250970 GAGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 250911
QY 714 GCGGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTGAGAAAGC 762
DB 250910 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 250862

Search completed: December 9, 2002, 00:44:00
Job time : 527.589 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 8, 2002, 21:26:48 : Search time 1307.27 Seconds
(without alignments)
11013.667 Million cell updates/sec

Title: US-09-591-500-3

Perfect score: 889

Sequence: 1 gggttcaggtttattgatt.....ctccaatcgtccctgaa 889

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estlin:*

4: em_estnu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_estti:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pin:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	729.8	82.1	894	9	AL533191
2	726.2	81.7	923	9	AL560249
3	724.2	81.5	875	9	AL535686
4	723.2	81.3	1034	9	AL518839
5	709.4	79.8	870	9	AL537874
6	705.8	79.4	875	9	AL547157

7	705.4	79.3	903	9	AL540827
8	693.6	78.0	992	9	AL517375
9	688	77.4	1035	14	BM904155
10	683.8	76.9	855	9	AL543743
11	668.6	75.2	853	9	AL535863
12	665.6	74.9	834	9	AL545880
13	661	74.4	895	14	BQ232856
14	659.6	74.2	1066	13	BM543218
15	645.2	72.6	894	9	AL571434
16	642.4	72.3	802	9	AL518247
17	627.2	70.6	999	13	BM460209
18	627	70.5	806	9	AL547462
19	620	69.7	749	13	BI860951
20	617	69.4	775	12	BF969229
21	612	68.8	961	13	BM475803
22	610.8	68.7	882	14	BQ427516
23	609.8	68.6	866	14	BQ687251
24	605.4	68.1	750	12	BG325466
25	600.2	67.5	902	9	AL516007
26	596.4	67.1	899	14	BQ890554
27	588.4	66.2	859	14	BQ212622
28	584	65.7	1141	11	AK020753
29	582.6	65.5	764	12	BG392351
30	581.6	65.4	1004	13	BM469555
31	566	63.7	737	9	AU122593
32	561.6	63.2	988	14	BQ216493
33	558.4	62.8	850	14	BQ229967
34	558.2	62.8	710	9	AL557479
35	555.2	62.5	764	10	BE561138
36	554.6	62.4	697	9	AU123726
37	551.8	62.1	883	10	BE544189
38	550.4	61.9	892	13	BI254991
39	547.6	61.6	790	10	BE409600
40	544.8	61.3	652	9	AL535685
41	541.4	60.9	762	10	BE561131
42	541.2	60.9	657	12	BF343748
43	533.2	60.0	728	9	AU130628
44	529.2	59.5	735	13	BI226535
45	528.8	59.5	742	12	BG287644

ALIGNMENTS

RESULT 1
AL533191
LOCUS AL533191 LTI_FL015_Brn1 Homo sapiens cDNA clone CS0DN003YK10 5
DEFINITION AL533191 LTI_FL015_Brn1 Homo sapiens cDNA clone CS0DN003YK10 5
prime, mRNA sequence.
ACCESSION AL533191
VERSION AL533191.1 GI:12796684
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 894)
AUTHORS Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Location/Qualifiers
1..894
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DN003YK10"
/clone_lib="LTI_FL015_Brn1"
/sex="male"
/tissue_type="Adult brain"
/note="Vector: PCMVSPORT 6; Site_1: NotI; 1st strand cDNA"

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 293 a 159 c 270 g 170 t 2 others
ORIGIN

Query Match 82.1%; Score 729.8; DB 9; Length 894;
Best Local Similarity 92.8%; Pred. No. 3.8e-151;
Matches 801; Conservative 1; Mismatches 48; Indels 13; Gaps 3;

Qy 1 GGGTTCGAGGTTTATGATTCGAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGCGC 60
Dy 31 GGGTTCGGGGTTTATGATTAATTCGCGCGCGGGAGCCCTCTGCAGAGAGAGCGC 90
Qy 61 GAGAGATGGAGATGGCAGCGGATTCATTTCAGAGCTGCGGAACAGGCGCCCTCTGATG 120
Dy 91 GAGAGATGGAGATGGCAGCGGATTCATTTCAGAGCTGCGGAACAGGCGCCCTCTGATG 150
Qy 121 TGAAGAACTTGCCTGGCAGCAACAGTGGTGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Dy 151 TGAAGAACTTGTCTGGCAGCAACAGTGGTGGTGAATGAAGGCAAACTCGAAGCCCTCACAG 210
Qy 181 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Dy 211 ATGAATTTGAAGAACTGGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCGCAA 270
Qy 241 ACTTACCAAAAGTTA---AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
Dy 271 ACTTACCAAAAGTTAACAACACTTAAGAGCTTGAACCTAAGCGATACAGAGTCTCAGGGG 330
Qy 289 GCCTGGAAGTATTGGCGAAGAGTGTCCAAACCTCAGCGATCTATATTTAAAGTGGCAACA 348
Dy 331 GCCTGGAAGTATTGGCGAAGAGTGTCCGAACCTCAGCGATCTAAATTTAAAGTGGCAACA 390
Qy 349 AAATTAAGACCTCAGCACATAGAGCCACTGAACAGATTAGAAAACCTCAAGAGCTTAG 408
Dy 391 AAATTAAGACCTCAGCACATAGAGCCACTGAAAAGATTAGAAAACCTCAAGAGCTTAG 450
Qy 409 ACCTTTTCAATTGCGAGGTAAACCA-ACCTGAACGACTACGGAGAAAACGTTTCAAGCTT 467
Dy 451 ACCTTTTCAATTGCGAGGTAAACCACTGACGACTACCGAGAAAATGTTTCAAGCTC 510
Qy 468 CTCCTGCAACTCACAATCTCGACAGCTGTTACTGGAACCAACAGGAGGCCCTTACTCA 527
Dy 511 CTCCTGCAACTCACAATCTCGACGGCTATGACCGGACGACAGGAGGCCCTGACTCG 570
Qy 528 GATATTGAGGACCACTGGAGGGGCTGGATGACGAGGAGGAGGTTGAGCATGAGGAGGAG 587
Dy 571 GATGCTGAGGGCTACGTTGAGGGGCTGGATGATGAGGAGGAGGATGAGGATGAGGAGGAG 630
Qy 588 TATGATGAAGATGCTCAGGTAGTGGAAAGTATGAGGAGGCGGAGGAGGAGGAGGAGGT 647
Dy 631 TATGATGAAGATGCTCAGGTAGTGGAAAGTATGAGGAGGCGGAGGAGGAGGAGGAGGT 690
Qy 648 GAAGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGTTATAACGATGAGAG 707
Dy 691 GAAGAGGAGGACGTGAGTGGAGGAGGAGGAGGATGAAGAAGTTATAACGATGAGAG 750
Qy 708 GTAGATGCGGAGGAGATGAAGAAGACTTGGTGAAGAAGAAAGGGGTCAAGACCGAANA 767
Dy 751 GTAGATGACGAGGAGATGAAGAAGACTTGGTGAAGAAGAAAGGGGTCAAGACCGAANA 810
Qy 768 TGAGAACTGAAGATGAGGAGGAGATGATGACTTAAGTGAATAAACCCTATTTTGAANAAT 827
Dy 811 CGAAGACCTGAAGATGAGGAGGAGATGATGACTTAAGTGAATAAACCCTATTTTGAANAAT 870
Qy 828 TCCTATTGTGATTGACTGTTTT 850

||||| 871 TCCTATTGTGATTGACTGTTTT 893
RESULT 2
AL560249 923 bp mRNA linear EST 16-FEB-2001
LOCUS AL560249 LTI_FLO11_BC1 Homo sapiens cDNA clone CS0DG002Y123 5 prime
DEFINITION mRNA sequence.
ACCESSION AL560249
VERSION AL560249.1 GI:12906528
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 923)
AUTHORS Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..923
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DG002Y123"
/clone_lib="LTI_FLO11_BC1"
/sex="male"
/tissue_type="B cells from Burkitt lymphoma"
/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 299 a 163 c 279 g 175 t 7 others
ORIGIN

Query Match 81.7%; Score 726.2; DB 9; Length 923;
Best Local Similarity 92.1%; Pred. No. 2.4e-150;
Matches 795; Conservative 6; Mismatches 49; Indels 13; Gaps 3;

Qy 1 GGGTTCGAGGTTTATGATTCGAATTCGGCTGGCAGAGAGCCCTCTGCAGACAGAGAGCGC 60
Dy 62 GGGTTCGGGGTTTATGATTCGAATTCGGCGCGGGAGCCCTCTGCAGAGAGAGAGCGC 121
Qy 61 GAGAGATGGAGATGGCAGCGGATTCATTTCAGAGCTGCGGAACAGGCGCCCTCTGATG 120
Dy 122 GAGAGATGGAGATGGCAGCGGATTCATTTCAGAGCTGCGGAACAGGAGCGCCCTCTGATG 181
Qy 121 TGAAGAACTTCCCTGGACACACAGTCGGTCCAATCAAGGCAAACTCGAAGCCCTCACAG 180
Dy 182 TGAAGAACTTCTCTGGACACACAGTCGGTCCAATCAAGGCAAACTCGAAGCCCTCACAG 241
Qy 181 ATGAATTTCAAGAACTTGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
Dy 242 ATGAATTTCAAGAACTTGAATTCCTTAAGTAAATCAACGAGGCGCTCACCTCAATCGCAA 301
Qy 241 ACTTACCAAAAGTTA---AAGTTGAGAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
Dy 302 ACTTACCAAAAGTTAAACAAACTTAAGAAGCTTGAACCTAAGCGATACAGAGTCTCAGGGG 361
Qy 289 GCCTGGAAGTATGGCAGAAAAGTGTCCAAACCTCAGCATCTATATTTAAAGTGGCAACA 348
Dy 362 GCCTGGAAGTATGGCAGAAAAGTGTCCGAACCTCAGCATCTAAATTTAAAGTGGCAACA 421

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Qy 349 AAATTAAAGACCTCAGCACAAATAGAGCCACTGAACACAGTTAGAAAACCTCAAGAGCTTAG 408
Dy 422 AAATTAAAGACCTCAGCACAAATAGAGCCACTGAACACAGTTAGAAAACCTCAAGAGCTTAG 481
Qy 409 ACCTTTTCATTTGCGAGGTACCAACCTGAACGACTACGGAGAAAACGTTTCAAGCTTC 468
Dy 482 ACCTTTTCATTTGCGAGGTACCAACCTGAACGACTACGGAGAAAACGTTTCAAGCTTC 541
Qy 469 TCCTGCAACTCACATATCTGCAGAGCTTTACTGGGACCACAGGAGGCCCTTACTCAG 528
Dy 542 TCCCGCAACTCACATATCTGCAGAGCTTTACTGGGACCACAGGAGGCCCTTACTCAG 601
Qy 529 ATATTGAGGACCACTGAGAGGCTTGTGATGACGAGGAGGAGGTTGATGAGGAGGAGT 588
Dy 602 ATGCTGAGGAGCTGAGTGGAGGCTTGTGATGAGGAGGAGGAGTGAAGGAGGAGT 661
Qy 589 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 648
Dy 662 ATGATGAAGATGCTCAGGTAGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGT 721
Qy 649 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 708
Dy 722 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 781
Qy 709 TAGATGCGAGGAGATGAAGAGAGCTTGTGTAAGAGAGGAGGAGGAGGAGGAGGAGG 768
Dy 782 TAGATGCGAGGAGATGAAGAGAGCTTGTGTAAGAGAGGAGGAGGAGGAGGAGGAGG 841
Qy 769 GAGAACCTGAAGATGAGGAGGAGATGACTAAGTGAAGTGAAGTGAAGTGAAGTGA 828
Dy 842 GAGAACCTGAAGATGAGGAGGAGATGACTAAGTGAAGTGAAGTGAAGTGAAGTGA 901
Qy 829 CCTATTGTGATTGACTGTTTTT 851
Dy 902 -CYATTGTGATTGACTGTTTTT 923

RESULT 3
AL535686 875 bp mRNA linear EST 13-FEB-2001
LOCUS AL535686 LTI_FL013_FBRn1 Homo sapiens cDNA clone CS0DF016YA23 5
DEFINITION prime, mRNA sequence.
VERSION AL535686
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..875
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DF016YA23"
/clone_lib="LTI_FL013_FBRn1"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
```

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BASE COUNT 291 a 156 c 287 g 160 t 1 others
ORIGIN
Query Match 81.5%; Score 724.2; DB 9; Length 875;
Best Local Similarity 92.9%; Pred. No. 6.6e-150;
Matches 785; Conservative 0; Mismatches 48; Indels 12; Gaps 2;
Qy 1 GGGTTCAGAGTTTATTGATTGGCTGGCAGCAGAGCCCTCTGCAGACAGAGAGCGC 60
Dy 31 GGGTTCAGAGTTTATTGATTGGCTGGCAGCAGAGCCCTCTGCAGACAGAGAGCGC 90
Qy 61 GAGAGATGAGATGGCCACACGAGATTCATTTCAGAGTCGCGAACAGGGGCCCTCTGATG 120
Dy 91 GAGAGATGAGATGGCCACACGAGATTCATTTCAGAGTCGCGAACAGGGGCCCTCTGATG 150
Qy 121 TGAAGAAGACTTGCCTGGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Dy 151 TGAAGAAGACTTGCCTGGGACACAGTCGGTCGAATGAAGGCAAACTCGAAGCCCTCACAG 210
Qy 181 ATGAATTTGAAGAAGCTGGAAATCTTTAAGTAAATCAACGAGGAGCCCTCACCTCAATCTCAG 240
Dy 211 ATGAATTTGAAGAAGCTGGAAATCTTTAAGTAAATCAACGAGGAGCCCTCACCTCAATCGCA 270
Qy 241 ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG 288
Dy 271 ACTTACCAAGTTAACAACAACTTAAGAAGCTTGAACCTAAGCGATAACAGAGTCTCAGGGG 330
Qy 289 GCGTGAAGCTATTGGCAGAAAAGTGTCCAAAGCTCAGCGATCTATATTTAACTGGCAACA 348
Dy 331 GCGTGAAGCTATTGGCAGAAAAGTGTCCAAAGCTCAGCGATCTAAATTTAAGTGGCAACA 390
Qy 349 AAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 408
Dy 391 AAATTAAGACCTCAGCACAAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG 450
Qy 409 ACCTTTTCAATTTGCGAGGTAAACCAACCTGACGACTACGGAGAAAACGTTGTTCAAGCTTC 468
Dy 451 ACCTTTTCAATTTGCGAGGTAAACCAACCTGACGACTACGGAGAAAATGTGTTCAAGCTCC 510
Qy 469 TCCTGCAACTCACATATCTGCAGAGCTGTTACTGGGACCACAGGAGGCCCTTACTCAG 528
Dy 511 TCCCGCAACTCACATATCTGCAGAGCTATGACCGGAGCAGCAAGAGGAGGCCCTGACTCGG 570
Qy 529 ATATTGAGGACCACTGAGGAGGCCCTGGATGACGAGGAGGAGGAGGAGGAGGAGT 588
Dy 571 ATGCTGAGGAGCTACGTTGGAGGAGGCCCTGGATGATGAGGAGGAGGAGGAGGAGT 630
Qy 589 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 648
Dy 631 ATGATGAAGATGCTCAGGTAGTGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGT 690
Qy 649 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 708
Dy 691 AAGAGGAGGAGCTGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 750
Qy 709 TAGATGGCAGGAGATGAAGAGAGCTTTGGTGAAGAGAAAAGGGGTCAGAACGCGAAAT 768
Dy 751 TAGATGACGAGGAGATGAAGAGAGCTTTGGTGAAGAGAAAAGGGGTCAGAACGCGAAAC 810
Qy 769 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 828
Dy 811 GAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 870
Qy 829 CCTAT 833
Dy 871 CCTAT 875
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AL518839
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LOCUS AL518839 1034 bp mRNA linear EST 13-FEB-2001
DEFINITION AL518839 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA011YH23 5
prime, mRNA sequence.
ACCESSION AL518839
VERSION AL518839.1 GI:12782332
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1034)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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source
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/db_xref="taxon:9606"
/clone="CS0DA011YH23"
/clone_lib="LTI_NFL011_NBC1"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 317 a 190 c 300 g 223 t 4 others
ORIGIN

Query Match 81.3%; Score 723.2; DB 9; Length 1034;
Best Local Similarity 92.2%; Pred. No. 1.1e-149;
Matches 797; Conservative 3; Mismatches 46; Indels 18; Gaps 3;

QY 44 CTGCAGACAGAGCGCGAGAGATGGAGTGGCAGACGGATTTCATTCAGAGCTGCGGAA 103
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Db 1 CTGCAGAGAGAGCGCGAGASACGAGATGGCAGACGGATTTCATTTAGAGCTGCGGAA 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 104 CAGGGCGCCCTCTGATGTGAAGAACTTTCCTCTGGACACAGTCGGTGAATGAAGGCAA 163
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 CAGGACGGCCCTCTGATGTGAAGAACTTTCCTCTGGACACAGTCGGTGAATGAAGGCAA 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 164 ACTCGAAGCCCTCAGAGATGAATTTGAAGAACTGGAATTCATTAAGTAAATCAACGGAGG 223
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Db 121 ACTCGAAGCCCTCAGAGATGAATTTGAAGAACTGGAATTCATTAAGTAAATCAACGTAGG 180
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QY 224 CCTCACTCAATCTCAGACTTACCAAGTGA---AAGTTGAGAAGCTTGAACATA----- 275
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 181 CCTCACCVCATCGCAACTTACCAAGTGAACATAAGTAAAGCTTGAAGCTTGAACATAAGCGGA 240
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QY 276 ----AGAGTCTCAGGGGCGCTGGAAGTATTTGGCGAAGAAAGTGTCCAAACCTCAGCGATCT 331
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 241 TAACAGAGTCTCAGGGGCGCTGGAAGTATTTGGCGAAGAAAGTGTCCGAACCTCAGCGATCT 300
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 332 ATATTTAAGTGCACACAAAATTAAGACCTCAGCACATAGAGCCACTGAACAGTTAGA 391
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 301 AAATTAAAGTGCACACAAAATTAAGACCTCAGCACATAGAGCCACTGAACAGTTAGA 360
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 392 AAACCTCAAGAGCTTAGACCTTTCAATTGGGAGGTAAACCAACCTGAACAGCTACGGAGA 451
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Db 361 AAACCTCAAGAGCTTAGACCTTTCAATTGGGAGGTAAACCAACCTGAACAGCTACCGAGA 420
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

QY 452 AAACGTGTTCAAGCTTCTCCTGCAACTCACAATATCTCGACAGCTGTCTACTGGGACACAA 511
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Db 421 AAATGTGTTCAAGCTTCTCCTCGCAACTCACAATATCTCGACAGCTGTCTACTGGGACACAA 480
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QY 512 GGAGGCCCTTACTCAGATATTGAGGACACCTGGAGGCGCTGGATGACGAGGAGGAGG 571
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Db 481 GGAGGCCCTTACTCAGATATTGAGGACACCTGGAGGCGCTGGATGACGAGGAGGAGG 540
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QY 572 TGAGCATGAGGAGGAGTATGTAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGA 631
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Db 541 TGAGCATGAGGAGGAGTATGTAAGATGCTCAGGTAGTGGAGATGAGGAGGCGGAGGA 600
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QY 632 GGAGGAGGAGGAGGTGAAGAGGAGGAGGAGTGTAGTGAGGAGGAGGAGGAGGAGGAGG 691
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QY 692 TTATAAGTGGAGGAGTGTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 751
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Db 661 TTATAAGTGGAGGAGTGTAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
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QY 752 GGTCAGAACGCGAAAAATGAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 811
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Db 721 GGTCAGAACGCGAAAAATGAGAACCTGAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
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QY 812 ACCTATTTGAAAAATTCCTATTGTGATTTGACTGTTTACCATATCCCT-----C 865
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Db 781 ACCTATTTGAAAAATTCCTATTGTGATTTGACTGTTTACCATATCCCTCTCCCTC 840
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QY 866 CCCCTCCCAATCTGCCCTGAA 889
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Db 841 CACCTCCCAATCTGCCCTGAA 864
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RESULT 5
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LOCUS AL537874 LTI_FL013_FBrnl Homo sapiens cDNA clone CS0DF028YN19 5
DEFINITION prime, mRNA sequence.
ACCESSION AL537874
VERSION AL537874.1 GI:12801367
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 870)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
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1..870
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/clone="CS0DF028YN19"
/clone_lib="LTI_FL013_FBrnl"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH10B"
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 290 a 156 c 265 g 155 t 4 others


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QY 589 ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGAGGGCGAGAGGAGAGGAGAGAGGTG 648
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Db 630 ATGATGAAGATGCTCAGGTAGTGGAAAGATGAGAGGGCGAGAGGAGAGGTG 689
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QY 649 AAGAGGAGGAGCTGAGTGGAGGGGAGGAGGAGGATGAGAGAGGTTATACCATGAGAGG 708
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Db 690 AAGAGGAGGAGCTGAGTGGAGGGGAGGAGGAGGATGAGAGAGGTTATACCATGAGAGG 749
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QY 709 TAGATGGCGAGGAACATGAAGAAGAGCTTGGTGAAGAAGAAGGGTCCAGAAAGGAAAT 768
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Db 750 TAGATGACGAGGAAGATGAGAGAGAGCTTGGTGAAGAAGAAGGGTCCAGAAAGGAAAT 809
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QY 769 GAGAACCTGAAGATGAGGAGGAGAGATGATGACTAAGTGAAGATAACCTTATTTGAAAAAT 828
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Db 869 C 869

RESULT 7
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LOCUS AL540827 LTI_FL002_P11 Homo sapiens cDNA clone CS0DE004YL15 5 prime
DEFINITION , mRNA sequence.
ACCESSION AL540827
VERSION AL540827.1 GI:12871345
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Location/Qualifiers
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/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 298 a 160 c 271 g 164 t 10 others
ORIGIN
Query Match 79.3%; Score 705.4; DB 9; Length 903;
Best Local Similarity 91.7%; Pred. No. 9.5e-146;
Matches 773; Conservative 8; Mismatches 49; Indels 13; Gaps 3;
QY 1 GGGTTGAGGTTTATGATGAATTCGGCTGGCAGCAGAGAGGCTCTGCAGACAGAGAGCGC 60
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Db 52 GGGTTGAGGTTTATGATGAATTCGGCTGGCAGCAGAGAGGCTCTGCAGARAGAGAGCGC 111
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QY 61 GAGAGATGAGATGGCAGACGAGTTCATTCAGACTCGGACAGGCGGCCCTCTGATG 120
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QY 181 ATGAATTTGAAGAACTTGGATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCTCAG 240
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Db 232 ATGAATTTGAAGAACTTGGATTTCTTAAGTAAATCAACGAGGCGCTCACCTCAATCGCAA 291
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QY 649 AAGAGGAGGACGTCAGTGGAGGGGACGAGGAGGATGAAGAAGCTTATAACGATGGAGAGG 708
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QY 709 TAGATGCGGAGGAGATGAAGAAGAGCTTGG-TGAAGAAGAAAGGGGTGAGAAGCGCAAAA 767
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QY 768 TGAGAACCTCAAGATGAGGAGGAGAGATGATGACTAAGTGAATAAATTTTGAATAAT 827
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QY 828 TCC 830
Db 892 TCY 894

RESULT 8
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LOCUS AL517375 LTI_NFL011_NBC1 Homo sapiens cDNA clone CS0DA003YC02 5
DEFINITION prime, mRNA sequence.
ACCESSION AL517375
VERSION AL517375.1 GI:12780868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

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FEATURES
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/clone="CS0DA003YC02"
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/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact : Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax : (1) 301 610 8371 Email :
fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 301 a 174 c 289 g 217 t 11 others
ORIGIN

Query Match 78.0%; Score 693.6; DB 9; Length 992;
Best Local Similarity 91.8%; Pred. No. 3.9e-143;
Matches 751; Conservative 7; Mismatches 48; Indels 12; Gaps 2;

Qy 68 GGAGATGGGCAGAGCGATTTCATTGAGCTGCGGAACAGGCGCCCTCTGATGTGAAGA 127
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Qy 128 ACTTGCCTGTGACACACAGTCGGTGCATGAAGCAAACTCGAAGCCCTCACAGATGAAT 187
Db 61 ACTTGTCTGTGACACACAGTCGGTGCATGAAGCAAACTCGAAGCCCTCACAGATGAAT 120

Qy 188 TGAAGAACTGGAATCTTAACTGAAATCAACGGAGGCGCTCACCTCAATCTCAGACTTACC 247
Db 121 TGAAGAACTGGAATCTTAACTGAAATCAACGGAGGCGCTCACCTCAATCTCAGACTTACC 180

Qy 248 AAAGTTA---AAGTTGAGAAAGCTTGAACTA-----AGAGTCTCAGGGGCGCTTGA 295
Db 181 AAAGTTAAACAAACTTAAGAAAGCTTGAACTAAGCGATAACAGAGTCTCAGGGGCGCTTGA 240

Qy 296 AGTATTGCGCAAAAAGTGTCAAACCTCAGCATCTATATTTAAGTGGCAACAAATTA 355
Db 241 AGTATTGCGCAAAAAGTGTCCGAACCTCAGCATCTATAATTTAAGTGGCAACAAATTA 300

Qy 356 AGACCTCAGCAATAGAGCCACTGAAACAGTTAGAAACCTCAAGAGCTTAGACCTTTT 415
Db 301 AAACCTCAGCAATAGAGCCACTGAAAGAGTTAGAAACCTCAAGAGCTTAGACCTTTT 360

Qy 416 CAATTGGGAGGTAAACCACTTGAACGACTACGGAGAAACGTGTCTCAAGCTTCTCTGCA 475
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Qy 476 ACTCACATATCTCAGACAGCTTTACTGGACCACAGAGGCCCTTACTCAGATATGA 535
Db 421 ACTCACATATCTCAGACAGCTTTACTGGAGGAGGATGAGGATGAGGAGGATGATGA 480

Qy 536 GGACACCTTGAGGCGCTTGGATGACGAGGAGGAGGTGACATGAGGAGGATGATGA 595
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Qy 596 AGATGCTCAGTGTGAAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 655
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Qy 656 GGACGTGAGTGGGAGGAGGAGGAGGATGAAGAGGTTATTAACGATGGAGGATGATGG 715
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Qy 836 TGATTTGACTGTTTTTACCCATATCCCTCCCTCCCTCC 873
Db 781 TGATTTGACTGTTTTTHHCCCATWTTCTYTYCCCAAC 818

RESULT 9
LOCUS BM904155
DEFINITION BM904155 1035 bp mRNA linear EST 12-MAR-2002
5', mRNA sequence.
AGENCOURT_6692842 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5499610
BM904155
VERSION BM904155.1 GI:193544489
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Place: LLNL12133 row: d column: 11
High quality sequence stop: 674.

FEATURES
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/lab_host="DH10B (phage-resistant)"
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Site:2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 325 a 204 c 301 g 205 t
ORIGIN

Query Match 77.4%; Score 688; DB 14; Length 1035;
Best Local Similarity 88.6%; Pred. No. 6.8e-142;
Matches 796; Conservative 0; Mismatches 85; Indels 17; Gaps 4;

Qy 1 GGGTTCGAGTTTATTGATTGATTCGGTGGCCAGAGAGCTCTGCACAGAGAGCGC 60
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Qy 61 GAGAGATGAGATGGGACAGCGGATTTCATTCAGAGCTCGGAAACAGGGCGCTCTGATG 120
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Qy 121 TGAAGAACTTGCCTTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 167 TGAAGAACTTGTCTTGGACACAGTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 226

Qy 181 ATCAATTTGAGAACTGGAATCTTAAAGTAAATCAACGAGGAGGCTCACCTCAATCTCAG 240
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Db 227 ATGAATTTGAAGAACTGGAATTTCTTAAGTACAACTAAGTAGGCTCACTCAATTCGCA 286
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QY 289 GCGTGAAGTATTGCGAGAAAGTGTCCAAACCTCAGCATCTATATTAAGTGGCAACA 348
Db 347 GCGTGAAGTATTGCGAGAAAGTGTCCGAACCTCAGCATCTGAATTTAAGTGGCAACA 406
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Db 647 ATGATGAAGTCTCAGGTAGTGGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGT 706
QY 649 AAGAGGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 708
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Db 767 TAGATGCCAGAGAGTGAAGAGAGCTGGTGAAGAGAGAGGAGGAGGAGGAGGAGGAG 826
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DEFINITION prime, mRNA sequence.
ACCESSION AL543743
VERSION AL543743.1 GI:12876222
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 855)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Location/Qualifiers
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enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
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BASE COUNT 280 a 151 c 265 g 152 t 7 others
ORIGIN
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Query Match 76.9%; Score 683.8; DB 9; Length 855;
Best Local Similarity 92.0%; Pred. No. 5.6e-141;
Matches 752; Conservative 5; Mismatches 47; Indels 13; Gaps 3;
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Db 40 GGGTTCGAGGTTTATTGATTTCGGCTGGCAGAGAGCCCTCTGCAGAGAGAGAGCGC 99
QY 61 GAGAGATGGAGATGGCAGACGAGTTCATTTCAGAGCTGCGGAACAGGCGGCCCTCTGATG 120
Db 100 GAGAGATGGAGATGGCAGACGAGTTCATTTCAGAGCTGCGGAACAGAGAGCCCTCTGATG 159
QY 121 TGAAGAACTTTGCCCTGGCAACAGCTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 180
Db 160 TGAARAACTTTGCTTGGCAACAGCTCGGTTCGAATGAAGGCAAACTCGAAGCCCTCACAG 219
QY 181 ATGAATTTGAAGAACTGGAATTTCTTAAGTAAAATCAACGAGGAGCCCTCACCTCAATCTCAG 240
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Db 460 ACCTTTTCAATTCGAGGTAAACCACTGAACGACTACGGAAGAAATGTTTCAAGCTTC 519
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Db 580 ATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 639
QY 589 ATGATGAAGTCTCAGGTAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 648
Db 640 ATGATGAAGTCTCAGGTAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 699
QY 649 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 708
Db 700 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 759
QY 709 TAGATGCCAGAGAGTGAAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGGAGT 768
Db 760 TAGATGCCAGAGAGTGAAGAGAGCTTGGTGAAGAGAGAGGAGGAGGAGGAGGAGT 819
QY 769 GAGAACTGAAGATGAGGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 805
Db 820 GAGAACTGAAGATGAGGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 855
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DEFINITION        prime, mRNA sequence.
ACCESSION         AL535863
VERSION           AL535863
KEYWORDS          EST.
SOURCE            human.
ORGANISM           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE          1 (bases 1 to 853)
AUTHORS           Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE             Full-length cDNA libraries and normalization
JOURNAL            Unpublished (2001)
COMMENT           Contact: Genoscope
                  Genoscope - Centre National de Sequencage
                  BP 191 91006 EVRY cedex - France
                  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                  Location/Qualifiers
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                     /dev_stage="pooled tissue from post conception fetuses (20
                     week, 24 week and 26 week)"
                     /lab_host="DH10B"
                     /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
                     cDNA was primed with a NotI-oligo(dT) primer. Five prime
                     end enriched, double-stranded cDNA was digested with Not I
                     and enriched into the Not I and Eco RV sites of the
                     pCMVSPORT 6 vector. Library was constructed by Life
                     Technologies. Contact : Feng Liang Life Technologies, a
                     division of Invitrogen 9800 Medical Center Drive Rockville
                     Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT        283 a 147 c 254 g 164 t 5 others
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Query Match       75.2%; Score 668.6; DB 9; Length 853;
Best Local Similarity 90.3%; Pred. No. 1.3e-137;
Matches 770; Conservative 5; Mismatches 59; Indels 19; Gaps 5;
QY 17 GATTGAATTCGGCTGGCAGCAGAGCCTCTGCAGACAGAGCGCGAGATGGAGATGGG 76
DB 1 GATTGAATTCGGCGCGGGAGGCCTCTGCAGAGAGAGCGCGAGARATGGAGATGGG 60
QY 77 CAGACGGATTCAATTCAGAGCTGCGGAACAGGGCGCCCTCTGTATGTGAAAGAACTTGCCT 136
DB 61 CAGACGGATTCAATTCAGAGCTGCGGAACAGAGCGCCCTCTGTATGTGAAAGAACTTGTCT 120
QY 137 GGACACAGTCGGTCGATGAAGCAACTCGAAGCCCTCACATGAATTTGAAGAACT 196
DB 121 GGACACAGTCGGTCGATGAAGCAACTCGAAGCCCTCACATGAATTTGAAGAACT 180
QY 197 GGAATCTTAAGTAAATCAACGGAGGCCTCACCTCAATCTCAGACTTACCAAGTTA-- 254
DB 181 GGAATCTTAAGTAAATCAACGTAGGCCTCACCTCAATCTCAGACTTACCAAGTTAAA 240
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QY 305 AGAAAAGTGTCCAAACCTCAGCATCTATATTTAAGTGGGCAACAAAATTAAGACCTCAG 364
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361 CACAATAGAGCCACTGAAAAAGTTAGAAAACCTCAAGAGCTTAGACCTTTCAATTGGCGA 420
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QY 485 TCTCGCAGCTGTTACTGGGACCAACAGAGGAGGCCCTTACTCAGATATTGAGG---ACC 540
DB 481 TCTCGAGGGCTATGACCGGGACGACAGAGGAGGCCCTGACTCGGATGCTGAGGTGCTAC 540
QY 541 ACCTGGAGGCCCTGGATGACGAG-GAGGAGGGTGAG--CATGAGGAGGAGTATGATGAAG 597
DB 541 GTGGTAGGTGCTGGATGATGAGTGAGGAGGATGAGGTATGAGTATGAGTATGATGAAG 600
QY 598 ATGCTCAGGTAGTGGAGATGAGGAGGAGGCCGAGGAGGAGGAGGAGGAGGAGGAGG 657
DB 601 ATGCTCAGGTAGTGGAGATGAGGAGGAGGCCGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 658 ACCTGAGTGGAGGGGACGAGGAGGATGAAGAGGTTTAAACGATGAGAGGAGTAGATGGCG 717
DB 661 ACCTGAGTGGAGGAGGAGGAGGATGAAGAGGTTTAAACGATGAGAGGAGTAGATGAGC 720
QY 718 AGGAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTGAGAGCGGAGGAGGAGGAGG 777
DB 721 AGCAAGATGAAGAGAGCTTGGTGAAGAGAAAGGGGTGAGAGCGGAGGAGGAGGAGG 780
QY 778 AAGATGAGGAGAGAGATGATGACTAAGTAGATAAAGCTATTTTGAAAAATTCCTATTG 837
DB 781 AAGATGAGGAGAGAGATGATGACTAAGTAGATAAAGCTATTTTGAAAAATTCCTATTG 840
QY 838 ATTGTGACTGTTTT 850
DB 841 ATTGTGACTGTTTT 853

RESULT 12
AL545880          834 bp      mRNA      linear      EST 16-FEB-2001
LOCUS             AL545880 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI023YE09 5
DEFINITION        prime, mRNA sequence.
ACCESSION         AL545880
VERSION           AL545880
KEYWORDS          EST.
SOURCE            human.
ORGANISM           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE          1 (bases 1 to 834)
AUTHORS           Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE             Full-length cDNA libraries and normalization
JOURNAL            Unpublished (2001)
COMMENT           Contact: Genoscope
                  Genoscope - Centre National de Sequencage
                  BP 191 91006 EVRY cedex - France
                  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                  Location/Qualifiers
FEATURES           source
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                     /db_xref="taxon:9606"
                     /clone="CS0DI023YE09"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
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BASE COUNT	272 a	153 c	257 g	148 t	4 others
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Query Match	74.9%; Score 665.6; DB 9; Length 834;				
Best Local Similarity	92.1%; Pred. No. 5.9e-137;				
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QY	61	GAGAGATGAGATGGCAGACGGATTCAATTCAGAGCTCGGGAACAGGGCGCCCTCTGATG	120		
Db	105	GARARATGGAGATGGCAGACGGATTCAATTCAGAGCTCGGGAACAGGAGCGCCCTCTGATG	164		
QY	121	TGAAGAAGCTTCGCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG	180		
Db	165	TGAAGAAGCTTCGCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTTCACAG	224		
QY	181	ATGAATTTGAAGAACTGGAATTTTAAAGTAAATCAACGGAGGCTCACCTCAATCTCAG	240		
Db	225	ATGAATTTGAAGAACTGGAATTTTAAAGTAAATCAACGGAGGCTCACCTCAATCTCAG	284		
QY	241	ACTTACCAAGTTA---AGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG	288		
Db	285	ACTTACCAAGTTAACAACAACTTAAGAAGCTTGAACCTAAGCGATAACACAGAGCTCTCAGGGG	344		
QY	289	GCCTGGAAGTATTGGCAGAAAAGTCTCAAACTCAGCAGCTATATATTAAGTGGCAACA	348		
Db	345	GCCTGGAAGTATTGGCAGAAAAGTCTCAAACTCAGCAGCTATATATTAAGTGGCAACA	404		
QY	349	AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG	408		
Db	405	AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG	464		
QY	409	ACCTTTTCAATTCGAGGTAAACCACTGAACGACTACGGAGAAAACGTTTCAAGCTTC	468		
Db	465	ACCTTTTCAATTCGAGGTAAACCACTGAACGACTACGGAGAAAACGTTTCAAGCTTC	524		
QY	469	TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAG	528		
Db	525	TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAG	584		
QY	529	ATATTGAGGACACGTGGAGGCGCTGGATGACGAGGAGGAGGGTGAGCATGAGGAGGAGT	588		
Db	585	ATGCTGAGGCGTACGTGGAGGCGCTGGATGATGAGGAGGAGGAGTGAAGGAGGAGT	644		
QY	589	ATGATGAAGATCCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGTG	648		
Db	645	ATGATGAAGATCCTCAGGTAGTGGAGATGAGGAGGCGGAGGAGGAGGAGGAGGAGTG	704		
QY	649	AAGAGGAGGACCTGAGTGGAGGCGGAGGAGGATGAAGAAGTTATAACGATGGAGAGG	708		
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QY	709	TAGATGGCGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTCAGAGGCGAAAT	768		
Db	765	TAGATGACGAGGAAGATGAAGAAGAGCTTGGTGAAGAAGAAGGGGTCAGAGGCGAAAC	824		
QY	769	GAGAAC	774		
Db	825	GARAAC	830		
RESULT 13					
BQ232856					
LOCUS	BQ232856 895 bp mRNA linear EST 02-MAY-2002				
DEFINITION	AGENCOURT_7567365 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6060491				
ACCESSION	BQ232856				
VERSION	BQ232856.1				
KEYWORDS	5', mRNA sequence.				
SOURCE	human.				

ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 895)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
CONTACT	Contact: Robert Strausberg, Ph.D.				
EMAIL	Email: cgapbs.r@mail.nih.gov				
TISSUE	Tissue Procurement: DCTD/Drp/Gazdar				
CDNA	CDNA Library Preparation: Life Technologies, Inc.				
DNA	DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
CLONE	DNA Sequencing by: Agencourt Bioscience Corporation				
FOUND	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:				
PLATE	http://image.llnl.gov				
SEQUENCE	Plate: LLAM1328 row: n column: 12				
FEATURES	High quality sequence stop: 676.				
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	/clone="IMAGE:6060491"				
	/clone_lib="NIH_MGC_68"				
	/tissue_type="large cell carcinoma"				
	/lab_host="PH10B (phage-resistant)"				
	/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies."				
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Query Match	74.4%; Score 661; DB 14; Length 895;				
Best Local Similarity	92.0%; Pred. No. 6.2e-136;				
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Db	46	GGGTCGGGTTTATGATTGAAATTCGCGCGCGGGAGCCCTCTGCAGAGAGAGAGCGC	105		
QY	61	GAGAGATGAGATGGGAGACGGATTTCATTTCAGAGCTGGGAACAGGGCCCTCTGTATG	120		
Db	106	GAGAGATGAGATGGGAGACGGATTTCATTTCAGAGCTGGGAACAGGGCCCTCTGTATG	165		
QY	121	TGAAGAAGCTTCGCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG	180		
Db	166	TGAAGAAGCTTCGCCCTGGACAAACAGTCGGTGAATGAAGGCAAACTCGAAGCCCTCACAG	225		
QY	181	ATGAATTTGAAGAACTGGAATTTTAAAGTAAAAATCAACGGAGGCGCTCACCTCAATCTCAG	240		
Db	226	ATGAATTTGAAGAACTGGAATTTTAAAGTAAAAATCAACGGAGGCGCTCACCTCAATCTCAG	285		
QY	241	ACTTACCAAGTTA---AAGTTGAGAAAGCTTGAACCTA-----AGAGTCTCAGGGG	288		
Db	286	ACTTACCAAGTTTAAACAACTTAAAGAAGCTTGAACCTAAGCGATAACAGAGTCTCAGGGG	345		
QY	289	GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGGCATCTATATTTAAGTGGCAACA	348		
Db	346	GCCTGGAAGTATTGGCAGAAAAGTGTCCAAACCTCAGGCATCTATATTTAAGTGGCAACA	405		
QY	349	AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG	408		
Db	406	AAATTAAGACCTCAGCACAATAGAGCCACTGAAACAGTTAGAAAACCTCAAGAGCTTAG	465		
QY	409	ACCTTTTCAATTCGAGGTAAACCACTGAACGACTACGGAGAAAACGTTTCAAGCTTC	468		
Db	466	ACCTTTTCAATTCGAGGTAAACCACTGAACGACTACGGAGAAAACGTTTCAAGCTTC	525		
QY	469	TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAG	528		
Db	526	TCCTGCAACTCACATATCTCGACAGCTGTTACTGGGACCAACAGGAGGCCCTTACTCAG	585		

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Db	121	GATGAATTTGAAGAACTGGAAATTTCTTAAGTAAATCAACGGAGGCGCTCACCCTCAATCTCGA	180
Qy	240	GACTTACCAAGTTA-- --AAGTTTGAGAAAGCTTTGAACCTA-----AGAGTCTCAGGG	287
Db	181	AACCTTACCAAGTTTAAACAACCTTGAAGACCTTGAACCTAAGCGATACAGAGTCTCAGGG	240
Qy	288	GGCCTGGAAGTATTTGGCAGAAAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGGCAAC	347
Db	241	GGCCTGGAAGTATTTGGCAGAAAAAGTGTCCAAACCTCAGCGATCTATATTTAAGTGGCAAC	300
Qy	348	AAATTTAAAGACCTCAGCACAATAGACCACTGAAACAGTTAGAAACCTTCAGAGAGCTTA	407
Db	301	AAATTTAAAGACCTCAGCACAATAGACCACTGAAACAGTTAGAAACCTTCAGAGAGCTTA	360
Qy	408	GACCTTTTCAATTTGCGAGGTAAACCAACCTTGAAGACCTTACGGAGAAAAAGTGTTCAGAGCTT	467
Db	361	GACCTTTTCAATTTGCGAGGTAAACCAACCTTGAAGACCTTACGGAGAAAAAGTGTTCAGAGCTT	420
Qy	468	CTCTGCAACTCACAATATCTGCAGAGCTGTTTACTGGACACACAGAGAGGCGCCCTTACTCA	527
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Qy	528	GATATTGAGGACACGCTGGAGGGCTCTGGATCACGAGGAGGAGGTGAGCATGAGGAGGAG	587
Db	481	GATCTTGAGGCTACGTGTGAGGGCTCTGGATGATGAGGAGGAGGTGAGCATGAGGAGGAG	540
Qy	588	TATGATGAAGATGCTCAGGTAGTGGGAAGATGAGGAGGGCGAGGAGGAGGAGGAGGAAGGT	647
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Qy	648	GAGGAGGAGGACGTGAGTGGAGGGGACGAGGAGGATGAAGAAGGTTATACGATGGAGAG	707
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Qy	708	GTAGATGCGGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTTCAGAACGGAATA	767
Db	661	GTAGATGCGGAGGAGATGAAGAAGAGCTTGGTGAAGAAGAAAGGGGTTCAGAACGGAATA	719
Qy	768	TGAGAACTGAAG-ATGAGGAGAGAGATGATGACTAGTACGAATAA-CCTATTTTGAATA	822
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Qy	826	ATTCCTATTGTGATTGACTGTTTTTACCCAT-----ATCCCTTCCCTCCCTCCCAATC	877
Db	780	AATCCAAATTGGATTTGACTGGTTTTTACCCTTATTTCCCTTTTCCCTCCCTCCCAATC	833
Qy	878	CTGCCCCCTGAA 889	
Db	840	CTGCCCCCTGAA 851	
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AL571434/c			
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DEFINITION	AL571434	LT1_NF1006_PL2 Homo sapiens cDNA clone CS0DI023YE09	EST 16-SEP-2001
ACCESSION	AL571434	prime, mRNA sequence.	
VERSION	AL571434.1	GI:12928726	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 894)		
JOURNAL	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
COMMENT	Full-length cDNA libraries and normalization		
	Unpublished (2001)		
	Contact: Genoscope		

